

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|-----------------------|---|
| | | | 621 626 649 679 719 725-726 738 793 803 831 834-836 838 844 857- 858 866 879 905 913 928 963 976 1005-1006 1012 1038 1050 1116- 1117 1151 1199 1204 1226 1243 1265 1274 1324-1325 1339 1353 1374 1377 1440-1441 1447 1504 1549 1600 1618-1619 1631 1641 1644 1653 1687-1688 1691-1692 1741 1771 |
| young liver | GIBCO | ALV001 | 5-8 11 20-21 46 50-51 58 65-66 75 79 82 93 97 102-103 108 110 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214- 215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116- 1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383- 1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550- 1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1641 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758 1760-1761 1763-1765 1769 |
| adult liver | Invitrogen | ALV002 | 5-8 17 20-21 32-33 41 55 58 64 75 77 86 89 102 108 117 119 175- 176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849- 850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408- 1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542 1547 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|-----------------------|---|
| | | | 1550 1567 1578 1581 1583 1594 1597 1601-1602 1611-1612 1615 1618-1619 1621 1625 1637 1645 1647 1652 1654-1655 1660 1666 1669-1671 1684 1706 1722 1737- 1738 1742-1744 1760-1761 1763- 1765 1772 1774 |
| adult liver | Clontech | ALV003 | 29 676 997 1063 1119 1536 1766 |
| adult ovary | Invitrogen | AOV001 | 1 4-18 20-23 29 35-40 42-48 50- 51 53-58 61-63 65-66 68-69 73-75 77-78 80 82 85 87 89 97 100-101 103-104 106-108 110 113 115 118 122-124 126 128 133-134 136-140 142 145-147 149-157 161 166 168- 170 174 177-178 180 182-186 188- 189 192-203 207 209 211-215 219 221-224 229-230 234 242-243 246- 247 255 258 260-262 265-269 271- 272 274 277-281 284-286 288 290 295 299 301-302 304 307 309-311 313-314 316 321 323-326 330 332- 333 335-338 341 344 349 352-353 356 358 360 362 370-372 376-377 379-384 387 390-392 394 397-398 400 403 408-410 412 414-416 423- 424 426-427 430-435 439 443-446 448-449 451 453-455 462-463 468- 471 473 476-479 481-484 487 489- 494 496-497 499-501 503-505 509- 514 516-517 519-520 522 524 526 528-534 541-544 546-547 549 552 554-555 561-564 566-567 569-570 572-573 575-576 579 581 583 585- 588 590-591 593 595 597 599 601- 605 607-613 615 618-622 624-627 630 632-633 636-640 642 644-647 649-652 654-655 657-665 667-675 677-678 681 683-684 692-695 697- 710 714-721 723 725-727 729 732 734-735 743-746 750-751 753 758 763 765 767 772-773 775-778 780 783-784 786 788 790-791 794-796 800 803 805 809-811 813-815 818- 819 821-824 826 828-829 831-832 837-838 843-850 852-857 859-864 867 869 871-872 874-875 878-883 887-888 890-895 898-910 912-914 916 919-922 924 926-927 929-939 941 943-946 948-951 953 955-958 961-964 966-967 970-979 981-982 985-986 988-990 992 995-997 999- 1001 1004-1009 1011-1013 1016 1019-1020 1024-1025 1029-1031 1033-1035 1037 1039 1041-1047 1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238- 1241 1243-1244 1247 1249 1252- 1254 1256-1258 1262 1265 1267- 1268 1270 1275 1278 1280-1283 1286-1289 1291 1293-1294 1298- |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| | | | 1299 1306 1308 1312 1317-1321 1323 1327 1329-1330 1332-1333 1338-1339 1341 1343-1351 1356 1359 1361 1365-1366 1371-1375 1377-1379 1383-1384 1386 1389 1394 1400 1404 1416-1417 1422- 1427 1429-1431 1435-1436 1439- 1443 1445-1450 1453-1454 1459 1463-1464 1466 1468 1470 1474- 1481 1484-1485 1488 1491 1493- 1494 1496-1498 1501-1504 1506- 1507 1511-1517 1519 1521-1524 1526-1527 1530-1531 1534-1536 1538-1539 1541 1546 1548-1550 1553 1555-1559 1561-1563 1566- 1567 1569-1570 1572 1574-1575 1578 1580-1581 1587-1588 1590- 1591 1595 1597-1598 1600-1606 1609 1611-1621 1623-1630 1634 1636 1638 1641 1643 1645 1647- 1657 1659-1662 1664 1667 1669- 1671 1673-1674 1676-1681 1683- 1690 1699 1702-1707 1710-1711 1713-1714 1716-1719 1723-1724 1726-1728 1731-1733 1735 1737- 1738 1740-1741 1743-1744 1748- 1751 1753 1755-1756 1760-1762 1765 1767-1768 1770-1771 1776 1778-1779 1783-1784 1786 |
| adult placenta | Clontech | APL001 | 5-8 44-45 90-91 107-108 159 178 311 351 414 476 503 545 574 624 636 719 755 773 860 890-891 924 947 955-956 962 990 992 1002 1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 |
| placenta | Invitrogen | APL002 | 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 |
| adult spleen | GIBCO | ASP001 | 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794 810-811 817 822 830 832 845 848 852-853 858 862 866 874 879 882 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| | | | 884 906-908 912 919 921-923 926- 927 934 942 949 957-958 963 977- 978 983 990 992-994 996-997 999 1005-1007 1010 1012 1031 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219- 1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760- 1761 1774 1779 1781-1782 |
| testis | GIBCO | ATS001 | 5-8 10 26 30-31 47 50-51 57 68- 69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 |
| Genomic DNA from BAC 63I18 | Research Genetics (CITB BAC Library) | BAC001 | 686 1352 1412 |
| Genomic DNA from BAC 393I6 | Research Genetics (CITB BAC Library) | BAC002 | 1411-1412 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|-------------------------------|---|--------------------|--|
| Genomic DNA from BAC 393I6 | Research Genetics (CITE BAC Library) | BAC003 | 1352 |
| adult bladder | Invitrogen | BLD001 | 5-8 17-18 22-23 33 37-39 56-57 80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382 413 415 424 430 443 483 502 542- 543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898 909 918 929 966 977 983 1016 1025 1055 1073 1082 1140 1167 1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636- 1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731- 1732 1739 1741 1760-1761 1779 |
| bone marrow | Clontech | BMD001 | 3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75 80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180 187 192-193 197-198 203-205 210- 213 215 217 219 222 224-226 233 235-237 242-244 255 258 260 263- 264 266 273 276 278 283 286 290 295 301-302 307 312-313 321 330 333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436- 437 439 441-442 445 447 454-456 461-462 471-472 475 477-479 481- 482 485 488 493 498 500 503-506 513 516 519 523-524 526 530 535- 540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656- 660 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772- 773 775-778 780 785-786 789-791 796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848- 855 858-859 866-867 869 878-880 883 890-892 896 903 905 908 912- 914 922-924 927 930-931 937 939- 941 952-953 955-958 963 969 973 976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025 1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054 1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144- 1145 1163 1172 1178 1197 1199- 1200 1202 1216-1217 1224 1227- 1228 1240 1246 1254 1261 1266 1270 1278 1281 1285 1287 1290- 1291 1293 1299-1301 1308 1314 1317-1320 1327 1331 1339 1343 1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394 1400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431 1433 1439 1443 1446-1449 1459 1463-1464 1482 1486 1493-1494 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| | | | 1506 1509 1513 1521-1522 1524 1526 1528 1531 1536-1537 1543 1546 1548-1549 1552 1554-1555 1557-1559 1571-1572 1581 1589- 1592 1597-1600 1609 1614 1621 1626-1628 1630-1632 1634 1636 1638-1639 1641 1646-1647 1651 1653-1655 1661-1662 1676-1681 1684 1686 1690 1702 1707 1711 1713-1714 1717 1720 1722-1723 1727 1737-1738 1740 1758 1767 1772 1781-1782 1785-1786 |
| bone marrow | Clontech | BMD002 | 11 15-16 19 30-31 35-36 68-69 75 83-84 93 99 103 108-109 118 137 139 169-170 174 177 180 190 193 212-213 219 222 225-226 232 237 255 259 264 273-274 284 286 290- 292 295 301 303-304 307 312-313 316 324 326 330 334-335 348 352- 353 357 360 370-373 384 386-387 397 403-404 414-416 421 425-427 429-430 433-436 440 444 451 454 465-466 472 475 478 491 493 516 520 523 525 531 545 548 552 566 569-570 581 583 590-591 597-598 601 616-617 621 641 650 652 656 659 671 674-675 679 684 710 718- 719 728 734 737-738 742 761 765 774-778 790 811 814 818 830 834- 836 854-855 859 866 869 871 878- 879 884 889 892 904 922-923 932 990 992 998 1001 1004 1016 1036 1042 1048 1051 1054-1055 1058 1088-1089 1106 1112-1114 1155 1157 1192 1200 1223 1227-1228 1236-1237 1260-1261 1282-1283 1285 1287 1295 1314 1317-1321 1324-1327 1330 1333 1341 1343 1347 1350 1353 1355-1357 1367 1369-1370 1373 1377 1379 1381 1383-1384 1394 1397 1400 1406 1413 1417 1425-1427 1438 1442 1446 1459-1460 1470 1493 1505 1521 1536 1546-1549 1560 1573- 1574 1578 1598-1600 1621 1626 1631 1634 1646 1649 1653 1656 1658 1669-1670 1683-1684 1687- 1688 1690-1693 1696 1699 1702 1704 1707-1709 1711 1720 1722- 1723 1725 1727 1729 1731-1733 1738-1740 1743-1746 1752 1755 1760-1761 1767 1777 1781-1782 1786 |
| bone marrow | Clontech | BMD004 | 73-74 503 922 1036 1711 |
| bone marrow | Clontech | EMD007 | 95-96 866 1320 1475 |
| adult colon | Invitrogen | CLN001 | 17 56-58 103 110 117 144 150 171 179 185 188-189 201 204-206 210 218-221 225-226 231 237 251 277 288 310 312 320 333 359 386 388 394 408 420 455 481 485 503 510- 512 590-591 615 635 647-648 665 672 684 697 710 725-726 743 780 786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068- 1069 1140 1153 1170 1185 1196 1199 1220 1280 1314-1315 1320 1345 1351 1355 1369 1428 1439 |

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| | | | 1462-1464 1512 1556 1583 1587 1594 1596 1614 1625-1626 1631 1639 1645 1650 1675-1677 1687- 1688 1701 1713-1714 1724 1740 1765 |
| Mixture of 16 tissues - mRNAs | Various Vendors | CTL016 | 401 1490 1686 |
| Mixture of 16 tissues - mRNAs* | Various Vendors | CTL021 | 312 782 1132-1133 1403 1712 1715 |
| adult cervix | BioChain | CVX001 | 1 4-8 11 13 18-21 25-26 30-31 33 37-39 43 46-47 58 61 64-66 71 73-74 82 85 94 100 103-104 113 118 122 126 130 134 140 147 153- 156 163 170 179 181 186 192 195- 196 198 201-202 218-219 222 229- 231 257 266 276-277 285-286 288 298 301-302 304 307 312-314 324 326 329-330 332 335 342 352 358 362 371-372 376 379 381-382 384 388 398 400 410 414 416 419-420 426-427 430-431 433-436 439 446 448 461-462 464 471-477 479 482- 483 491 493 496 503 506 510-513 516-517 526 530 535 542-544 546- 547 557 561 572-573 575-577 581- 582 585-586 588-589 593-594 600 602 604-605 607-609 612 615-619 623 644 650 654 657-658 662-665 670 672 680 683 691-694 698 706 708-709 711 713 720-721 727 729 731-732 737 745-747 753-754 760 765 771 774-777 780 790 793 796 798 800 803 805 818 826 828 831- 832 834-836 843 847-848 851-855 857-860 864-866 869 871 876 878- 880 882 887 890-891 897 899-902 905-908 912-913 916 918-919 922 927 932 934-938 944 948 955-956 958 963-964 967 969-970 972 976 978-979 983 985 990 992 1000 1005-1007 1016-1017 1024 1027 1033 1036 1038 1045 1047 1053- 1056 1066-1067 1071 1073 1075 1079 1082 1098 1113 1124 1129 1134 1139 1146-1149 1163 1167 1170 1173 1175 1177 1181 1197 1200 1202 1211 1214 1216 1221- 1222 1225 1227 1232-1234 1240- 1241 1243 1258 1264-1265 1268 1270 1279 1287-1290 1308 1310- 1311 1316 1320 1323 1327 1345 1349 1353-1354 1360 1372-1374 1383-1384 1386 1394 1397 1405- |

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|-------------------|------------|--------------------|--|
| | | | 1406 1416 1425-1427 1431 1436-1437 1442 1446 1448 1453 1459 1466 1472 1478 1482 1496 1501-1503 1506 1512 1522 1527-1528 1531 1533 1541 1547 1569 1571 1585 1589 1597-1598 1600 1608-1609 1614-1616 1620 1623-1624 1626-1628 1630 1638 1641 1643 1649 1653 1656 1662 1667 1669 1674-1675 1683 1685-1688 1699 1702 1709-1710 1715 1717 1722 1724 1729 1731-1732 1735-1739 1741 1743-1744 1748-1749 1755 1760-1762 1767 1773 1778 1785-1786 |
| diaphragm | BioChain | DIA002 | 137 282 289 730 780 986 1409 1478 1599 1614 |
| endothelial cells | Strategene | EDT001 | 3 5-10 13 15-21 24-26 29 34 37-39 42 44-45 50-51 53-55 57-58 60-61 65-66 68-69 73-74 77-78 80 82-83 85 87 89 93-96 101-105 108 110 112-114 116 118-122 124 128 133-134 137-142 147-150 152-153 161-163 166-172 176-179 187 190 192 194 196-201 204-207 210 212-214 220 224 229-230 233 235-236 240-241 251-252 258 261-262 265 267-269 272 276-277 279-281 284-285 288 290 295-296 301-302 310-311 313 316 321 325 329 331-333 335 340-342 351-355 360 371 375 380-382 384 387 390 392 397 400 407-408 410 412 414 416 425-427 431 434-436 439 444-445 449 454 463-464 472-475 477-479 486 488-490 497-498 500-504 510-513 516-519 522 524 526-528 532-534 536-540 542-546 548 561-563 566-567 572-576 579 581 585-586 589 593 595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641 644 647 656-660 662-664 670 673 678 680-682 692-697 707 709-710 712-713 719 730 732 734 736 738 743-746 751 759 768 771 773 775-778 783 786-789 793 800 803 805-807 810-811 814 816-818 821-822 824 826 828-829 832 834-838 842-845 848-850 854-860 862 864 869 871 874 876-879 883 885 887 890-891 894-895 898-900 903 908 910-913 916 919-922 924 926-928 930-935 939 943 948-949 951-954 957 959-961 964 969-970 973 975-978 983-984 988-990 992-993 996-997 1000 1002 1004-1013 1016-1020 1022-1025 1028 1031 1033-1034 1038-1046 1050 1055-1056 1059-1060 1062-1064 1067-1070 1072-1074 1076 1078 1082 1086-1087 1089-1090 1093-1097 1099-1103 1107 1109-1113 1116-1117 1124-1126 1128-1131 1134-1135 1138 1140 1144-1145 1148-1149 1153 1157 1160 1163 1171 1183-1184 1198-1199 1202 1205-1207 1211 1216-1217 1219 1221 1225 1229 1232-1235 1238-1241 1243-1244 1246 1250 1253 1257-1258 1261 |

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| | | | 1265-1266 1268 1270-1271 1274- 1277 1280-1283 1285-1286 1288- 1290 1293 1295 1298 1308 1312 1317-1320 1324-1325 1327 1329- 1330 1334-1335 1338 1342-1343 1345-1347 1350 1355-1356 1359 1367 1369 1374 1376 1379 1398 1400 1406 1408 1414 1417 1419 1424-1426 1428-1431 1434-1438 1440-1442 1448 1450 1462-1466 1468 1472 1474 1478 1487-1488 1491-1493 1501-1504 1506 1509 1511 1516 1520-1521 1526 1529 1531 1536-1537 1539-1540 1546- 1547 1549 1552 1555 1557-1559 1561-1565 1568 1571 1575 1578- 1579 1581-1583 1587-1588 1590 1592 1597 1605-1606 1611 1613 1615 1618-1621 1624-1628 1630- 1631 1634 1636 1638 1641 1643- 1650 1652-1659 1664 1666-1667 1669 1671 1675-1681 1683-1688 1696-1698 1703 1711 1715-1716 1719 1722-1723 1726 1731-1733 1736 1739-1741 1743-1744 1749 1755 1760-1761 1765 1767-1768 1771-1773 1776 1779 1783-1786 |
| Genomic clones from the short arm of chromosome 8 esophagus | Genomic DNA from Genetic Research BioChain | EPM001 ESO002 | 286 686 1297 1303-1304 1352 1411-1412 1754 131-132 261 289 380 503 860 892 1000 1007 1397 |
| fetal brain | Clontech | FBR001 | 62-63 89 112 126 194 322 336-338 379 391 411 481 546 563 607 679 710 867 1012 1031 1055 1251 1262 1320 1407 1643 1652 1686 1731- 1732 1746 1765 |
| fetal brain | Clontech | FBR004 | 68-69 90-91 139 212-213 301 331 362 374 403 436 611 645-646 659 668 670 691 785 805 845 1163 1209 1216 1232-1233 1238-1239 1387 1410 1416 1430 1496 1536 1547 1593 |
| fetal brain | Clontech | FBR006 | 5-9 25 43 60 62-63 65-66 70 72 80 87 92 101 103 108 114 136 139 149 152-153 157 168 171-172 175 207-208 210 212-213 221-226 237- 238 251-253 266 272 279-281 295 301-302 307 310 317-318 321-324 330 333-334 336-338 346-347 352 357 370 373 377 379-380 382 384 391-392 397 399 402 406-408 410- 411 417 421 424 426-427 430 436- 437 440-443 454 460 464 467 473 476 483 488-489 495 497 508 510- 513 516 519-520 524 530 537-540 544 547 550 561 567 572-574 582 590-591 595 597 604 607-609 615 623 628-629 631 634 638-640 655 657-658 660 665 669 674-675 679 689 691-694 696-697 699 701 706 710 716 720 728 732 734 736 742- 744 757-760 763 775-778 780 799 806-807 810 817-818 826 839 843 858 861 864 871-872 884 890-891 894-895 898 904 915 921-923 935- 936 938 945 950 952 955-956 958- 959 961 963 967 969-971 990 992 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| fetal brain | Clontech | FBRs03 | 235-236 520 864 1068 1188 1587 |
| fetal brain | Invitrogen | FBT002 | 15-18 20-21 24-25 29 34 43 61-63 77-78 98 101 103 107-108 128 130 136 146 148 165-166 171 174 181 185 196-198 204-205 208 223 230 235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786 |
| fetal heart | Invitrogen | FHR001 | 105 124 180 289 864 1036 1148 1229 1614 1616 1762 1785 |
| fetal kidney | Clontech | FKD001 | 5-8 11 40 47 57 65-66 82 85 102 124 163 171 216 222 224 235-236 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| | | | 258 277 280-281 307 310 314 330 371 387 392 395 403 422-423 431 436 443 455 469 500 519 522 542 563 572-573 585 600 619 623 650 654 657-658 660 679 719 731 780 798 821 833 844 854-855 857 864 868 878 911 929 958 960 969 990 992 1007 1046 1087 1103 1129 1139 1285 1312 1331 1355 1369 1371 1376 1391 1422 1425-1426 1440-1441 1470 1543 1598 1601 1618 1631 1651 1654-1655 1669 1678-1679 1691-1692 1733 1785 |
| fetal kidney | Clontech | FKD002 | 352 384 426-427 440 583 602 1060 1131 1324-1325 1636 |
| fetal kidney | Invitrogen | FKD007 | 20-21 82 163 335 679 988-989 1000 1227 1230 1320 1554 |
| fetal lung | Clontech | FLG001 | 35-36 94 323 371 398 426-427 445 473 549 560 604 616-617 626 631 649 651 719 746 786-787 832 842 849-850 864 894-895 1075 1178 1182 1200 1206 1309 1311 1345 1429 1493 1567 1576 1620 1686 |
| fetal lung | Invitrogen | FLG003 | 9 15-16 29 41 47 68-69 83 88-89 102 124 137 152-153 165 196 224 229 231 249 254 256 267 291-292 300 325 333 344-345 352 373 376 379 384 408 426-427 430 432 467- 468 475 483 488 493 516 531 535 545 547 549 564 582 602 623 644 660 662-664 670 673 725-726 728 761 766-767 774 805 830 852-853 864 875 921 932 937 946 949 963 988-989 1014 1016-1017 1024 1027 1090 1097 1170 1185 1200 1215- 1216 1224 1258 1290 1309 1320 1342 1347 1355 1369 1381 1413- 1414 1431 1438 1449 1491 1512 1536 1547 1557-1560 1567 1590 1601 1636 1644 1653-1655 1662 1667 1671 1675 1680-1681 1706 1739 1760-1761 1769 |
| fetal lung | Clontech | FLG004 | 103 276 334 465-466 737 843 1131 1614 1658 |
| fetal liver- spleen | Columbia University | FLS001 | 3-11 13 15-21 25 30-39 41-48 50- 51 54 56-58 60-66 68-69 72 75 77-80 82-83 85 87 89 92-103 105- 110 112 116-124 126-127 130 133 135-139 141 144 147-149 152-153 157 163-165 167-172 174 176-178 180 186 188-190 193-194 196 198- 200 202-206 210-214 219 221-231 233-236 240-244 246-247 250-251 255-256 258 261-265 268-269 272 274 276-278 280-281 284-286 288 293 295 299-301 304 306-307 309 311 314 316 318 320-321 326 329- 332 342 344-345 350 352-353 356- 358 360 362 370-374 376 378-384 386-387 390 392-393 400-401 403 406 408 410-412 415 417 419 422- 437 439-442 444-445 448 452-454 456 459 461-470 472-479 481-483 487-488 490-491 493 500-501 503- 506 509-513 515-520 522-524 526- 529 531 534 536-540 542 547-549 553-554 561-562 564 567-568 571- 576 579 581 583 585-597 599-605 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| | | | 607 610-613 615-621 623-624 626 628-634 636-640 644 647-650 655- 660 665 669-670 672 674-675 678 681-682 684 690-695 697 702 708- 710 713-714 716-719 725-728 730- 731 734 736 738 740-741 743-746 748 750-751 759-766 768 772 774- 777 779 783-788 793 796 798 800- 805 808 810-812 814 818-819 821- 824 826-832 834-837 843-847 849- 867 869-876 878-883 887 889-895 897-898 902 904-914 916 919 921- 928 930-937 939 945-950 953-958 960-961 963-965 967 969 971 974- 978 980-983 986 988-990 992-993 995-997 1000-1002 1004-1008 1012 1014 1016-1019 1025-1026 1028- 1031 1033 1035-1036 1039-1044 1047 1049-1050 1053-1056 1058- 1059 1061-1064 1067-1070 1072- 1074 1076 1078 1082 1085-1087 1089-1090 1097 1099-1103 1107- 1113 1115-1119 1121-1123 1125 1127-1128 1131-1134 1136-1137 1144-1150 1153 1159-1160 1163 1170 1175 1177-1178 1188 1190- 1192 1195-1200 1202 1206 1208- 1211 1214 1216 1218 1221-1222 1225 1227 1234 1237 1241 1244 1246-1247 1251 1254 1258 1261 1266 1268 1270-1273 1277-1282 1284-1285 1287-1290 1294 1299- 1300 1306-1308 1313-1320 1324- 1325 1327 1330 1332-1333 1338 1341 1343 1345-1347 1349-1350 1353-1360 1362-1363 1365-1367 1369-1370 1372-1374 1376 1378- 1381 1383-1384 1386 1389-1391 1400 1402-1403 1405-1410 1413 1415 1417-1419 1422-1429 1431 1435-1437 1439-1442 1445-1446 1448-1449 1454 1458-1459 1466- 1470 1472 1474 1477-1478 1480 1482 1485 1491-1493 1496-1498 1501-1507 1509 1511-1512 1516- 1519 1524-1526 1529 1532 1536- 1541 1546-1547 1549-1550 1552- 1554 1562 1564 1569 1572 1574- 1575 1578 1581 1583 1587-1588 1591-1592 1594-1595 1597-1598 1600-1604 1611-1612 1614-1615 1617-1618 1620-1622 1624-1625 1627-1628 1630-1632 1634-1639 1645-1651 1653-1662 1664 1667- 1669 1671 1673-1674 1676-1688 1690 1696 1701-1703 1706-1709 1711 1713-1714 1718-1719 1722 1724-1727 1731-1733 1738 1740- 1741 1743-1744 1746 1748 1751- 1752 1754 1760-1765 1767-1773 1780 1783-1786 |
| fetal liver- spleen | Columbia University | FLS002 | 3-11 13 15-21 26 29 32 35-39 42 44-45 48 50-51 54-55 57-58 61 64 68-69 73-75 78 80 82 84 87 95-98 100 103 105 107-108 110 112-113 116-119 122-125 128 130 137-138 145 147-153 155 157 159 161-163 166 168 171-172 174-175 177 181 188-189 193-194 196-198 200-203 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| fetal liver-spleen | Columbia University | FLS003 | 103 300 318 321 352 372 379 381 384 392-393 403 422 424 429 434- 435 440 444 453 503 515 544 592 978 1064 1324-1325 1327 1333 1357 1369 1378 1418 1424 1622 1646 1649 1680-1681 1689-1690 1717 1743-1744 1769 |
| fetal liver | Invitrogen | FLV001 | 15-16 26 34 58 61 64 70 75 78 89 98 105 112 116 120-121 123 133 151 165 176 180 194-196 198 200 204-206 210-211 220 225-226 230 235-236 239 247 259 261 267 272 277 280-281 303 310 313 317 320- 321 329 344 356 371 374 376 379- 382 395 408 412 414 419 429 434- 435 441-442 465-466 490 494 504- 506 509 522 527 534 552-553 562 567 569-570 572-574 607 631 657- 658 667 669 672 685-686 702 717 725-726 732 748 759 761 778 784 786 809 817 829 837 857 861 872- 873 875 881 889 894-895 909 911 916 954 963 967 974 977 986 988- 989 993 995 997 1000 1005-1006 1008 1014-1015 1020 1042-1043 1070 1086-1087 1089-1090 1118- 1119 1122 1144-1145 1148 1153 1157 1159 1183 1195-1196 1227 1250 1257-1258 1262 1267 1280 1285 1307 1312 1314 1317-1320 1344-1345 1349-1350 1355 1362- 1363 1403 1405 1415 1419 1425- 1426 1429 1431 1442 1448 1463- 1464 1469-1470 1489 1528 1536 1539 1549-1550 1557-1562 1577 1583 1598 1601 1611 1615 1622 1644 1649 1666 1674 1706 1721 1738 1746 1763-1765 1774 1776 1779 |
| fetal liver | Clontech | FLV002 | 676 998 1719 |
| fetal liver | Clontech | FLV004 | 93 133 214 301 355 374 379 555 581 601 679 837 847 859 1123 1236 1270 1313 1324-1325 1327 1355 1367 1425-1426 1536 1690 1733 1760-1761 |
| fetal muscle | Invitrogen | FMS001 | 26 37-39 50-51 58 84 86 89 98 113 128 131-132 139 155 172 186 194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935 970 980 986 988-990 992 1000- 1001 1007 1014 1027 1035-1036 1045 1060 1064 1070 1083 1097 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| fetal muscle | Invitrogen | FMS002 | 119 221 273 402 426-427 463 547 599 736 869 1000 1033 1083 1266 1431 1440-1441 1468 1545 1599 1673 1678-1679 1687-1688 1710 1712-1714 1723 1725 1731-1733 1743-1744 1760-1761 1767 |
| fetal skin | Invitrogen | FSK001 | 1 4-11 15-16 20-23 25 29 33 40 43 46 56-57 60-61 64-66 75 82 87 97-98 105 107-108 113 118-119 123 133 135-137 139 144 146 148 151-153 156 163 170 176 180 188- 189 197-198 200 202-203 210 218 222 231 246-247 261 263 265-270 277 285-286 290 293 299 301 307 311 321 325 328 330 333-335 339 341 345 351-352 355-356 358-359 362 368 370 372 376 379-382 384 388 394 404-405 408-409 411-412 419-420 424 426-427 436 441-442 445 448-449 454 462 465-466 472 476 490 493 504 506 509 515-517 519 526 531 537-540 547 549 560- 561 567 572-573 581 584 589 611- 612 615 623 630-631 635 647 649 651 657-658 660 662-665 667 669 672 676 678 681 688 701 704-705 709-710 713 717 720-721 725-726 728-729 732 748 750 753 759 764 766 770 775-777 780-781 786 788- 789 798 809 811 814 816-817 822 824-826 831 842 857 859 861 863- 864 881 894-895 908 910-911 916 918 922-923 928 932-933 935 937 946 948-949 953 960-961 966-967 970 975 977 986 990 992-993 999- 1000 1004 1007 1013 1018 1025 1027 1032 1035 1041-1043 1054 1057-1058 1060 1062-1064 1069 1072 1077 1090-1091 1097 1099- 1103 1108 1113 1119 1123 1128 1131 1134 1140 1148-1149 1152- 1153 1156 1163 1167 1178 1182 1189 1192 1195-1196 1198 1201- 1205 1208 1211-1212 1216 1219- 1220 1222 1225 1240 1243 1258 1266-1267 1274 1277 1280 1282- 1285 1299 1310 1317-1322 1324- 1325 1329-1330 1342 1344 1346 1349-1351 1354-1357 1365-1366 1369 1371 1373 1376 1378 1380 1383-1384 1387 1399-1400 1405 1410 1427 1429 1431 1433-1435 1439-1441 1448-1449 1454 1457 1468 1470 1472 1475 1480-1481 1487 1490-1491 1493 1498 1509 1512 1521 1525-1526 1529 1535- 1536 1547 1549 1557-1559 1588 1592 1595 1597-1598 1601 1603- 1604 1608 1611 1614 1618 1624- |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| fetal skin | Invitrogen | FSK002 | 13 286 302 307 313 321 330 335 339 341 354 370 372 385 400 402 408 414 426-427 433 436 450 454 515 544 585 598 767 810 845 939 1076 1109 1155 1317-1320 1326 1333-1335 1343 1347 1350 1369- 1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687- 1688 1693 1718 1721 1725 1731- 1732 1739 1755 |
| fetal spleen | BioChain | FSP001 | 110 137 211 353 589 927 1108 1639 1771 |
| umbilical cord | BioChain | FUC001 | 4-8 10 12 14 17 33-36 44-46 57 64 68-69 75 82 85 101 104 113- 114 116 119 122-124 133 137 153- 154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 |
| fetal brain | GIBCO | HFB001 | 4 9 11-13 17-18 22-23 25 37-39 42-47 50-51 54-55 58 60-61 65-66 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
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| macrophage | Invitrogen | HMP001 | 5-8 110 204-205 503 634 678 859 878 933 988-989 1379 1448 1504 |
| infant brain | Columbia University | IB2002 | 10 12-13 15-18 22-23 25 29 34 37-39 43 47 50-51 54-56 58 60-63 65-66 68-69 72-74 80 82-83 86 88-92 97 100 102-104 106-108 110 112-113 115-116 118 123 128 130 134-136 138-139 143 147-149 151- 152 154-155 163 165-167 169 172- 175 181-184 186 193-196 198 201 203-205 209-210 214-215 222 224- 226 231-232 235-236 239 246-247 252 257 260 268-269 272 276-277 279-281 286 288 291-292 295 298 300-301 304 307 310 313 321-323 330-331 333-334 339 346-347 349 352 356-357 362 371-372 377 379- 380 383-384 392 397 401 406 408 411 413-414 416 418-419 422 428 430-431 434-435 438 443 449 453- 454 461 464-466 469-470 472-473 475-476 478 482-483 487 490 492 494 497 503 507-508 510-513 516 519-520 524-526 530-534 536-540 547 550-551 561 563-564 566-567 572-576 579 581-582 584-587 590- 591 593 595-597 607-609 611-613 616-617 620 622-624 627 631 637 641 645-647 650-655 657-658 660- 665 667-675 689 691 695 697 699 703 707 713-715 717 721 728-731 733-736 739 743 745 751 755 759 763 769-770 772 778 780-781 785 788-789 793-794 799 803 808 811 814 825-826 830 834-836 840-843 845 848-850 854-855 860 862 864- 865 870 872 875-876 878 886 888 890-891 894-896 898 903-904 916- 917 919 922-925 927-928 930-932 934-936 938 941 945-946 948-950 953-954 959-962 966-969 977 979 981 986-990 992 997 999-1000 1004-1006 1014 1016 1018-1019 1024-1025 1033 1036 1047 1051- 1052 1054-1055 1057-1059 1063- 1064 1068-1070 1073 1081-1082 1085 1089 1108-1113 1118-1120 1123-1124 1130 1132-1138 1140 1149 1151 1153-1154 1163-1170 1172 1174-1175 1183-1184 1188 1190 1193-1194 1196-1197 1199 1204 1208-1209 1211 1218-1222 1226-1227 1229 1231 1234 1241 1247 1249 1251 1256 1258 1261- 1262 1269 1274 1279 1281 1283 1285 1287-1289 1294-1295 1305 1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356 1362-1363 1365-1366 1368-1370 1374 1381 1383-1384 1388 1400 1403 1406-1407 1413 1417 1420 |

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| infant brain | Columbia University | IB2003 | 17-18 20-23 29 34 43 60 68-69 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572-576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 |
| infant brain | Columbia University | IBM002 | 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 |
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| lung, fibroblast | Stratagene | LFB001 | 5-9 17 20-21 25 68-69 82 94 105 153 157 197-198 203 207-208 212- 213 223 262 266 283 302 321 326 333 356 370 427 430 436 446 462 472 493 498 503 516 519 527 535 537-540 542-544 562 565 567 586 599-600 607 615 630 647 662-664 692-694 712 719 745 748 775-777 794-796 810 837 843-847 849 854- 856 869 876 903 934 953 955-956 964 975-976 984 1000 1005-1007 1024-1025 1033 1039 1053 1064 1070 1072 1082 1112-1113 1134 1136-1138 1140 1195 1223 1232- 1233 1246 1279 1285 1295 1311 1320 1334-1335 1343 1427-1428 1446 1478 1482 1493 1504 1537 1552 1555 1567 1575 1582 1598 1620 1625 1632 1638 1645 1654- 1655 1662 1680-1681 1684 1686 1690 1696 1702 1711 1733 1741 1760-1761 1778 1785 |
| lung tumor | Invitrogen | LGT002 | 5-10 18 20-21 29 33-36 40 43 52 54-55 61 65-66 68-70 73-75 80 85 88-89 93-94 100 103 106-108 112- 113 115-116 118-119 123-124 126 130-132 135-137 139-141 143-144 147-148 151-153 155-156 159 161 164 169 171 179-180 185 190 192 194 196-199 203-208 210 212-214 216-217 219 222 233 240-241 244 246 251-252 255-256 261-262 266 272 276-277 279-281 284 286 288 290 295 298 301-302 309-312 317 321 329 332 341-342 344-345 348 352 358-360 363 368 370-371 376 380-381 384 389-390 398 400 409 414 423 426-427 430 432-436 443- 444 450-451 454 462 468 472-477 480-483 487-488 490-491 493 496- 498 500 503-506 509-512 515-516 519 521-523 526 530 534 541 544 547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956 961 963 966-967 969 971 977-979 981 984 986-987 990 992-993 995 997 999-1001 1005-1007 1009 1012-1013 1018 1020 1022-1024 1026 1029-1030 1033 1038 1041 |

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| lymphocytes | ATCC | LPC001 | 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466 1470 1472 1474 1482 1492 1506 1528 1537 1546 1549 1591 1598 1600 1603-1604 1606 1627 1636 |

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| leukocyte | GIBCO | LUC001 | 3-4 10-11 13 15-18 20-21 24-25 30-31 35-36 40 43-45 48 50-51 54-58 60-63 68-69 75 79-80 82-83 85 88-91 93-96 98 100 103-104 107-108 112 116 119 123 125-128 134-140 142 147-149 151 153 155 157 162-163 167 169-172 174 177- 179 186 190 192-199 203-207 210 212-215 217-219 222-223 229 235- 236 247 251 255-258 260 262 272 274-277 280-281 285-286 297-301 307-310 313-314 316-317 321 325- 330 333-334 340-342 348-349 352 354-358 370-371 380-385 387-388 400 405 408-410 412 414-416 421- 425 430-431 434-435 437 439 441- 442 445-451 453-454 456 459 461- 464 468-472 474-479 481 483-485 487-491 496 499-501 503-504 509- 513 516-519 522 526-527 529-531 534 536-540 542 547-549 553-559 566-567 571 574-577 579 582 584- 586 589 593 595-597 601-602 604 606-607 611-613 615-621 623 627- 629 633 636-637 642 644-650 655 659-660 662-665 667 669 674-675 678 682-684 692-696 698 700 706 708 710 716-720 725-726 729-736 738-739 743-746 749 751 753 756 759 765-766 768 770-778 780 784- 786 788-790 793 796 798 800 802- 803 810-811 814 817 819 826 828- 830 832 834-836 838 843 845-860 863-864 866-871 877-879 881-892 894-896 898 902 904-914 916 919- 925 927 930-932 935-936 941-942 945 948-949 953 955-956 958 960- 962 964 967 970-971 973 975 977 985-990 992-993 995-996 999-1002 1004-1009 1011 1014 1017-1019 1022-1023 1025 1027 1029-1031 1033-1036 1038 1041 1043 1047 1050 1053-1054 1058-1059 1061- 1062 1064 1068 1070 1072 1078 1085-1086 1089-1091 1093 1097 1106-1107 1110-1113 1115-1117 1122-1123 1125 1129 1132-1133 1135-1137 1140-1145 1152 1158 1163 1168 1170-1174 1176-1178 1180 1182-1183 1186 1195 1198- 1200 1202 1205-1206 1211 1216 1219-1221 1223-1227 1230-1236 1238-1242 1247 1252 1254 1256 1258 1261-1262 1264-1265 1269- 1270 1272-1275 1277 1280-1284 1287-1293 1299-1300 1306 1308 1312-1313 1317-1320 1322 1324- 1330 1333-1335 1339 1341 1343- 1347 1349 1353-1357 1359-1361 1365-1367 1369-1370 1373-1374 1377 1379-1381 1386-1387 1394 1400 1403 1409 1419 1423 1425- 1428 1430-1431 1433-1434 1437- 1438 1440-1442 1446-1448 1450 |

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| leukocyte | Clontech | LUC003 | 4 35-36 44-45 61 68-69 75 82 102 119 139 154 179 197 244 280-281 324 372 404 430-431 455 461 476- 477 481 503 537-540 554 575-576 581 589 608-609 621-622 624 630 632 647 662-664 669 679 698 764 773 775-777 802 848 851 856-857 879 905-907 915 949 952 990 992 1002 1113 1119 1170 1183 1216 1236-1237 1241 1275 1346 1353 1357 1359 1377 1506 1515 1534 1553 1591 1600 1613-1614 1621 1628 1670 1676-1677 1691-1692 1699 1733 1738 1772 |
| melanoma from cell line ATCC #CRL 1424 | Clontech | MEL004 | 25 35-36 43 80 104 126 128 150 163 166 188-189 197 210 215 220 271 277 280-281 310 317 336-338 345 351 372 380-381 383 387 412 415-416 430 445 448 454 456 467 481 490 499 503 526 528 546 548 567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 |
| mammary gland | Invitrogen | MMG001 | 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165- 166 170-172 174 176 178 181-185 188-190 194-198 201-206 210 217- 222 224 227-228 231 233-237 247 251 253-254 256 261-263 266-267 271 276-277 279-281 284-286 288 |

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| induced neuron cells | Stratogene | NTD001 | 29 35-36 80 116 123 156 163 181 214 230 280-281 284-285 307 321 330 340 358 371 375 377 380 382 422 424 492 497 532-533 542 546 |

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| retinoid acid induced neuronal cells | Stratagene | NTR001 | 5-8 78 268-269 277 383 431 506 623 677 731 999-1000 1199 1425- 1426 1547 |
| neuronal cells | Stratagene | NTU001 | 29 65-66 80 82 110 119 146 152 166 174 181-185 198 227-228 253 284 309 325 332 334 336-338 375 391 393 406 414-416 454 465-466 470 488 503 506 510-512 519 537- 540 572-574 597 602 607 623 647 661 700 702 716 743 771 792 858 904 948 954 977 1000 1005-1006 1025 1064 1068 1122 1148 1185 1219 1226 1234 1246 1271 1283 1295-1296 1311 1317-1320 1329- 1330 1350 1355 1365-1366 1378 1383-1384 1400 1412 1445 1505 1539 1547 1578 1647 1656 1683 1690 1738 1749 1783-1784 |
| pituitary gland | Clontech | PIT004 | 311 314 379 408 419 430 454 1055 1095-1096 1272-1273 1312 1320 1378 1652 1671 1720 1725 1736 1741 1755 |
| placenta | Clontech | PLA003 | 5-8 124 208 277 370 843 906-907 1280 1317-1319 1369 1609 1621 1737 |
| prostate | Clontech | PRT001 | 9 46 57 71 107 147 171 177 197 201 229 231 242-243 274 280-281 307 310 317 330 358 373 382-383 400 430 434-436 461-462 469 477 489 497 500 505-506 513 521 526 531-533 547 618 649 657-658 662- 664 710 729 767 771 789 820 861 871 874 890-891 905 938 945 963- 964 988-989 1002 1025 1033 1045 1061 1095-1096 1112 1125 1142 1196 1198 1202 1232-1233 1241 1258 1272-1273 1287 1295 1313 1333 1341 1344 1349 1360 1362- 1363 1367 1437 1442 1447 1475 1478-1479 1482 1489 1513 1517 1527 1531 1536 1598-1599 1628 1636 1657 1680-1681 1687-1688 1717 1738 1743-1744 |
| rectum | Invitrogen | REC001 | 17-18 29 33 62-63 71 73-74 83 86 113 126 146 153 158 167-169 195 200 206 261 309 312 341 344 368 373 388 395 408 414 420 430 441- 442 446 448 464 468 483 517 537- 540 547 567 585 589 602 623 628- 629 632 645-647 651 657-658 669 717-719 721 725-726 738 748 750 756 762-763 766 770 774 790 819 825 843 849 851 881 903 909 948- 949 960 986 996 1020 1023 1033- 1034 1064 1067 1070 1075 1086 1108-1109 1113 1130 1139 1153 1159 1172 1178 1185 1187-1189 1205 1220 1225 1240 1244 1271 1317-1320 1323 1334-1335 1350- 1351 1355 1369 1373 1375 1425- |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|--------------------|------------|--------------------|--|
| | | | 1426 1436 1439 1469 1474 1477 1482 1546 1587-1588 1592 1596 1610 1622 1627 1644 1658 1662 1665-1666 1669 1675-1677 1749 1786 |
| salivary gland | Clontech | SAL001 | 10 55 97 103 110 140 149 152 158 198 217-218 242-243 256 301 308 312 321 333 351 354 360 410 437 448 473 487 494 496 501 535 555 569-570 572-573 590-591 624 636 651 759 762 764 768 771 788 800 809 826 848 865 879 906-907 925 933 963 1016 1020 1025 1040 1046 1055 1066 1103 1150 1172 1181 1234 1281-1282 1288-1289 1298 1315 1320 1333 1336-1337 1346 1359 1373 1379 1424 1447 1449 1474 1482 1492 1494 1498 1511 1523-1524 1537 1554 1596 1626- 1627 1636 1652-1655 1658 1665 1671-1672 1691-1692 |
| salivary gland | Clontech | SALs03 | 158 326 1423 1463-1464 |
| skin fibroblast | ATCC | SFB001 | 1320 1400 |
| skin fibroblast | ATCC | SFB002 | 262 736 1025 1253 |
| skin fibroblast | ATCC | SFB003 | 709 1119 1350 1631 1653 |
| small intestine | Clontech | SIN001 | 25 142 146-147 151 155 198 203 244 260 271 280-281 286 288 298 301-302 308 312 334 340 371 398 408 412 414 416 423 426-427 430 434-435 445 452 454 478 503 516 519 521 523 543 547 549 555 559 563 569-570 585 592 604 611 626 628-629 632 650 659 681 710 714 718 750 764 780 798 829 842 857 859 866 887 892 894-895 901 904 906-907 912 919 935 997-998 1000 1007-1008 1026-1028 1044 1055 1089 1097 1116-1117 1131 1148 1169 1199 1219 1234 1247 1264 1279 1316 1320 1326 1341 1343 1349 1351 1374 1387 1398 1400 1403 1407 1423 1428 1468 1498 1501 1521 1550 1556 1585 1597 1636 1638-1639 1645 1653 1656 1662 1671 1675 1684 1691-1692 1704 1711 1717 1719 1722 1725- 1726 1729 1733-1734 1743-1744 1762 1767 1780 1785 |
| skeletal muscle | Clontech | SKM001 | 18 20-21 82 84 101 118 134 148 151 153 166 225-226 258 274 277 289 329 361 412 414 424 440 452 459 470 488 503-504 537-540 647 660 673-675 715 773 780 786 830 905 922 950 963 982 990 992 1020 1047 1063 1115-1117 1121 1134 1228 1268 1284 1298 1321 1329 1336-1337 1343 1409 1413-1414 1509 1599 1624 1644 1653 1712 |
| skeletal muscle | Clontech | SKM002 | 168 1683 1712 |
| skeletal muscle | Clontech | SKMs03 | 235-236 1409 |
| skeletal muscle | Clontech | SKMs04 | 235-236 |
| spinal cord | Clontech | SPC001 | 4 9 11 17 30-31 35-36 43 46 60 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|--------------------|--|
| | | | 82 85 92 94 108 110 116 139 157 167 198 204-205 210 215 229 256 259 277 280-281 300-302 304 315 317 372 379 387 392 419 426-427 430 433 448 467 473 487 489 506 509 513 519 524 526 537-540 543 547 549 551 559 567 569-570 593 607 616-617 623 625 637 649-650 652 657-658 670-671 673 679 681- 682 709 711 715 719 728-729 734 749-750 753 775-777 781 789 791 809 820 832 834-836 847-849 854- 855 858 861 864 871-872 875 884 898 906-908 917 919 924 934 942 944 970 985 990 992-993 998 1013 1039 1053 1059 1065 1072 1075 1077 1082 1085 1097 1103 1109 1116-1117 1128 1134 1151 1170 1174 1192-1194 1215 1225 1241 1243 1283 1294 1307 1312 1320 1323 1327 1330 1350 1353-1354 1356 1359 1368 1375 1400 1406- 1407 1423 1429 1437 1443 1448 1454 1470 1482 1492 1501 1508 1511 1529 1538 1548-1549 1565 1571 1578 1598 1600 1614 1625 1627 1630 1639 1646 1651-1652 1670 1686 1696 1740 1751 1755 1771 |
| adult spleen | Clontech | SPLc01 | 117 312 326 348 424 426-427 431 845 866 1320 1330 1333 1344 1355-1357 1371 1387 1397 1446 1538 1579 1669 1686 1739 1767 |
| stomach | Clontech | STO001 | 10 15-16 61 68-69 100 117 149 197 201 227-228 231 249 273 280- 281 287 291-292 302 312 358 362 426-427 430 446 462 475 479 535 597 620 630 651 662-664 722 739 780 782 785 846 919 960 964 966- 967 976 1008 1012 1032 1042 1063 1071 1135 1170 1208 1234-1235 1259 1277 1280-1281 1322 1349 1359 1369 1449 1468 1474 1478 1487 1493 1498 1557-1559 1622 1634 1651 1653 1729 |
| thalamus | Clontech | THA002 | 9 11 25 85 87 112 137 146 180 190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753 |
| thymus | Clontech | THM001 | 44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307 327 330 333 342 351 358 371 410 430 445 465-466 468 471 483 487 493 503 506 509 517 526 535 537- |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|-----------------------|--|
| | | | 540 546 548 554 567 584 586 590- 591 604 612 621 638-640 645-647 649 656 660 665 670 698 710 720 728 735 739 746 759 762 766-767 775-777 780 784-785 800 802 809 824 826 828 845 851 858-859 864 866 870-871 878 884 887 892 899- 900 927 930-931 967 983 986 990 992 999 1014 1029-1030 1033 1059 1066 1073 1103 1107 1113 1116- 1117 1119 1140-1142 1158 1163 1172 1177 1195 1206 1209 1213 1216 1218-1219 1221-1222 1227 1271 1277 1282 1320 1329 1349 1367 1369 1383-1384 1417 1419 1423 1425-1427 1448 1477 1488 1493 1536 1554 1620 1644 1646 1649 1654-1655 1661-1662 1669- 1670 1674 1676-1677 1685-1688 1707 1711 1731-1732 1737 |
| thymus | Clontech | THMc02 | 5-9 15-21 25 33 35-36 43-45 48 50-51 54-55 60 75 83 87 89 93 98-100 102 105 112 117 135-137 141 143 146 157 167 169 192 196 211 217-219 222 224 229 233 235- 236 240-241 244 251-252 256 261- 262 268-269 286 288 290 295 297 301-302 309-310 315-317 321 324 327 334 342 350 352-353 360 370- 373 382 384 400 403 410 414-416 424 430-431 436 445 454-456 461 464-467 470 472 474-476 483 488 497 500 504 506 513 516 519-520 524 526 530-531 534 537-540 549 554-555 565-566 569-570 572-573 575-577 586-587 595 603-604 606 612 630-632 634 636 647 650 657- 660 666-667 669 673-675 678 698 700 703 708 720 725-726 731 738- 739 743-744 750-753 757 759 763- 765 767 772-779 787 789-790 798 800 810 823 829 834-836 841 848 854-856 859 861 864 870-871 881 890-891 898 908-909 913 928 933 941 949 958 961 963 967 969 975 981 986 988-990 992 999 1007- 1008 1014 1016 1039 1041 1073- 1074 1079 1089 1097 1109 1114- 1117 1122 1131 1140-1141 1144- 1145 1163 1172 1175-1177 1186 1196 1198 1206 1211 1216 1220 1223 1227 1234-1243 1261-1262 1267 1271 1280-1281 1284 1290 1308 1317-1320 1322 1324-1325 1327 1330 1334-1335 1339 1346 1350-1351 1355 1357 1360 1370 1374 1377-1379 1386 1389-1390 1392 1397 1400 1402 1406-1407 1417 1423 1425-1427 1440-1441 1466 1474 1477 1483 1493 1498 1504 1506 1525 1536 1545 1549 1566 1594 1598-1600 1608 1611 1614 1621 1623 1625 1632 1639 1641 1644 1647 1649 1653-1656 1658 1662-1663 1671 1673 1678- 1681 1686-1688 1693 1705 1707 1711 1717-1718 1726-1727 1731- 1733 1737-1738 1743-1745 1758- 1761 1771-1772 1779 1786 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|-----------------------|---|
| thyroid gland | Clontech | THR001 | 4 9-10 20-21 37-39 48 50-51 54- 57 60-61 65-66 71 83 94-96 98- 100 102 104 110 112 115-117 119 123 127 133 136-137 140 149 152- 153 155-158 163-164 168-169 171 186 190-192 197 201-203 219-220 229 233-237 246-247 253 256 258 262 265-266 268-269 277 280-281 284-286 288-289 298-299 302 309- 311 317 321 326 332 335 341-342 344 348 350 354 358-359 363 368 371-373 382-383 385 394 398 400- 401 411 414-415 421 424 430-431 433-436 443-446 450-452 454-455 458 472-474 476-478 482 484-485 487-488 490-494 496-497 500-501 503-504 506 509-513 516-517 519 524 526-527 529 535-540 547 549 562 564 569-570 575-576 588 594- 595 601-602 604 606 610 612 615- 617 619-623 628-630 634-635 642 647 649-651 660 662-665 668 670 681 690-694 696 698 700 709 721 727-729 732 734 738 740-741 743 745 750 759 761 763 765 770 773 780 785 795-796 798 802 804 823- 824 826 828 833 838 841-845 847 849 857-860 867 874-875 878 880- 881 887-888 890-892 894-895 898 908 910-911 913-914 922-923 926- 927 929 932-934 937 939 941-942 948 953 957 961 963-964 966 978- 979 981-982 987 990 992 1001 1004-1006 1010 1014 1020 1024 1033 1038-1039 1044 1047 1050 1052-1054 1056 1058 1068 1070- 1071 1077-1079 1088 1094-1097 1105-1106 1112-1113 1116-1117 1124 1126 1128-1129 1131 1134 1136-1137 1142-1143 1146-1147 1149-1150 1156 1161-1164 1167 1170-1173 1177-1181 1190 1192 1197 1200 1204 1208-1209 1214 1217 1219 1222 1230 1232-1233 1235 1241 1245 1247 1254 1257- 1258 1260 1262 1271-1273 1283 1286-1289 1299 1306 1314 1320 1330-1332 1334-1335 1342 1345 1349 1365-1367 1370-1372 1374 1381 1394 1407 1419 1428-1436- 1437 1440-1441 1443 1446-1449 1454 1459 1461-1462 1468 1470- 1471 1475 1477 1479 1482 1491 1497-1498 1504-1505 1507 1513 1522 1524-1526 1528 1531 1534 1536-1537 1548 1550 1553 1555- 1559 1562 1567 1578 1590-1591 1597 1599-1601 1612 1614 1616 1619-1620 1622 1624-1626 1628 1631-1632 1634 1636 1639 1644- 1645 1648 1651 1653-1656 1658 1660 1662-1663 1667 1669 1671 1675 1678-1681 1683-1686 1689 1691-1692 1703 1709-1711 1717 1724-1726 1729 1734 1737-1738 1740 1743-1744 1749 1753 1759- 1761 1770 1777 1786 |
| trachea | Clontech | TRC001 | 9 29-31 46 48 87 104 107 110 135 158 222 262 266 286 301 318 331 |

| Tissue Origin | RNA Source | Hyseq Library Name | SEQ ID NOS: |
|---------------|------------|-----------------------|--|
| | | | 352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099- 1102 1113 1208 1215 1232-1233 1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691- 1692 1711 1717 1726 1772 |
| uterus | Clontech | UTR001 | 17 19 25 41 46 57-58 61 89 104 108 139 152 174 198 200-201 206 263-265 274 290 387 408 420 438 446 448 452 473 491 493 499 503 506 513 519 522 526 530 542-543 560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912 929 934 937 996 1009-1011 1018 1050 1075 1107 1124 1170 1219 1258 1279 1287 1310 1320 1323 1343-1344 1375 1437 1451-1452 1478 1481 1498 1519 1521 1536 1552 1579 1597 1602 1606 1620 1626-1627 1649 1652 1661 1670 1719 1722-1723 |

TRADOCs:1416191.1(%CQN011.DOC)

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
| 1 | Y41736 | Homo sapiens | Human PRO1114 protein sequence. | 1398 | 100 |
| 2 | Y66656 | Homo sapiens | Membrane-bound protein PRO943. | 2389 | 99 |
| 3 | AF113136 | Homo sapiens | IL-1 receptor-associated-kinase-M; IRAK-M | 3043 | 100 |
| 4 | AF017806 | Mus musculus | Zn-15 transcription factor | 6351 | 77 |
| 5 | X02761 | Homo sapiens | fibronectin precursor | 10535 | 98 |
| 6 | X02761 | Homo sapiens | fibronectin precursor | 8990 | 89 |
| 8 | X02761 | Homo sapiens | fibronectin precursor | 12564 | 99 |
| 9 | AJ011679 | Homo sapiens | Rab6 GTPase activating protein, GAPCenA | 5251 | 99 |
| 10 | W88501 | Homo sapiens | Human stomach carcinoma clone HP10415-encoded protein. | 2381 | 100 |
| 11 | AF117754 | Homo sapiens | thyroid hormone receptor-associated protein complex component TRAP240 | 11336 | 98 |
| 12 | Z97630 | Homo sapiens | dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G))) | 896 | 100 |
| 13 | Y58620 | Homo sapiens | Protein regulating gene expression PRGE-13. | 1894 | 98 |
| 14 | AF213457 | Homo sapiens | triggering receptor expressed on myeloid cells 2 | 1238 | 100 |
| 16 | AF233453 | Homo sapiens | RACK-like protein PRKCBP1 | 3124 | 99 |
| 17 | AF201303 | Homo sapiens | dhfr oribeta-binding protein RIP60 | 3130 | 98 |
| 18 | AF064205 | Homo sapiens | dynactin 1 p150 isoform | 6377 | 100 |
| 19 | U00059 | Saccharomyces cerevisiae | Yhr121wp | 174 | 26 |
| 20 | AB032903 | Homo sapiens | guanosine monophosphate reductase isolog | 1801 | 99 |
| 21 | AB032903 | Homo sapiens | guanosine monophosphate reductase isolog | 1485 | 99 |
| 22 | AF140507 | Homo sapiens | Ca2+/calmodulin-dependent protein kinase kinase beta | 3083 | 99 |
| 23 | AF140507 | Homo sapiens | Ca2+/calmodulin-dependent protein kinase kinase beta | 2300 | 99 |
| 24 | AJ289131 | Homo sapiens | chondroitin 4-O-sulfotransferase | 2211 | 99 |
| 25 | U33460 | Homo sapiens | DNA-directed RNA polymerase I, largest subunit | 8777 | 98 |
| 26 | Y44488 | Homo sapiens | ACRP30R2 variant protein. | 1387 | 100 |
| 27 | U43701 | Homo sapiens | ribosomal protein L23a | 791 | 100 |
| 28 | U02032 | Homo sapiens | ribosomal protein L23a | 767 | 97 |
| 29 | Y41324 | Homo sapiens | Human secreted protein encoded by gene 17 clone HNF1Y77. | 1083 | 99 |
| 30 | W71749 | Homo sapiens | Human ubiquitin conjugation system protein 2. | 715 | 90 |
| 31 | W71749 | Homo sapiens | Human ubiquitin conjugation system protein 2. | 631 | 82 |
| 32 | AF231917 | Homo sapiens | long-chain 2-hydroxy acid oxidase HAOX2 | 1811 | 100 |
| 33 | Z29481 | Homo sapiens | 3-hydroxyanthranilic acid dioxygenase | 1507 | 99 |
| 34 | AB001451 | Homo sapiens | Sck | 2869 | 100 |
| 35 | Y00644 | Homo sapiens | precursor polypeptide (AA -34 to 287) | 1667 | 99 |
| 36 | Y00644 | Homo sapiens | precursor polypeptide (AA -34 to 287) | 1104 | 98 |
| 37 | Y78795 | Homo sapiens | Human antizual-2 (AZ-2) amino acid sequence. | 3586 | 78 |
| 38 | Y78795 | Homo sapiens | Human antizual-2 (AZ-2) amino acid sequence. | 4726 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 39 | Y78795 | Homo sapiens | Human antizual-2 (AZ-2) amino acid sequence. | 3556 | 77 |
| 40 | U93121 | Homo sapiens | M-phase phosphoprotein-1 | 3747 | 100 |
| 41 | Y42750 | Homo sapiens | Human calcium binding protein 1 (CaBP-1). | 795 | 100 |
| 42 | AF282626 | Homo sapiens | latexin | 1189 | 100 |
| 43 | G02150 | Homo sapiens | Human secreted protein, SEQ ID NO: 6231. | 384 | 94 |
| 44 | U19617 | Mus musculus | Elf-1 | 2724 | 88 |
| 45 | U19617 | Mus musculus | Elf-1 | 2062 | 86 |
| 46 | AF100758 | Homo sapiens | osteoinductive factor OIF | 1538 | 100 |
| 47 | Y87591 | Homo sapiens | Human SPROUTY-1 protein, SEQ ID NO:24. | 1737 | 99 |
| 49 | X04145 | Homo sapiens | T3 gamma precursor (aa -22 to 160) | 942 | 99 |
| 51 | X63547 | Homo sapiens | oncogene | 5845 | 99 |
| 52 | M94043 | Rattus norvegicus | rab-related GTP-binding protein | 1089 | 96 |
| 53 | L31783 | Mus musculus | uridine kinase | 917 | 71 |
| 54 | X83973 | Homo sapiens | transcription factor | 4486 | 98 |
| 55 | AF224741 | Homo sapiens | chloride channel protein 7 | 4128 | 99 |
| 56 | W74805 | Homo sapiens | Human secreted protein encoded by gene 77 clone HOEAS24. | 1491 | 100 |
| 57 | Z50907 | Homo sapiens | Human TBC-1 cDNA from second transcript. | 4824 | 100 |
| 58 | D79994 | Homo sapiens | similar to ankyrin of Chromatium vinosum. | 6089 | 99 |
| 59 | D79994 | Homo sapiens | similar to ankyrin of Chromatium vinosum. | 4014 | 91 |
| 60 | Y59738 | Homo sapiens | Human normal ovarian tissue derived protein 15. | 601 | 100 |
| 61 | AB031069 | Homo sapiens | protein containing CXXC domain 1 | 1390 | 100 |
| 62 | Y66660 | Homo sapiens | Membrane-bound protein PRO783. | 2492 | 99 |
| 63 | Y66660 | Homo sapiens | Membrane-bound protein PRO783. | 1709 | 99 |
| 64 | S70011 | Rattus sp. | tricarboxylate carrier | 895 | 55 |
| 65 | AF139518 | Rattus norvegicus | A-kinase anchor protein | 178 | 24 |
| 66 | W29666 | Homo sapiens | Homo sapiens DH1308_1 clone secreted protein. | 157 | 30 |
| 67 | AJ245738 | Homo sapiens | claudin-15 | 1206 | 100 |
| 68 | AF099138 | Rattus norvegicus | GLUT4 vesicle protein | 4183 | 87 |
| 69 | AF099138 | Rattus norvegicus | GLUT4 vesicle protein | 4906 | 86 |
| 70 | Z82059 | Caenorhabditis elegans | Similarity to Drosophila ring canal protein comes from this gene | 1285 | 44 |
| 71 | AF224278 | Homo sapiens | PMEPA1 protein | 1282 | 100 |
| 72 | AF126426 | Homo sapiens | neurotrimin | 1809 | 100 |
| 73 | Y41652 | Homo sapiens | Human MEK2 protein sequence. | 2065 | 99 |
| 74 | Y41652 | Homo sapiens | Human MEK2 protein sequence. | 1207 | 100 |
| 75 | AF188622 | Mus musculus | selectively expressed in embryonic epithelia protein-1 | 1485 | 74 |
| 76 | AE000406 | Escherichia coli | putative DNA topoisomerase | 950 | 100 |
| 77 | X99302 | Homo sapiens | Pop1 | 655 | 100 |
| 78 | AL136538 | Schizosaccharomyces pombe | similarity to S. cerevisiae kti12 protein | 210 | 31 |
| 79 | AF129756 | Homo sapiens | G4 | 1554 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|----------------------|--|----------------------|------------|
| 80 | AL096768 | Homo sapiens | dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65)) | 2033 | 100 |
| 81 | AL096768 | Homo sapiens | dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65)) | 1220 | 96 |
| 82 | X57351 | Homo sapiens | 1-8D | 677 | 98 |
| 83 | AC005594 | Homo sapiens | R26984_1 | 2700 | 98 |
| 84 | X73113 | Homo sapiens | fast MyBP-C | 5959 | 99 |
| 85 | AF097330 | Homo sapiens | H1 chloride channel; p64H1; CLIC4 | 1305 | 99 |
| 86 | AB018423 | Mus musculus | SH2 domain-containing protein | 1360 | 78 |
| 87 | AF272151 | Homo sapiens | adaptor protein CIKS | 3084 | 99 |
| 88 | AF196329 | Homo sapiens | triggering receptor expressed on monocytes 1 | 1214 | 100 |
| 89 | AB016879 | Arabidopsis thaliana | contains similarity to pre-mRNA splicing factor-gene_id:MRB17.2 | 634 | 36 |
| 90 | AJ133721 | Mus musculus | homeodomain protein | 654 | 57 |
| 91 | AJ242864 | Mus musculus | phtf protein | 619 | 61 |
| 92 | A61971 | unidentified | MCSP | 11676 | 99 |
| 93 | Y99365 | Homo sapiens | Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86. | 3890 | 100 |
| 94 | Y87231 | Homo sapiens | Human signal peptide containing protein HSPP-8 SEQ ID NO:8. | 1031 | 100 |
| 95 | AF227741 | Rattus norvegicus | protein kinase WNK1 | 2428 | 95 |
| 96 | AF227741 | Rattus norvegicus | protein kinase WNK1 | 1961 | 94 |
| 97 | Y92513 | Homo sapiens | Human OXRE-10. | 1626 | 100 |
| 98 | AL021366 | Homo sapiens | cICK0721Q.3 (Kinesin related protein) | 3423 | 100 |
| 99 | AC005783 | Homo sapiens | R33083_1 | 1974 | 99 |
| 100 | Y95293 | Homo sapiens | Human GEF containing NEK-like kinase substrate sGNK. | 4092 | 99 |
| 101 | AL118501 | Homo sapiens | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 1509 | 100 |
| 102 | AJ006267 | Homo sapiens | ClpX-like protein | 3233 | 100 |
| 103 | AF100753 | Homo sapiens | ancient ubiquitous 46 kDa protein AUP1 | 2042 | 96 |
| 104 | AB015982 | Homo sapiens | serine/threonine kinase | 4718 | 100 |
| 105 | AF151074 | Homo sapiens | HSPC240 | 831 | 64 |
| 106 | M35522 | Canis familiaris | GTP-binding protein (rab7) | 354 | 50 |
| 107 | R99800 | Homo sapiens | NTII-1 nerve protein, facilitates regeneration of nerve cells. | 2337 | 93 |
| 108 | AF125533 | Homo sapiens | NADH-cytochrome b5 reductase isoform | 1290 | 93 |
| 109 | AC005614 | Homo sapiens | P23269_2 | 3369 | 99 |
| 110 | AF064729 | Homo sapiens | RAN binding protein 16 | 3285 | 100 |
| 111 | X52425 | Homo sapiens | interleukin 4 receptor | 4496 | 100 |
| 112 | Y41686 | Homo sapiens | Human PRO274 protein sequence. | 2285 | 100 |
| 113 | W15506 | Homo sapiens | Mitogen activating protein kinase ERK1. | 1991 | 100 |
| 114 | Y71071 | Homo sapiens | Human membrane transport protein, MTRP-16. | 1190 | 99 |
| 115 | AL049548 | Homo sapiens | dJ398G3.1 (ortholog of rat CPG2) | 3497 | 99 |
| 116 | AF189817 | Mus musculus | evectin-2 | 1124 | 90 |
| 117 | W30891 | Homo | Human cytostatin III protein. | 715 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | IDENTITY |
|------------|------------------|--------------------------|---|----------------------|----------|
| | | sapiens | | | |
| 118 | AF116618 | Homo sapiens | PRO1038 | 1469 | 100 |
| 119 | Y08915 | Homo sapiens | alpha 4 protein. | 1748 | 100 |
| 120 | AF098070 | Drosophila melanogaster | Lis1 homolog | 192 | 39 |
| 121 | AF052432 | Homo sapiens | katanin p80 subunit | 181 | 37 |
| 122 | Y70743 | Homo sapiens | PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling. | 2637 | 98 |
| 123 | AF083246 | Homo sapiens | HSPC028 | 2132 | 100 |
| 124 | Y27096 | Homo sapiens | Human viral receptor protein (ACVRP). | 833 | 99 |
| 125 | M63109 | Leishmania major | glycoprotein 96-92 | 172 | 27 |
| 126 | U75467 | Drosophila melanogaster | Atu | 935 | 36 |
| 127 | Z68220 | Caenorhabditis elegans | Similarity to Human ADP/ATP carrier protein | 438 | 43 |
| 128 | AF095927 | Rattus norvegicus | protein phosphatase 2C | 1927 | 94 |
| 129 | W92958 | Homo sapiens | Human zsig44 protein. | 463 | 100 |
| 130 | AF115391 | Lactobacillus sakei | ribokinase RbsK | 508 | 37 |
| 131 | X93498 | Homo sapiens | 21-Glutamic Acid-Rich Protein | 1250 | 100 |
| 132 | X93498 | Homo sapiens | 21-Glutamic Acid-Rich Protein | 916 | 87 |
| 133 | W52811 | Homo sapiens | Human DBI/ACBP-like protein (DBIH). | 705 | 97 |
| 134 | Y84444 | Homo sapiens | Amino acid sequence of a human RNA-associated protein. | 3230 | 100 |
| 135 | M69181 | Homo sapiens | non-muscle myosin B | 189 | 20 |
| 136 | W74882 | Homo sapiens | Human secreted protein encoded by gene 154 clone HE6FL83. | 480 | 100 |
| 137 | W78200 | Homo sapiens | Human secreted protein encoded by gene 75 clone HHGAU81. | 855 | 99 |
| 138 | AL033520 | Homo sapiens | dJ349A12.1 (similar to KIAA0701 protein) | 424 | 39 |
| 139 | AF020261 | Santalum album | proline rich protein | 119 | 30 |
| 140 | X70394 | Homo sapiens | zinc finger protein | 1634 | 100 |
| 141 | Y06439 | Homo sapiens | Human protease HUPM-8. | 936 | 100 |
| 142 | Z68493 | Caenorhabditis elegans | predicted using Genefinder | 365 | 42 |
| 143 | AB018107 | Arabidopsis thaliana | ADP-ribosylation factor-like protein | 596 | 65 |
| 144 | AF161483 | Homo sapiens | HSPC134 | 580 | 51 |
| 145 | Y84902 | Homo sapiens | A human proliferation and apoptosis related protein. | 480 | 100 |
| 146 | AB004906 | Ipomoea purpurea | transposase | 146 | 20 |
| 147 | AC007357 | Arabidopsis thaliana | F3F19.18 | 647 | 31 |
| 148 | W75155 | Homo sapiens | Human secreted protein encoded by gene 41 clone HNTME13. | 1494 | 98 |
| 149 | AF056490 | Homo sapiens | cAMP-specific phosphodiesterase 8A | 3710 | 99 |
| 150 | Y58171 | Homo sapiens | Human hydrolase homologue HHH-7. | 785 | 99 |
| 151 | U10397 | Saccharomyces cerevisiae | Yhr148wp | 515 | 53 |
| 152 | X73478 | Homo sapiens | phosphotyrosyl phosphatase activator | 1719 | 99 |
| 153 | AL049697 | Homo sapiens | dJ382I10.5.1 (novel protein | 2034 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|--|----------------------|------------|
| | | | similar to arginyl-tRNA) | | |
| 154 | AF169802 | Homo sapiens | cytochrome b5 reductase b5R.2 | 1455 | 99 |
| 155 | X94703 | Homo sapiens | rab28 | 1126 | 99 |
| 156 | Y25716 | Homo sapiens | Human secreted protein encoded from gene 6. | 1471 | 100 |
| 158 | W77404 | Homo sapiens | Secreted salivary polypeptide zsig32. | 937 | 100 |
| 159 | Y17248 | Homo sapiens | Human protein kinase inhibitor-2 (PKI-2). | 383 | 100 |
| 160 | J04970 | Homo sapiens | carboxypeptidase M precursor | 2395 | 100 |
| 161 | W54040 | Homo sapiens | Human interferon-inducible protein, HIFI. | 484 | 98 |
| 162 | AL022724 | Homo sapiens | dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1) | 1357 | 100 |
| 163 | AF125535 | Homo sapiens | pp21 homolog | 193 | 45 |
| 164 | G03632 | Homo sapiens | Human secreted protein, SEQ ID NO: 7713. | 463 | 97 |
| 165 | AJ250839 | Homo sapiens | serine/threonine protein kinase | 1442 | 71 |
| 166 | L09649 | Zymomonas mobilis | zm2 | 173 | 37 |
| 167 | Y73337 | Homo sapiens | HTRM clone 1944530 protein sequence. | 1204 | 100 |
| 168 | W88645 | Homo sapiens | Secreted protein encoded by gene 112 clone HUKFC71. | 1084 | 100 |
| 169 | AF214731 | Homo sapiens | ATP-dependent RNA helicase | 4402 | 100 |
| 170 | AE000871 | Methanobacterium thermoautotrophicum | conserved protein | 166 | 27 |
| 171 | Y27684 | Homo sapiens | Human secreted protein encoded by gene No. 118. | 821 | 100 |
| 172 | AF226044 | Homo sapiens | HSNFRK | 2904 | 100 |
| 173 | AJ245946 | Homo sapiens | neuroglobin | 779 | 100 |
| 174 | D43949 | Homo sapiens | This gene is novel. | 3202 | 100 |
| 175 | Y07923 | Homo sapiens | GTP-binding protein | 1205 | 100 |
| 176 | W90338 | Homo sapiens | Human DP1 homologue protein. | 966 | 100 |
| 177 | Y41675 | Homo sapiens | Human channel-related molecule HCRM-3. | 1122 | 100 |
| 178 | Y41674 | Homo sapiens | Human channel-related molecule HCRM-2. | 936 | 99 |
| 179 | AF220492 | Homo sapiens | krueppel-like zinc finger protein HZF2 | 4100 | 99 |
| 180 | X03084 | Homo sapiens | Clq B-chain precursor | 1240 | 100 |
| 181 | U57344 | Mus musculus | Meis3 | 1813 | 89 |
| 183 | U57344 | Mus musculus | Meis3 | 1743 | 86 |
| 184 | U57344 | Mus musculus | Meis3 | 1070 | 86 |
| 185 | AF033120 | Homo sapiens | p53 regulated PA26-T2 nuclear protein | 1389 | 58 |
| 186 | AF200357 | Mus musculus | pantothenate kinase 1 beta | 1605 | 82 |
| 187 | W75058 | Homo sapiens | Human secreted protein encoded by gene 2 clone HLDBG33. | 1188 | 99 |
| 188 | AJ292529 | Homo sapiens | suppressor of sterile four 1 | 2424 | 100 |
| 190 | X54134 | Homo sapiens | protein-tyrosine phosphatase | 3705 | 100 |
| 191 | Y22203 | Homo sapiens | Human calcium-binding phosphoprotein, CBPP-1, protein sequence. | 1083 | 99 |
| 192 | W63692 | Homo sapiens | Human secreted protein 12. | 1975 | 100 |
| 193 | W87772 | Homo sapiens | Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide. | 2605 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 194 | AF084259 | Mus musculus | bromodomain-containing protein BP75 | 693 | 54 |
| 195 | Y00752 | Rattus norvegicus | serine dehydratase (AA 1 - 327) | 994 | 61 |
| 196 | W95349 | Homo sapiens | Human foetal brain secreted protein fh170_7. | 2596 | 100 |
| 197 | AB028859 | Homo sapiens | hDj9 | 1890 | 100 |
| 198 | W95633 | Homo sapiens | Homo sapiens secreted protein gene clone hm236_1. | 1614 | 100 |
| 199 | Y44277 | Homo sapiens | Human nucleic acid methylase-2. | 2096 | 99 |
| 200 | AB030039 | Homo sapiens | hPACPL1 | 2258 | 100 |
| 201 | X54162 | Homo sapiens | 64 Kd autoantigen | 2918 | 99 |
| 202 | G02061 | Homo sapiens | Human secreted protein, SEQ ID NO: 6142. | 558 | 99 |
| 203 | X13885 | Nicotiana tabacum | extensin (AA 1-620) | 185 | 33 |
| 204 | J04204 | Bos taurus | 32 kd accessory protein | 1837 | 100 |
| 205 | J04204 | Bos taurus | 32 kd accessory protein | 1101 | 100 |
| 207 | Y87283 | Homo sapiens | Human signal peptide containing protein HSPP-60 SEQ ID NO:60. | 1318 | 100 |
| 208 | Y02860 | Homo sapiens | Fragment of human secreted protein encoded by gene 65. | 936 | 98 |
| 209 | AL121889 | Homo sapiens | dJ1076E17.1 (XIAA0823 protein (continues in AL023803)) | 694 | 54 |
| 210 | AF226732 | Homo sapiens | NPD007 | 1345 | 76 |
| 211 | X66295 | Mus musculus | C1q C chain | 970 | 73 |
| 212 | Z29328 | Homo sapiens | Ubiquitin-conjugating enzyme UbcH2 | 966 | 100 |
| 213 | Z29328 | Homo sapiens | Ubiquitin-conjugating enzyme UbcH2 | 542 | 98 |
| 214 | AJ002030 | Homo sapiens | progesterone binding protein | 1163 | 100 |
| 215 | X70649 | Homo sapiens | member of DEAD box protein family | 3933 | 100 |
| 216 | AF250558 | Homo sapiens | claudin-2 | 1169 | 99 |
| 217 | AL021453 | Homo sapiens | dJ821D11.1 (PUTATIVE protein) | 259 | 100 |
| 218 | Y08565 | Homo sapiens | UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase | 3331 | 99 |
| 219 | Y94452 | Homo sapiens | Human inflammation associated protein | 2067 | 100 |
| 220 | AL035521 | Arabidopsis thaliana | putative protein | 315 | 42 |
| 221 | AL031786 | Schizosaccharomyces pombe | putative proline-trna synthetase | 811 | 41 |
| 222 | AL109736 | Schizosaccharomyces pombe | WD repeat protein | 626 | 40 |
| 223 | X52493 | Glycine max | DNA-directed RNA polymerase | 136 | 23 |
| 224 | AL035659 | Homo sapiens | dJ979N1.1 (dJ979N1.1) | 5199 | 98 |
| 225 | AB032401 | Mus musculus | mmDj4 | 1761 | 92 |
| 226 | AB032401 | Mus musculus | mmDj4 | 1988 | 92 |
| 227 | X83502 | Saccharomyces cerevisiae | J1007 | 112 | 26 |
| 228 | X83502 | Saccharomyces cerevisiae | J1007 | 79 | 25 |
| 229 | AF143723 | Homo sapiens | heat shock protein HSP60 | 2557 | 99 |
| 230 | Y66677 | Homo sapiens | Membrane-bound protein PRO828. | 982 | 100 |
| 231 | AB027466 | Homo sapiens | spondin 2 | 1756 | 99 |
| 232 | W95634 | Homo sapiens | Homo sapiens secreted protein. | 1391 | 100 |
| 233 | W00365 | Homo sapiens | Human cyclin B1. | 2218 | 99 |
| 234 | Y53762 | Homo sapiens | A GTP-binding polypeptide | 1017 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|---|----------------------|------------|
| | | | designated RAQ. | | |
| 235 | Z50749 | Homo sapiens | yeast sds22 homolog | 1800 | 100 |
| 236 | Z50749 | Homo sapiens | yeast sds22 homolog | 1754 | 98 |
| 237 | AB026491 | Homo sapiens | PICK1 | 2137 | 100 |
| 238 | AJ270205 | Entodinium caudatum | putative phosphatidylinositol-4-phosphate 5-kinase | 114 | 37 |
| 239 | AB030189 | Mus musculus | contains transmembrane (TM) region and ATP binding region | 710 | 93 |
| 240 | W56538 | Homo sapiens | Human hedgehog interacting protein (HIP). | 3785 | 99 |
| 241 | W56538 | Homo sapiens | Human hedgehog interacting protein (HIP). | 3436 | 99 |
| 242 | AF155107 | Homo sapiens | NY-REN-37 antigen | 996 | 99 |
| 243 | AF155107 | Homo sapiens | NY-REN-37 antigen | 1005 | 100 |
| 244 | AL031320 | Homo sapiens | dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase) | 763 | 99 |
| 245 | U37026 | Rattus norvegicus | sodium channel beta 2 subunit | 162 | 30 |
| 246 | AL078599 | Homo sapiens | dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086)) | 2391 | 98 |
| 247 | U32274 | Saccharomyces cerevisiae | Ydr386wp; CAI: 0.12 | 191 | 37 |
| 248 | Y41719 | Homo sapiens | Human PRO864 protein sequence. | 1879 | 100 |
| 249 | AB029434 | Homo sapiens | ghrelin precursor | 611 | 100 |
| 250 | X97831 | Rattus norvegicus | carnitine/acylcarnitine carrier protein | 246 | 38 |
| 251 | W80993 | Homo sapiens | Human RIP-interacting factor RIF. | 1724 | 100 |
| 252 | Y94873 | Homo sapiens | Human protein clone HP02632. | 1876 | 100 |
| 253 | W59878 | Homo sapiens | Amino acid sequence of the cDNA clone AIF-2 (HEBGM49). | 765 | 100 |
| 254 | AL354533 | Leishmania major | possible adenylate kinase | 265 | 34 |
| 255 | AF233322 | Mus musculus | zinc transporter like 2 | 1916 | 95 |
| 256 | Y78113 | Homo sapiens | Human cytokine signal regulator CKSR-1 SEQ ID NO:1. | 2247 | 99 |
| 257 | AL035539 | Arabidopsis thaliana | putative amino acid transport protein | 390 | 27 |
| 258 | W74787 | Homo sapiens | Human secreted protein encoded by gene 58 clone HHFHN61. | 1171 | 100 |
| 259 | AL035689 | Homo sapiens | dJ187J11.1 (novel protein similar to protein kinase C inhibitors) | 974 | 100 |
| 260 | AE000909 | Methanobacterium thermoautotrophicum | serine/threonine protein kinase related protein | 363 | 30 |
| 261 | AL050131 | Homo sapiens | hypothetical protein | 626 | 100 |
| 262 | AF019661 | Mus musculus | zeta proteasome chain; PSMA5 | 1214 | 100 |
| 263 | AL035593 | Homo sapiens | dJ310J6.1 (novel protein) | 821 | 100 |
| 264 | AL022318 | Homo sapiens | bK150C2.3 (PUTATIVE novel protein similar to APOBEC1) | 1072 | 100 |
| 265 | AF205940 | Homo sapiens | endomucin | 1289 | 100 |
| 266 | AL023583 | Homo sapiens | dJ500L14.1 (novel protein) | 789 | 100 |
| 267 | AL034548 | Homo sapiens | dJ1103G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW) | 1888 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH- WATERMAN SCORE | IDENTITY |
|------------------|---------------------|----------------------|---|-----------------------------|----------|
| 268 | AF161470 | Homo sapiens | HSPC121 | 1884 | 98 |
| 269 | AF161470 | Homo sapiens | HSPC121 | 1232 | 96 |
| 270 | X90763 | Homo sapiens | HMa5 hair keratin type I intermediate filament | 2190 | 99 |
| 271 | AF207600 | Homo sapiens | ethanolamine kinase | 1952 | 100 |
| 272 | M32334 | Homo sapiens | intercellular adhesion molecule 2 | 1436 | 100 |
| 273 | AF161483 | Homo sapiens | HSPC134 | 663 | 61 |
| 274 | Y53052 | Homo sapiens | Human secreted protein clone df202_3 protein sequence SEQ ID NO:110. | 587 | 100 |
| 276 | Y77576 | Homo sapiens | Human cytoskeletal protein (HCYT) (clone 2195418). | 762 | 100 |
| 277 | AF077042 | Homo sapiens | 30S ribosomal protein S7 homolog | 1269 | 100 |
| 278 | Y94907 | Homo sapiens | Human secreted protein clone ca106_19x protein sequence SEQ ID NO:20. | 1619 | 98 |
| 279 | Y68788 | Homo sapiens | Amino acid sequence of a human phosphorylation effector PHSP-20. | 2801 | 99 |
| 280 | Z75134 | Canis familiaris | rod transducin | 1816 | 100 |
| 281 | Z75134 | Canis familiaris | rod transducin | 1718 | 96 |
| 282 | AF249873 | Homo sapiens | muscle-specific protein | 1395 | 100 |
| 283 | AL050007 | Homo sapiens | hypothetical protein | 405 | 98 |
| 284 | AF201931 | Homo sapiens | DC1 | 1859 | 99 |
| 285 | AF156102 | Homo sapiens | ELL complex EAP30 subunit | 1318 | 99 |
| 286 | Y35897 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 146. | 1250 | 99 |
| 287 | U88964 | Homo sapiens | HEM45 | 923 | 100 |
| 288 | AL050143 | Homo sapiens | hypothetical protein | 598 | 100 |
| 289 | AJ011098 | Homo sapiens | telethonin | 574 | 100 |
| 290 | Y66724 | Homo sapiens | Membrane-bound protein PRO836. | 2321 | 100 |
| 291 | AF034801 | Homo sapiens | liprin-alpha4 | 2565 | 98 |
| 292 | AF034801 | Homo sapiens | liprin-alpha4 | 2590 | 100 |
| 293 | AL049851 | Homo sapiens | dJ889J22B.1 (novel protein (isoform 1)) | 1738 | 100 |
| 294 | Y73348 | Homo sapiens | HTRM clone 839651 protein sequence. | 1245 | 99 |
| 295 | L11672 | Homo sapiens | zinc finger protein | 1694 | 44 |
| 296 | AL035423 | Homo sapiens | dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1)) | 1024 | 79 |
| 297 | AF198532 | Homo sapiens | lymphoid enhancer binding factor-1 | 2173 | 100 |
| 298 | AF161417 | Homo sapiens | HSPC299 | 1147 | 85 |
| 299 | AF159141 | Homo sapiens | breast cancer metastasis-suppressor 1 | 1236 | 99 |
| 300 | U26397 | Rattus norvegicus | inositol polyphosphate 4-phosphatase | 160 | 30 |
| 301 | AF036145 | Homo sapiens | meningioma-expressed antigen 5 | 3458 | 100 |
| 302 | Z82022 | Homo sapiens | GlcNac-1-P transferase | 2067 | 99 |
| 303 | AF269232 | Mus musculus | butyrophilin-like protein BUTR-1 | 271 | 50 |
| 304 | AJ222644 | Arabidopsis thaliana | asparaginyl-tRNA synthetase | 659 | 50 |
| 305 | AF054180 | Homo sapiens | hematopoietic cell derived zinc finger protein | 351 | 79 |
| 306 | AJ272079 | Homo sapiens | APOBEC-1 stimulating protein | 3056 | 100 |
| 308 | Y44486 | Homo sapiens | Human GPRW receptor polypeptide. | 1721 | 100 |
| 309 | AJ131891 | Homo sapiens | DNA polymerase mu | 2598 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
| 310 | AF293335 | Homo sapiens | p30 DBC | 1248 | 92 |
| 311 | AF176525 | Mus musculus | F-box protein FBL12 | 1501 | 93 |
| 312 | X57802 | Homo sapiens | immunoglobulin lambda light chain | 959 | 81 |
| 313 | Z36715 | Homo sapiens | Net | 2048 | 98 |
| 314 | AF161532 | Homo sapiens | HSPC047 | 727 | 100 |
| 315 | AF208068 | Homo sapiens | kelch-like protein KLHL3a | 3046 | 100 |
| 316 | Y66666 | Homo sapiens | Membrane-bound protein PRO1013. | 1166 | 100 |
| 317 | Y29666 | Homo sapiens | Human Ras protein RAPR-1. | 1253 | 98 |
| 318 | AJ387747 | Homo sapiens | sialin | 2614 | 99 |
| 319 | AF161362 | Homo sapiens | HSPC099 | 224 | 40 |
| 320 | Y68773 | Homo sapiens | Amino acid sequence of a human phosphorylation effector FHSP-5. | 2243 | 99 |
| 321 | AJ238379 | Homo sapiens | putative TH1 protein | 3013 | 100 |
| 322 | AB040812 | Homo sapiens | protein kinase PAK5 | 3792 | 99 |
| 323 | Y95013 | Homo sapiens | Human secreted protein vc48_1, SEQ ID NO:66. | 913 | 100 |
| 324 | Y13381 | Homo sapiens | Amino acid sequence of protein PRO271. | 1976 | 100 |
| 325 | Y94944 | Homo sapiens | Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94. | 2305 | 98 |
| 326 | Y76884 | Homo sapiens | Retinoblastoma binding protein-7sequence. | 6728 | 99 |
| 327 | AF198532 | Homo sapiens | lymphoid enhancer binding factor-1 | 2173 | 100 |
| 328 | Z78013 | Caenorhabditis elegans | Similarity to Drosophila Cadherin-related tumor suppressor | 569 | 33 |
| 329 | AF212921 | Mus musculus | MMTV receptor variant 1 | 484 | 94 |
| 330 | Z75330 | Homo sapiens >R65207 R65207 02-MAR-1995 27-AUG-1993 Human stromalin-1. [Homo sapiens] | nuclear protein SA-1 | 6492 | 99 |
| 331 | AL008583 | Homo sapiens | dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE) | 2133 | 99 |
| 332 | Y36104 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 489. | 310 | 41 |
| 333 | AJ271669 | Homo sapiens | putative sialoglycoprotease | 1747 | 100 |
| 334 | AF156598 | Mus musculus | p53-regulated DDA3 | 997 | 64 |
| 335 | M99058 | Eimeria maxima | em100 gene is homologous the Eimeria tenella gene et100 | 154 | 26 |
| 336 | Y85564 | Homo sapiens | Human homologue of UNC-53 (Hs-UNC-53/1) sequence. | 3386 | 97 |
| 337 | Y85564 | Homo sapiens | Human homologue of UNC-53 (Hs-UNC-53/1) sequence. | 2602 | 94 |
| 338 | Y85564 | Homo sapiens | Human homologue of UNC-53 (Hs-UNC-53/1) sequence. | 3447 | 98 |
| 339 | Z66561 | Caenorhabditis elegans | Similarity to Human rab13 protein (PIR Acc. No. A49647). | 716 | 34 |
| 340 | AB021643 | Homo sapiens | gonadotropin inducible transcription repressor-3 | 2761 | 99 |
| 341 | G01946 | Homo sapiens | Human secreted protein, SEQ ID NO: 6027. | 465 | 98 |
| 342 | AF020591 | Homo sapiens | zinc finger protein | 1091 | 48 |
| 343 | L29154 | Homo sapiens | immunoglobulin heavy chain | 439 | 84 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| | | | VDJ region | | |
| 344 | U10281 | Sus scrofa | gastric mucin | 279 | 24 |
| 345 | AK000404 | Homo sapiens | unnamed protein product | 1177 | 99 |
| 346 | L22557 | Rattus norvegicus | calmodulin-binding protein | 1949 | 84 |
| 347 | L22557 | Rattus norvegicus | calmodulin-binding protein | 2363 | 91 |
| 348 | AL049481 | Arabidopsis thaliana | AIG1-like protein | 316 | 30 |
| 350 | AJ251516 | Mus musculus | cysteine and histidine-rich protein | 1460 | 99 |
| 351 | AK024477 | Homo sapiens | FLJ00070 protein | 1773 | 100 |
| 352 | U50133 | Homo sapiens | ankyrin | 502 | 33 |
| 353 | AK000625 | Homo sapiens | unnamed protein product | 721 | 100 |
| 354 | AF161420 | Homo sapiens | HSPC302 | 2623 | 97 |
| 355 | AJ010014 | Homo sapiens | M96A protein | 1269 | 47 |
| 356 | AF151029 | Homo sapiens | HSPC195 | 941 | 91 |
| 357 | AL022327 | Homo sapiens | dJ355C18.1 (KIAA0027) | 1911 | 100 |
| 358 | W78128 | Homo sapiens | Human secreted protein encoded by gene 3 clone HOSBI96. | 1117 | 100 |
| 359 | X03414 | Drosophila melanogaster | Kr polypeptide | 316 | 45 |
| 360 | AF151079 | Homo sapiens | HSPC245 | 643 | 100 |
| 361 | Y53886 | Homo sapiens | A suppressor of cytokine signalling protein designated HSCOP-6. | 530 | 41 |
| 362 | AF254741 | Drosophila melanogaster | Centaurin Gamma 1A | 681 | 46 |
| 363 | AF213465 | Homo sapiens | dual oxidase | 2016 | 100 |
| 364 | AF181562 | Homo sapiens | proSAAS | 1319 | 100 |
| 365 | AF181562 | Homo sapiens | proSAAS | 1024 | 99 |
| 366 | U73200 | Mus musculus | p116Rip | 884 | 82 |
| 367 | AF263744 | Homo sapiens | erbB2-interacting protein ERBIN | 4973 | 99 |
| 368 | U37501 | Mus musculus | laminin alpha 5 chain | 5867 | 72 |
| 369 | AF043695 | Caenorhabditis elegans | similar to the protein phosphates 2c family | 549 | 36 |
| 370 | Y73440 | Homo sapiens | Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102. | 1484 | 99 |
| 371 | AF272833 | Homo sapiens | misato | 2869 | 97 |
| 372 | AF198454 | Homo sapiens | epithelial protein lost in neoplasm beta | 3927 | 100 |
| 373 | Y73345 | Homo sapiens | HTRM clone 438283 protein sequence. | 273 | 80 |
| 374 | AF169017 | Homo sapiens | formiminotransferase cyclodeaminase | 2717 | 98 |
| 375 | A95106 | unidentified | RED ALPHA | 1202 | 99 |
| 376 | W74828 | Homo sapiens | Human secreted protein encoded by gene 100 clone HLQAB52. | 1012 | 99 |
| 377 | Y32131 | Homo sapiens | Human LYST-2 protein. | 3556 | 99 |
| 378 | M14912 | Homo sapiens | pol | 132 | 86 |
| 379 | AF090934 | Homo sapiens | PRO0518 | 382 | 100 |
| 380 | X66363 | Homo sapiens | serine/threonine protein kinase | 2499 | 100 |
| 381 | Y41699 | Homo sapiens | Human PRO703 protein sequence. | 2362 | 100 |
| 382 | AF174498 | Homo sapiens | GR AF-1 specific protein phosphatase | 7008 | 98 |
| 383 | U64608 | Caenorhabditis elegans | coded for by C. elegans cDNA yk173c12.5 | 246 | 36 |
| 384 | U50133 | Homo sapiens | ankyrin | 502 | 33 |
| 385 | AJ238520 | Homo sapiens | putative transcription factor-like nuclear regulator | 4123 | 97 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 387 | AF208845 | Homo sapiens | BM-003 | 1375 | 99 |
| 389 | X57821 | Homo sapiens | immunoglobulin lambda light chain | 797 | 76 |
| 390 | AF182404 | Homo sapiens | mitochondrial uncoupling protein 1 | 1670 | 99 |
| 391 | Y85564 | Homo sapiens | Human homologue of UNC-53 (Hs-UNC-53/1) sequence. | 3386 | 97 |
| 393 | AF178432 | Homo sapiens | SH3 protein | 3700 | 100 |
| 394 | AF229928 | Drosophila melanogaster | cytoplasmic protein 89BC | 1616 | 62 |
| 395 | AF181721 | Homo sapiens | RU2S | 2254 | 100 |
| 396 | Y69197 | Homo sapiens | Amino acid sequence of a human betaIV-spectrin protein. | 1626 | 98 |
| 397 | U48238 | Mus musculus | zinc finger protein neuro-d4 | 749 | 60 |
| 398 | AL390137 | Homo sapiens | hypothetical protein | 263 | 51 |
| 399 | AF217525 | Homo sapiens | Down syndrome cell adhesion molecule | 5337 | 60 |
| 400 | AL022599 | Schizosaccharomyces pombe | WD repeat protein | 447 | 27 |
| 401 | AC004859 | Homo sapiens | similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g1352618) | 4176 | 78 |
| 402 | AB010266 | Mus musculus | tenascin-X | 10246 | 62 |
| 403 | AL133288 | Homo sapiens | dJ671D7.1 (similar to D.melanogaster CG5986 protein) | 761 | 100 |
| 404 | Z68753 | Caenorhabditis elegans | ZC518.3b | 888 | 48 |
| 405 | Z78013 | Caenorhabditis elegans | Similarity to Drosophila Cadherin-related tumor suppressor | 569 | 33 |
| 406 | AB031230 | Homo sapiens | protein containing CXXC domain 2 | 1196 | 97 |
| 407 | AF155106 | Homo sapiens | NY-REN-36 antigen | 1168 | 100 |
| 408 | Y57945 | Homo sapiens | Human transmembrane protein HTPN-69. | 1538 | 99 |
| 409 | Z18361 | Ovis aries | trichohyalin | 184 | 30 |
| 410 | AF249744 | Homo sapiens | RhoGEF | 2733 | 100 |
| 411 | AF176529 | Mus musculus | F-box protein FBX13 | 2072 | 94 |
| 412 | AF210842 | Homo sapiens | HARP | 4880 | 100 |
| 413 | AL031658 | Homo sapiens | dJ310013.7 (novel protein similar to H. roretzi HRPET-3) | 776 | 98 |
| 414 | X57398 | Homo sapiens | pm5 protein | 6131 | 99 |
| 415 | AB029826 | Homo sapiens | 3-methylcrotonyl-CoA carboxylase biotin-containing subunit | 2961 | 99 |
| 416 | U43503 | Saccharomyces cerevisiae | Lphlp | 115 | 42 |
| 417 | AL160493 | Leishmania major | possible t26f17.21 | 239 | 35 |
| 418 | Y08100 | Homo sapiens | Human PRO331 protein. | 330 | 29 |
| 419 | U15131 | Homo sapiens | p126 | 2228 | 54 |
| 420 | AF117946 | Homo sapiens | Link guanine nucleotide exchange factor II | 2363 | 100 |
| 421 | AF190635 | Drosophila melanogaster | ankyrin 2 | 755 | 30 |
| 422 | AF302150 | Homo sapiens | phosphoinositol 3-phosphate-binding protein-2 | 1962 | 100 |
| 423 | AL137530 | Homo sapiens | hypothetical protein | 433 | 94 |
| 424 | X63753 | Homo sapiens | son-a | 7269 | 100 |
| 425 | AB027249 | Homo sapiens | MAPKK like protein kinase | 1693 | 100 |
| 426 | AF279144 | Homo sapiens | tumor endothelial marker 7 precursor | 1084 | 55 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 427 | AF279144 | Homo sapiens | tumor endothelial marker 7 precursor | 1259 | 56 |
| 428 | AE003683 | Drosophila melanogaster | CG8312 gene product | 149 | 29 |
| 429 | Y07829 | Homo sapiens | RING finger protein | 2201 | 99 |
| 430 | AF096897 | Drosophila melanogaster | pushover | 4442 | 47 |
| 431 | U41387 | Homo sapiens | Gu protein | 4021 | 99 |
| 432 | AF023674 | Homo sapiens | nephrocystin | 3783 | 100 |
| 433 | AF146760 | Homo sapiens | septin 2-like cell division control protein | 2284 | 100 |
| 434 | AB006697 | Arabidopsis thaliana | cleft lip and palate associated transmembrane protein-like | 886 | 42 |
| 437 | Y94247 | Homo sapiens | Human calcium binding protein hCBP. | 1704 | 100 |
| 438 | AB040672 | Homo sapiens | UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase | 1075 | 63 |
| 439 | AF105228 | Bos taurus | tuftelin | 285 | 33 |
| 440 | R06463 | Homo sapiens | Derived protein of clone ICA13 (ATCC 40553). | 3073 | 99 |
| 441 | X14971 | Mus musculus | alpha-adaptin (A) (AA 1-977) | 4897 | 98 |
| 442 | X53773 | Rattus norvegicus | alpha-c large chain (AA 1-938) | 3979 | 81 |
| 443 | Y66689 | Homo sapiens | Membrane-bound protein PRO1136. | 3299 | 99 |
| 444 | AC067754 | Arabidopsis thaliana | unknown protein; 20348-23707 | 114 | 33 |
| 445 | AF229032 | Mus musculus | pIL | 2077 | 93 |
| 446 | AF056035 | Rattus norvegicus | s-nexilin | 2662 | 85 |
| 447 | AF132484 | Mus musculus | unknown | 478 | 51 |
| 448 | W89024 | Homo sapiens | Polypeptide fragment encoded by gene 156. | 528 | 45 |
| 449 | AF161445 | Homo sapiens | HSPC327 | 1606 | 100 |
| 450 | Z68753 | Caenorhabditis elegans | ZC518.3b | 951 | 49 |
| 451 | W39160 | Homo sapiens | Human partial complement factor H protein fragment 3. | 155 | 32 |
| 452 | W85727 | Homo sapiens | Novel protein (Clone BM46_10). | 2799 | 99 |
| 453 | Y53629 | Homo sapiens | A bone marrow secreted protein designated BMS115. | 2810 | 100 |
| 454 | D87438 | Homo sapiens | Similar to a C.elegans protein in cosmid C14H10 | 4069 | 100 |
| 455 | AF240468 | Homo sapiens | nicastatin | 3687 | 100 |
| 456 | Z15005 | Homo sapiens | CENP-E | 13305 | 99 |
| 457 | M59216 | Homo sapiens | gamma-aminobutyric acid receptor beta-1 subunit | 2477 | 100 |
| 458 | Y73467 | Homo sapiens | Human secreted protein clone yd61.1 protein sequence SEQ ID NO:156. | 966 | 100 |
| 459 | W67824 | Homo sapiens | Human secreted protein encoded by gene 18 clone HSLFM29. | 535 | 100 |
| 460 | AF163151 | Homo sapiens | dentin sialophosphoprotein precursor | 279 | 19 |
| 461 | D87446 | Homo sapiens | Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) | 9196 | 99 |
| 462 | G04044 | Homo sapiens | Human secreted protein, SEQ ID NO: 8125. | 486 | 93 |
| 463 | AC002398 | Homo sapiens | F25965_1 | 1018 | 100 |
| 464 | AF064856 | Rattus sp. | 7acomp protein | 1845 | 84 |
| 465 | AF223408 | Homo sapiens | B99 | 3686 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 466 | AF223408 | Homo sapiens | B99 | 2878 | 87 |
| 467 | AF104415 | Mus musculus | gene trap locus-13 | 6336 | 91 |
| 468 | U53450 | Rattus norvegicus | Jun dimerization protein 1 JDP-1 | 196 | 49 |
| 469 | AL031297 | Homo sapiens | dJ97220.1 (novel gene) | 3564 | 99 |
| 470 | AF257077 | Homo sapiens | eukaryotic translation initiation factor EIF2B subunit 3 | 1274 | 95 |
| 471 | L28125 | Podospora anserina | beta transducin-like protein | 284 | 38 |
| 472 | Y84903 | Homo sapiens | A human proliferation and apoptosis related protein. | 2337 | 100 |
| 473 | AF144237 | Homo sapiens | LOMP protein | 252 | 44 |
| 474 | Y71213 | Homo sapiens | Human irritable bowel disease related polypeptide IMX39. | 838 | 100 |
| 475 | Y95006 | Homo sapiens | Human secreted protein ve13_1, SEQ ID NO:52. | 3411 | 100 |
| 476 | D38549 | Homo sapiens | hal025 is new | 6533 | 99 |
| 477 | AF241230 | Homo sapiens | TAK1-binding protein 2 | 3656 | 100 |
| 478 | AL031534 | Schizosaccharomyces pombe | putative asparagine synthase | 482 | 40 |
| 479 | L28125 | Podospora anserina | beta transducin-like protein | 233 | 26 |
| 480 | AF161544 | Homo sapiens | HSPC059 | 434 | 77 |
| 481 | AJ238248 | Homo sapiens | centaurin beta2 | 3986 | 99 |
| 482 | Z38061 | Saccharomyces cerevisiae | mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3) | 295 | 23 |
| 483 | AF161381 | Homo sapiens | HSPC263 | 1404 | 100 |
| 484 | AF223468 | Homo sapiens | AD021 protein | 1314 | 100 |
| 486 | X57527 | Homo sapiens | alpha 1(VIII) collagen | 4166 | 99 |
| 487 | Y19062 | Homo sapiens | 39k3 protein | 2475 | 100 |
| 488 | Y73373 | Homo sapiens | HTRM clone 921803 protein sequence. | 555 | 56 |
| 489 | AL021918 | Homo sapiens | b34f8.1 (Kruppel related Zinc Finger protein 184) | 4184 | 100 |
| 490 | X53773 | Rattus norvegicus | alpha-c large chain (AA 1-938) | 4675 | 97 |
| 491 | U52426 | Homo sapiens | GOK | 1459 | 59 |
| 492 | AL359773 | Leishmania major | possible threonine synthase | 702 | 45 |
| 493 | AF226614 | Homo sapiens | ferroportin1 | 2929 | 100 |
| 494 | Z93241 | Homo sapiens | dJ222E13.1 (novel protein with some similarity to Drosophila KRAKEN) | 513 | 96 |
| 495 | AF036977 | Homo sapiens | unknown | 1812 | 100 |
| 496 | U93564 | Homo sapiens | p40 | 133 | 45 |
| 497 | Y91405 | Homo sapiens | Human secreted protein sequence encoded by gene 2 SEQ ID NO:126. | 357 | 100 |
| 498 | AF069781 | Drosophila melanogaster | Bem46-like protein | 653 | 43 |
| 499 | Y16601 | Homo sapiens | Human cell-cycle phosphoprotein CECYP-2. | 1658 | 98 |
| 500 | X70944 | Homo sapiens | PTB-associated splicing factor | 3883 | 100 |
| 501 | AF027503 | Mus musculus | putative membrane-associated guanylate kinase 1 | 205 | 36 |
| 502 | AF282874 | Homo sapiens | nectin 3; PRR3 | 2856 | 99 |
| 503 | AJ249732 | Homo sapiens | G8 protein | 669 | 100 |
| 504 | AF208861 | Homo sapiens | BM-019 | 1629 | 100 |
| 505 | L09708 | Homo sapiens | complement component C2 | 4022 | 100 |
| 507 | X66285 | Mus musculus | HCl ORF | 115 | 43 |
| 508 | D00189 | Rattus norvegicus | Na ⁺ , K ⁺ -ATPase alpha-subunit | 5227 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|---|----------------------|------------|
| 509 | Y94971 | Homo sapiens | Human secreted protein clone fa171_1 protein sequence SEQ ID NO:148. | 2176 | 100 |
| 510 | AB019038 | Homo sapiens | beta-1,4 mannosyltransferase | 781 | 77 |
| 511 | AB019038 | Homo sapiens | beta-1,4 mannosyltransferase | 1347 | 100 |
| 512 | AB019038 | Homo sapiens | beta-1,4 mannosyltransferase | 1520 | 99 |
| 513 | X84908 | Homo sapiens | phosphorylase kinase | 5729 | 99 |
| 514 | X52851 | Homo sapiens | peptidylprolyl isomerase | 650 | 76 |
| 515 | AF186084 | Homo sapiens | epidermal growth factor repeat containing protein | 3046 | 99 |
| 516 | G03602 | Homo sapiens | Human secreted protein, SEQ ID NO: 7683. | 505 | 99 |
| 517 | U04706 | Bos taurus | 50 kDa protein | 1749 | 77 |
| 518 | G00653 | Homo sapiens | Human secreted protein, SEQ ID NO: 4734. | 530 | 100 |
| 519 | AF161475 | Homo sapiens | HSPC126 | 1368 | 100 |
| 520 | Y99366 | Homo sapiens | Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88. | 3394 | 97 |
| 521 | AF266852 | Homo sapiens | PTPLA | 1295 | 100 |
| 522 | AE000995 | Archaeoglobus fulgidus | chromosome segregation protein (smc1) | 153 | 20 |
| 523 | AF062249 | Homo sapiens | immunoglobulin heavy chain variable region | 605 | 97 |
| 524 | AJ223830 | Rattus norvegicus | ARE1 | 2950 | 98 |
| 525 | W01535 | Homo sapiens | Cellular homologue of the SV40 large T antigen. | 1276 | 83 |
| 526 | AF145658 | Drosophila melanogaster | BcDNA.GH10229 | 320 | 33 |
| 527 | AF112213 | Homo sapiens | putative Rab5-interacting protein | 524 | 79 |
| 528 | D49387 | Homo sapiens | NADP dependent leukotriene b4 12-hydroxydehydrogenase | 1616 | 100 |
| 529 | Y30819 | Homo sapiens | Human secreted protein encoded from gene 9. | 328 | 32 |
| 530 | AL079335 | Homo sapiens | dJ132F21.3 (72.1 kDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induce MG11.) | 1059 | 99 |
| 531 | Y91506 | Homo sapiens | Human secreted protein sequence encoded by gene 56 SEQ ID NO:179. | 1159 | 98 |
| 532 | X76116 | Caenorhabditis elegans | carrier protein (c2) | 576 | 50 |
| 533 | X76116 | Caenorhabditis elegans | carrier protein (c2) | 506 | 50 |
| 534 | X12966 | Homo sapiens | 3-oxoacyl-CoA thiolase propeptide (424 AA) | 1972 | 100 |
| 535 | Y09267 | Homo sapiens | flavin-containing monooxygenase 2 | 2486 | 100 |
| 536 | Z11773 | Homo sapiens | SRE-ZBP | 2201 | 99 |
| 537 | D84224 | Homo sapiens | methionyl tRNA synthetase | 4741 | 99 |
| 538 | D84224 | Homo sapiens | methionyl tRNA synthetase | 3887 | 99 |
| 539 | D84224 | Homo sapiens | methionyl tRNA synthetase | 2933 | 96 |
| 540 | D84224 | Homo sapiens | methionyl tRNA synthetase | 4529 | 99 |
| 541 | J03244 | Bos taurus | H+ ATPase 31kDa subunit (EC 3.6.1.3) | 848 | 77 |
| 542 | Y92514 | Homo sapiens | Human OXRE-11. | 2301 | 99 |
| 543 | AF221712 | Homo sapiens | Smad- and Olf-interacting zinc finger protein | 2151 | 61 |
| 544 | AE000919 | Methanobacterium thermoautotrophicum | conserved protein | 207 | 38 |
| 545 | A06669 | synthetic construct | preTGF-beta1 | 2070 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 546 | Y02698 | Homo sapiens | Human secreted protein encoded by gene 49 clone HTPCS60. | 854 | 98 |
| 547 | AF112205 | Homo sapiens | WSB-1 protein | 2275 | 100 |
| 548 | X60271 | Mus musculus | c-rel | 2264 | 74 |
| 549 | AC016827 | Arabidopsis thaliana | putative GTPase | 810 | 42 |
| 550 | Y70400 | Homo sapiens | Human cell-signalling protein-2. | 429 | 68 |
| 551 | AB048365 | Homo sapiens | NEDD4-like ubiquitin ligase 1 | 8290 | 99 |
| 552 | Y57880 | Homo sapiens | Human transmembrane protein HTPMN-4. | 1112 | 95 |
| 553 | AF119855 | Homo sapiens | PRO1847 | 265 | 67 |
| 554 | M17236 | Homo sapiens | MHC HLA-DQ alpha precursor | 1332 | 100 |
| 555 | AL078468 | Arabidopsis thaliana | putative protein | 540 | 40 |
| 556 | AC006963 | Homo sapiens | similar to Kelch proteins; similar to BAA77027 (PID:g4650844) | 515 | 44 |
| 557 | AK024487 | Homo sapiens | FLJ00086 protein | 1623 | 98 |
| 558 | M12140 | Homo sapiens | pol gene protein; Xxx | 117 | 48 |
| 559 | W74825 | Homo sapiens | Human secreted protein encoded by gene 97 clone HAQBF73. | 225 | 56 |
| 560 | X56681 | Homo sapiens | jund protein | 373 | 88 |
| 561 | AF003136 | Caenorhabditis elegans | contains weak similarity to an AMP-binding motif | 2926 | 54 |
| 562 | AL109839 | Homo sapiens | dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)) | 877 | 100 |
| 563 | AF181640 | Drosophila melanogaster | BcDNA.GH09817 | 289 | 42 |
| 564 | AF052723 | Feline leukemia virus | gag-pol precursor polyprotein gPr80 | 1547 | 43 |
| 565 | AF161472 | Homo sapiens | HSPC123 | 439 | 44 |
| 566 | Y28817 | Homo sapiens | pt326_4 secreted protein. | 3338 | 100 |
| 567 | U09848 | Homo sapiens | zinc finger protein | 1738 | 100 |
| 569 | AF155113 | Homo sapiens | NY-REN-55 antigen | 3603 | 93 |
| 570 | AF155113 | Homo sapiens | NY-REN-55 antigen | 3951 | 99 |
| 571 | AL032821 | Homo sapiens | dJ55C23.1 (vanin 1) | 1821 | 98 |
| 572 | M69181 | Homo sapiens | non-muscle myosin B | 7350 | 99 |
| 573 | M69181 | Homo sapiens | non-muscle myosin B | 7311 | 98 |
| 574 | Y59678 | Homo sapiens | Secreted protein 108-008-5-0-E6-FL. | 772 | 100 |
| 575 | AL365234 | Arabidopsis thaliana | putative protein | 788 | 40 |
| 576 | AL365234 | Arabidopsis thaliana | putative protein | 788 | 40 |
| 577 | X06745 | Homo sapiens | DNA polymerase alpha-subunit (AA 1 - 1462) | 7619 | 99 |
| 578 | AB041642 | Homo sapiens | PAR-6 | 1342 | 100 |
| 579 | D86984 | Homo sapiens | similar to yeast adenylate cyclase (S56776) | 2446 | 100 |
| 580 | AF165124 | Homo sapiens | gamma-aminobutyric acid A receptor gamma 2 | 2499 | 99 |
| 581 | W88812 | Homo sapiens | Polypeptide fragment encoded by gene 58. | 2339 | 99 |
| 582 | U82319 | Homo sapiens | novel ORF | 342 | 100 |
| 583 | P92219 | Homo sapiens (human) | CR1 protein. | 11425 | 99 |
| 584 | AJ223948 | Homo sapiens | RNA helicase | 6608 | 99 |
| 585 | Y08612 | Homo sapiens | 88kDa nuclear pore complex protein | 3874 | 99 |
| 586 | Y42384 | Homo sapiens | Amino acid sequence of lv310_7. | 1007 | 37 |
| 587 | AF129756 | Homo sapiens | BAT4 | 1873 | 98 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|--|----------------------|------------|
| 588 | AF131775 | Homo sapiens | Unknown | 1929 | 99 |
| 589 | AJ250865 | Homo sapiens | TESS 2 | 2348 | 100 |
| 591 | Z98885 | Homo sapiens | dJ522J7.2 (bromodomain-containing 1 (similar to peregrin, BR140)) | 4167 | 100 |
| 592 | L76571 | Homo sapiens | nuclear hormone receptor | 1355 | 100 |
| 593 | AF091622 | Homo sapiens | PHD finger protein 3 | 9054 | 100 |
| 594 | X56807 | Homo sapiens | desmocollin type 2a | 4443 | 100 |
| 595 | AL137802 | Homo sapiens | dJ798A10.1 (novel protein) | 212 | 55 |
| 596 | AL022329 | Homo sapiens | bK407F11.2 (adrenergic, beta, receptor kinase 2) | 3653 | 100 |
| 597 | AF226048 | Homo sapiens | GL003 | 2009 | 99 |
| 598 | AJ278112 | Homo sapiens >Y49635 Y49635 21-OCT-1999 15-APR-1998 Human sdp3.5 protein. [Homo sapiens] | putative cell cycle control protein | 335 | 23 |
| 599 | Y59741 | Homo sapiens | Human normal ovarian tissue derived protein 18. | 1574 | 99 |
| 600 | L36531 | Homo sapiens | integrin alpha 8 subunit | 5386 | 99 |
| 601 | Y38458 | Homo sapiens | Human secreted protein encoded by gene No. 20. | 895 | 100 |
| 602 | AF218584 | Homo sapiens | GGA1 | 3265 | 100 |
| 603 | Y13115 | Homo sapiens | serine/threonine protein kinase | 5071 | 99 |
| 604 | AL132776 | Homo sapiens | dJ393D12.1 (KIAA0776) | 2413 | 99 |
| 605 | AL034452 | Homo sapiens | dJ682J15.1 (novel Collagen triple helix repeat containing protein) | 1979 | 100 |
| 606 | Y14494 | Homo sapiens | aralar1 | 3465 | 99 |
| 607 | AJ001981 | Homo sapiens | OXAL1 | 2603 | 100 |
| 608 | X86098 | Homo sapiens | binds directly to adenovirus type 5 E1A protein | 3069 | 100 |
| 610 | AF163572 | Homo sapiens | Forssman glycolipid synthetase | 1865 | 99 |
| 611 | AF161503 | Homo sapiens | HSPC154 | 1261 | 97 |
| 612 | L41834 | Ensis minor | nuclear protein | 345 | 30 |
| 613 | Y91954 | Homo sapiens | Human cytoskeleton associated protein 9 (CYSKP-9). | 3668 | 100 |
| 614 | AL022327 | Homo sapiens | dJ355C18.1 (KIAA0027) | 361 | 94 |
| 615 | X85786 | Homo sapiens | binding regulatory factor | 3203 | 100 |
| 616 | Y08319 | Homo sapiens | kinesin-2 | 3487 | 99 |
| 617 | DL2644 | Mus musculus | KIF2 protein | 3609 | 97 |
| 618 | U28789 | Mus musculus | PACT | 5936 | 89 |
| 619 | Y35914 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 163. | 1684 | 99 |
| 620 | AB046382 | Mus musculus | testis-abundant finger protein | 199 | 23 |
| 621 | Y00062 | Homo sapiens | precursor polypeptide (AA -23 to 1120) | 3440 | 99 |
| 622 | AF068286 | Homo sapiens | HDCMD38P | 861 | 100 |
| 623 | X98248 | Homo sapiens | sortilin | 4436 | 99 |
| 624 | X61100 | Homo sapiens | 75 kDa subunit NADH dehydrogenase precursor | 3734 | 99 |
| 625 | S58544 | Homo sapiens | 75 kDa infertility-related sperm protein | 2125 | 99 |
| 626 | AF151027 | Homo sapiens | HSPC193 | 582 | 93 |
| 627 | X14968 | Homo sapiens | R11-alpha subunit (AA 1-404) | 2079 | 100 |
| 628 | Y50911 | Homo sapiens | Human fetal brain cDNA clone vb7_1 derived protein | 1983 | 100 |

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| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 629 | Y50911 | Homo sapiens | Human fetal brain cDNA clone vb7.1 derived protein | 1694 | 100 |
| 630 | AF098786 | Homo sapiens | 17 beta-hydroxysteroid dehydrogenase type VII | 1754 | 100 |
| 631 | AL034555 | Homo sapiens | dJ134O19.3 (zinc finger protein 151 (pHZ-67)) | 4273 | 100 |
| 632 | W74826 | Homo sapiens | Human secreted protein encoded by gene 98 clone HAQBT94. | 794 | 96 |
| 633 | AF288288 | Homo sapiens | HPT protein | 2236 | 100 |
| 634 | AF041429 | Homo sapiens | pRGR1 | 823 | 99 |
| 635 | X66357 | Homo sapiens | serine/threonine protein kinase | 1589 | 100 |
| 636 | Y11284 | Homo sapiens | AFX1 | 2571 | 98 |
| 637 | AB004884 | Homo sapiens | PKU-alpha | 3718 | 99 |
| 638 | AJ002303 | Homo sapiens | synaptogyrin 1c | 1020 | 100 |
| 639 | AJ002304 | Homo sapiens | synaptogyrin 1b | 1002 | 100 |
| 640 | AJ002303 | Homo sapiens | synaptogyrin 1c | 933 | 94 |
| 641 | D87682 | Homo sapiens | similar to a C.elegans protein encoded in cosmid T26A5. | 2676 | 100 |
| 642 | M14660 | Homo sapiens | ISG-K54 | 2473 | 99 |
| 643 | X06661 | Homo sapiens | calbindin (AA 1-261) | 1358 | 100 |
| 644 | AF119900 | Homo sapiens | PRO2822 | 185 | 76 |
| 645 | AB031048 | Drosophila melanogaster | microtubule associated-protein orbit | 738 | 27 |
| 646 | AF250842 | Drosophila melanogaster | multiple asters | 834 | 29 |
| 647 | X86691 | Homo sapiens | Mi-2 protein | 10110 | 99 |
| 648 | U67934 | Homo sapiens | 44.9 kDa protein C18B11 homolog | 827 | 96 |
| 649 | AF236061 | Oryctolagus cuniculus | RING-finger binding protein | 3830 | 91 |
| 650 | AL034553 | Homo sapiens | dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp)) | 5708 | 100 |
| 653 | X14766 | Homo sapiens | GABA-A receptor alpha 1 subunit | 2388 | 99 |
| 654 | AC004614 | Homo sapiens | similar to f-spondin proteins AB006086 (PID:g2529225) | 3026 | 99 |
| 655 | Y57908 | Homo sapiens | Human transmembrane protein HTMPN-32. | 608 | 99 |
| 656 | Z34975 | Homo sapiens | ldlCp | 3733 | 100 |
| 658 | AL050306 | Homo sapiens | dJ475B7.2 (novel protein) | 1942 | 99 |
| 659 | W76734 | Homo sapiens | Human mDia Rho targeting protein. | 781 | 34 |
| 660 | AF202724 | Homo sapiens | Sad1 unc-84 domain protein 1 | 2172 | 100 |
| 661 | Z21966 | Homo sapiens | mPOU homeobox protein | 1529 | 100 |
| 662 | AJ242954 | Mus musculus | dysferlin | 4752 | 59 |
| 663 | AF182316 | Homo sapiens | myoferlin | 6232 | 99 |
| 665 | AL161516 | Arabidopsis thaliana | hypothetical protein | 209 | 30 |
| 667 | X59303 | Homo sapiens | valyl-tRNA synthetase | 3393 | 99 |
| 668 | Y13355 | Homo sapiens | Amino acid sequence of protein PRO220. | 3692 | 100 |
| 669 | AB010692 | Arabidopsis thaliana | contains similarity to endo-beta-N-acetylglucosaminidase gene | 611 | 52 |
| 671 | X56123 | Mus musculus | talin | 4474 | 76 |
| 672 | AB039371 | Homo sapiens | mitochondrial ABC transporter 3 | 2902 | 99 |
| 673 | AF269223 | Homo sapiens | TCP11 | 806 | 42 |
| 674 | AF229633 | Mus musculus | groucho-related protein 4 | 4053 | 99 |
| 675 | L14463 | Rattus | transducin | 3619 | 92 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-----------------------|---|----------------------|------------|
| | | norvegicus | | | |
| 676 | AC005757 | Homo sapiens | R32611_1 | 2779 | 100 |
| 677 | S61069 | Homo sapiens | reverse transcriptase homolog=pol {retroviral element} | 252 | 65 |
| 678 | AF271388 | Homo sapiens | CMP-N-acetylneuraminic acid synthase | 2273 | 100 |
| 679 | X79066 | Homo sapiens | ERF-1 | 1783 | 100 |
| 680 | AF118566 | Mus musculus | hematopoietic zinc finger protein | 769 | 50 |
| 681 | Y51415 | Homo sapiens | Human wild type pKe83 protein. | 2621 | 99 |
| 682 | AL133545 | Homo sapiens | bA386N14.1 (novel protein similar to a dual specificity phosphatase) | 700 | 68 |
| 683 | Y86214 | Homo sapiens | Nuclear transport protein clone hfb341 protein sequence. | 5888 | 99 |
| 684 | Y94952 | Homo sapiens | Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110. | 354 | 98 |
| 685 | AL021878 | Homo sapiens | dJ257I20.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2)) | 154 | 67 |
| 686 | AE000198 | Escherichia coli | orf, hypothetical protein | 628 | 100 |
| 687 | M58378 | Homo sapiens | synapsin I | 3730 | 99 |
| 688 | AF039697 | Homo sapiens | antigen NY-CO-31 | 508 | 98 |
| 689 | U09355 | Oryctolagus cuniculus | protein phosphatase 2A1 B gamma subunit | 2356 | 99 |
| 690 | AF155106 | Homo sapiens | NY-REN-36 antigen | 265 | 50 |
| 691 | AC004774 | Homo sapiens | DLX-5 | 1542 | 100 |
| 692 | X90530 | Homo sapiens | ragB | 1926 | 99 |
| 693 | X90530 | Homo sapiens | ragB | 1405 | 99 |
| 694 | X90530 | Homo sapiens | ragB | 1590 | 85 |
| 695 | G01563 | Homo sapiens | Human secreted protein, SEQ ID NO: 5644. | 330 | 100 |
| 696 | AC011810 | Arabidopsis thaliana | Putative methionine aminopeptidase | 669 | 52 |
| 697 | AJ250425 | Rattus norvegicus | Collybistin I | 2455 | 98 |
| 698 | AB037901 | Homo sapiens | gene amplified in squamous cell carcinoma-1 | 5364 | 99 |
| 699 | Y99401 | Homo sapiens | Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218. | 1386 | 100 |
| 701 | AF221712 | Homo sapiens | Smad- and Olf-interacting zinc finger protein | 6705 | 100 |
| 702 | X83573 | Homo sapiens | ARSE | 3184 | 99 |
| 703 | AJ243274 | Homo sapiens | AP-2rep protein | 2078 | 99 |
| 704 | Y71262 | Homo sapiens | Human chondromodulin-like protein, Zchm1. | 1697 | 94 |
| 705 | Y71262 | Homo sapiens | Human chondromodulin-like protein, Zchm1. | 1736 | 99 |
| 706 | Y41257 | Homo sapiens | Amino acid sequence of long human FAIM. | 1060 | 100 |
| 707 | AL022237 | Homo sapiens | bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1)) | 2030 | 100 |
| 708 | AJ006266 | Homo sapiens | AND-1 protein | 5942 | 100 |
| 709 | G01571 | Homo sapiens | Human secreted protein, SEQ ID NO: 5652. | 777 | 99 |
| 710 | Y08698 | Homo sapiens | ranbp3 | 2849 | 98 |
| 711 | Y68770 | Homo sapiens | Amino acid sequence of a human phosphorylation effector PHSP-2. | 754 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|---|----------------------|------------|
| 712 | U93574 | Homo sapiens | putative p150 | 799 | 59 |
| 713 | AC004531 | Homo sapiens | Gene with similarity to DEAD box helicases | 2715 | 99 |
| 714 | D89016 | Homo sapiens | Neuroblastoma | 538 | 48 |
| 715 | Y92175 | Homo sapiens | Human cardiovascular system associated protein tyrosine phosphatase 2. | 734 | 98 |
| 716 | AL137013 | Homo sapiens | bA311P8.3 (probable uracil phosphoribosyltransferase) | 862 | 100 |
| 717 | AB035123 | Mus musculus | GDI alpha/GT1a alpha/GQ1b alpha synthase | 1696 | 93 |
| 718 | Y96290 | Homo sapiens >P40254 P40254 25-OCT-1984 09-APR-1983 Human IgD. [Homo sapiens] | Human IGFAM-2 immunoglobulin. | 2345 | 85 |
| 719 | X07979 | Homo sapiens | integrin beta 1 subunit precursor | 4347 | 99 |
| 720 | AJ224819 | Homo sapiens | tumor suppressor | 2149 | 99 |
| 721 | Y07595 | Homo sapiens | transcription factor TFIIH | 2373 | 100 |
| 722 | W41565 | Homo sapiens >W41564 W41564 08-OCT-1997 05-APR-1996 Human calpain. [Homo sapiens] | Human calpain. | 1591 | 99 |
| 723 | AF161341 | Homo sapiens | HSPC078 | 1097 | 98 |
| 724 | AF187318 | Homo sapiens | F-box protein Fbx2 | 1607 | 100 |
| 725 | AC006708 | Caenorhabditis elegans | contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876) | 1143 | 46 |
| 726 | AC006708 | Caenorhabditis elegans | contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876) | 988 | 46 |
| 727 | AC024818 | Caenorhabditis elegans | contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 | 950 | 44 |
| 728 | AJ005897 | Homo sapiens | JM5 | 831 | 47 |
| 729 | Y45377 | Homo sapiens | Human secreted protein fragment encoded from gene 27. | 908 | 97 |
| 730 | G03931 | Homo sapiens | Human secreted protein, SEQ ID NO: 8012. | 578 | 100 |
| 731 | AB012720 | Oncorhynchus masou | GTP-binding protein | 3865 | 76 |
| 732 | W73404 | Homo sapiens | Human secreted protein encoded by Gene No. 8. | 862 | 97 |
| 733 | G02650 | Homo sapiens | Human secreted protein, SEQ ID NO: 6731. | 644 | 97 |
| 734 | AC024813 | Caenorhabditis elegans | Hypothetical protein Y54F10AL.a | 152 | 24 |
| 735 | AL035461 | Homo sapiens | dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) | 1562 | 98 |
| 736 | U00033 | Caenorhabditis elegans | similar to S. cerevisiae YJU2 protein | 605 | 41 |
| 737 | AF079098 | Homo sapiens | arginine-tRNA-protein transferase 1-1p; ATE1-1p | 2733 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|------------------------|--|----------------------|------------|
| 738 | AJ131712 | Homo sapiens | nucleolar RNA-helicase | 2793 | 100 |
| 739 | AJ133115 | Homo sapiens | TSC-22-like protein | 2054 | 99 |
| 740 | X98258 | Homo sapiens | M-phase phosphoprotein 9 | 953 | 100 |
| 741 | X98258 | Homo sapiens | M-phase phosphoprotein 9 | 564 | 74 |
| 742 | U97191 | Caenorhabditis elegans | strong similarity to the YPT1 sub-family of RAS proteins | 960 | 85 |
| 743 | X76057 | Homo sapiens | phosphomannose isomerase | 2191 | 100 |
| 744 | G03209 | Homo sapiens | Human secreted protein, SEQ ID NO: 7290. | 496 | 98 |
| 745 | X97064 | Homo sapiens | Sec23 protein | 4034 | 99 |
| 746 | W93946 | Homo sapiens | Human regulatory molecule HRM-2 protein. | 994 | 100 |
| 747 | Y73388 | Homo sapiens | HTRM clone 3376404 protein sequence. | 1565 | 99 |
| 748 | M19529 | Sus scrofa | folliculin A | 1906 | 98 |
| 749 | AJ249457 | Trichomonas vaginalis | centrin, putative | 183 | 28 |
| 750 | AC004410 | Homo sapiens | fos39554.1 | 2094 | 100 |
| 751 | AF074968 | Homo sapiens | p47ING3 protein | 2167 | 100 |
| 752 | AF252284 | Homo sapiens | transcription specificity factor Sp1 | 4005 | 100 |
| 753 | AB049629 | Homo sapiens | phospholysine phosphohistidine inorganic pyrophosphate phosphatase | 1375 | 99 |
| 754 | D79205 | Homo sapiens | ribosomal protein L39 | 160 | 77 |
| 755 | AB008430 | Homo sapiens | CDEP | 142 | 29 |
| 758 | L32162 | Homo sapiens | transcription factor | 574 | 80 |
| 759 | AF037204 | Homo sapiens | RING zinc finger protein | 295 | 54 |
| 760 | Y44250 | Homo sapiens | Human cell signalling protein-13. | 625 | 100 |
| 761 | AF218586 | Homo sapiens | Cide-b | 1136 | 100 |
| 762 | U38934 | Gallus gallus | histone H2A | 625 | 97 |
| 763 | AF226053 | Homo sapiens | HSKM-B | 606 | 32 |
| 764 | X13403 | Homo sapiens | Oct-1 protein (AA 1 - 743) | 3626 | 100 |
| 765 | D87446 | Homo sapiens | Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) | 568 | 38 |
| 766 | AL023828 | Caenorhabditis elegans | Y17G7B.14 | 200 | 27 |
| 767 | Y82777 | Homo sapiens | Human chordin related protein (Clone dw665.4). | 2551 | 99 |
| 768 | X92475 | Homo sapiens | ITBA1 | 1429 | 100 |
| 769 | Y42752 | Homo sapiens | Human calcium binding protein 3 (CaBP-3). | 1426 | 100 |
| 770 | X51416 | Homo sapiens | hormone receptor hERR1 (AA 1-521) | 2641 | 97 |
| 771 | AJ006591 | Homo sapiens | cysteine-rich protein | 1793 | 100 |
| 772 | A08695 | Homo sapiens | rap2 | 935 | 100 |
| 773 | Z12173 | Homo sapiens | N-acetylglucosamine-6-sulphatase | 2970 | 100 |
| 774 | Y91950 | Homo sapiens | Human cytoskeleton associated protein 5 (CYSKP-5). | 565 | 43 |
| 776 | AL023799 | Homo sapiens | dJ322P7.1 (zinc finger) | 855 | 56 |
| 777 | AL023799 | Homo sapiens | dJ322P7.1 (zinc finger) | 855 | 56 |
| 778 | G01880 | Homo sapiens | Human secreted protein, SEQ ID NO: 5961. | 849 | 98 |
| 779 | AJ012590 | Homo sapiens | glucose 1-dehydrogenase | 4155 | 99 |
| 780 | AL078582 | Homo sapiens | dJ130E4.2 (KIAA0796) | 1321 | 68 |
| 781 | Z75955 | Caenorhabditis elegans | similar to mitochondrial carrier protein | 384 | 34 |
| 782 | AL109965 | Homo sapiens | dJ1121G12.2 (SCAN domain-containing 1 protein) | 900 | 100 |
| 783 | AF061262 | Mus musculus | semaF cytoplasmic domain associated protein 2 | 1316 | 83 |
| 784 | G03873 | Homo sapiens | Human secreted protein, SEQ | 649 | 95 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|----------------------------|---|----------------------|------------|
| | | | ID NO: 7954. | | |
| 785 | Y84441 | Homo sapiens | Amino acid sequence of a human RNA-associated protein. | 2074 | 100 |
| 786 | Y00918 | Homo sapiens | Human Rab protein, RABP-1, protein sequence. | 1048 | 99 |
| 787 | Z97029 | Homo sapiens | ribonuclease HI large subunit | 1548 | 99 |
| 788 | AB035384 | Homo sapiens | SRp25 nuclear protein | 962 | 94 |
| 789 | AF024631 | Homo sapiens | ANG2 | 2644 | 100 |
| 790 | AJ006710 | Rattus norvegicus | phosphatidylinositol 3-kinase | 4508 | 97 |
| 792 | V00638 | bacteriophage lambda | reading frame ea10 | 600 | 100 |
| 793 | AF049103 | Homo sapiens | Huntingtin interacting protein | 819 | 100 |
| 795 | Z26317 | Homo sapiens | desmoglein 2 | 4810 | 99 |
| 796 | Y76884 | Homo sapiens | Retinoblastoma binding protein-7 sequence. | 5080 | 99 |
| 797 | U15155 | Gallus gallus | trypsinogen | 372 | 37 |
| 798 | U97189 | Caenorhabditis elegans | strong similarity to the P13/P14 family of kinases | 227 | 28 |
| 799 | AF112201 | Homo sapiens | neuronal protein NP25 | 1053 | 100 |
| 800 | AF234765 | Rattus norvegicus | serine-arginine-rich splicing regulatory protein SRRP86 | 958 | 63 |
| 801 | AF267852 | Homo sapiens | placental protein 13-like protein | 743 | 99 |
| 802 | AF208851 | Homo sapiens | BM-009 | 766 | 80 |
| 803 | Z81097 | Caenorhabditis elegans | Similarity to Human retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene | 152 | 27 |
| 804 | G02113 | Homo sapiens | Human secreted protein, SEQ ID NO: 6194. | 496 | 98 |
| 805 | AL121673 | Homo sapiens | ba305P22.1 (novel protein) | 1160 | 100 |
| 806 | AC013483 | Arabidopsis thaliana | putative GTPase activator protein | 264 | 30 |
| 807 | AC013483 | Arabidopsis thaliana | putative GTPase activator protein | 264 | 30 |
| 808 | AB013885 | Homo sapiens | beta-ureidopropionase | 1494 | 100 |
| 809 | AF078842 | Homo sapiens | HOTTL protein | 1581 | 99 |
| 810 | AF161421 | Homo sapiens | HSPC303 | 2134 | 96 |
| 811 | AF261689 | Homo sapiens | DNA polymerase epsilon p17 subunit | 734 | 100 |
| 812 | Z74029 | Caenorhabditis elegans | Similarity to C.elegans alcohol dehydrogenase comes from this gene | 610 | 71 |
| 813 | Z73497 | Homo sapiens | cU240C2.2 (Core histone H2A/H2B/H3/H4) | 324 | 100 |
| 814 | W87689 | Homo sapiens | Human HTXFT19 polypeptide. | 1484 | 99 |
| 815 | X16282 | Homo sapiens | zinc finger protein (217 AA) (1 is 2nd base in codon) | 1109 | 99 |
| 816 | Z92539 | Mycobacterium tuberculosis | pth | 300 | 36 |
| 818 | AB030483 | Mus musculus | B9 | 197 | 27 |
| 819 | AL117555 | Homo sapiens | hypothetical protein | 321 | 94 |
| 820 | AC005328 | Homo sapiens | R26660_2, partial CDS | 865 | 97 |
| 821 | G03951 | Homo sapiens | Human secreted protein, SEQ ID NO: 8032. | 700 | 99 |
| 822 | L34807 | Musca domestica | transposase | 174 | 20 |
| 823 | G02928 | Homo sapiens | Human secreted protein, SEQ ID NO: 7009. | 558 | 78 |
| 824 | Z99531 | Schizosaccharomyces pombe | caffeine-induced death | 184 | 29 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| | | romyces pombe | protein 1 | | |
| 825 | AJ006692 | Homo sapiens | ultra high sulfur keratin | 693 | 68 |
| 826 | U23037 | Oryctolagus cuniculus | eIF-2Bepsilon | 3406 | 90 |
| 827 | G03412 | Homo sapiens | Human secreted protein, SEQ ID NO: 7493. | 464 | 100 |
| 828 | Y30827 | Homo sapiens | Human secreted protein encoded from gene 17. | 113 | 44 |
| 829 | Y32199 | Homo sapiens | Human receptor molecule (REC) encoded by Incyte clone 2022379. | 1012 | 100 |
| 830 | W78279 | Homo sapiens | Fragment of human secreted protein encoded by gene 33. | 1264 | 99 |
| 832 | AB011542 | Homo sapiens | MEGF9 | 2097 | 100 |
| 833 | G02639 | Homo sapiens | Human secreted protein, SEQ ID NO: 6720. | 223 | 70 |
| 834 | AF119664 | Homo sapiens | transcriptional regulator protein HCNGP | 1574 | 100 |
| 835 | AF119664 | Homo sapiens | transcriptional regulator protein HCNGP | 1144 | 89 |
| 836 | AF119664 | Homo sapiens | transcriptional regulator protein HCNGP | 1448 | 94 |
| 837 | X12517 | Homo sapiens | C protein (AA 1-159) | 918 | 100 |
| 838 | U32865 | Drosophila melanogaster | linotte protein | 164 | 24 |
| 839 | AF067730 | Homo sapiens | TLS-associated protein TASR-2 | 631 | 56 |
| 840 | U27831 | Homo sapiens | striatum-enriched phosphatase | 2840 | 98 |
| 841 | AF286366 | Homo sapiens | CamKI-like protein kinase | 1796 | 100 |
| 842 | G02309 | Homo sapiens | Human secreted protein, SEQ ID NO: 6390. | 278 | 98 |
| 843 | AE003615 | Drosophila melanogaster | ade3 gene product | 113 | 48 |
| 844 | G01350 | Homo sapiens | Human secreted protein, SEQ ID NO: 5431. | 629 | 100 |
| 845 | U27838 | Mus musculus | glycosyl-phosphatidyl-inositol-anchored protein homolog | 3305 | 96 |
| 847 | Y87788 | Homo sapiens | Human RBP-26 protein. | 2026 | 100 |
| 848 | AF164794 | Homo sapiens | Diff33 protein homolog | 2398 | 100 |
| 849 | U41315 | Homo sapiens | ZNF127-Xp | 2458 | 93 |
| 850 | AF192784 | Homo sapiens | makorin 1 | 2062 | 97 |
| 851 | Y58628 | Homo sapiens | Protein regulating gene expression PRGE-21. | 1548 | 100 |
| 852 | Z22968 | Homo sapiens | M130 antigen | 6205 | 100 |
| 853 | Z22971 | Homo sapiens | M130 antigen extracellular variant | 6380 | 100 |
| 854 | G03362 | Homo sapiens | Human secreted protein, SEQ ID NO: 7443. | 330 | 96 |
| 855 | G03362 | Homo sapiens | Human secreted protein, SEQ ID NO: 7443. | 203 | 100 |
| 856 | AF285118 | Homo sapiens | CGI-203 | 452 | 100 |
| 857 | AC006069 | Arabidopsis thaliana | putative cleavage and polyadenylation specificity factor | 1383 | 55 |
| 858 | AL021546 | Homo sapiens | Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) | 593 | 100 |
| 859 | L02956 | Xenopus laevis | ribonucleoprotein | 1664 | 85 |
| 860 | AF201947 | Homo sapiens | MEK binding partner 1 | 616 | 100 |
| 861 | L31783 | Mus musculus | uridine kinase | 1266 | 92 |
| 862 | AF161472 | Homo sapiens | HSPC123 | 602 | 73 |
| 863 | Z49068 | Caenorhabditis elegans | mitochondrial carrier protein | 370 | 43 |
| 864 | AF154108 | Homo sapiens | tumor necrosis factor type 1 | 3559 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
| | | | receptor associated protein | | |
| 865 | AE001530 | Helicobacter pylori J99 | putative | 230 | 32 |
| 866 | X57807 | Homo sapiens | immunoglobulin lambda light chain | 699 | 91 |
| 867 | AL031673 | Homo sapiens | dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains) | 4066 | 99 |
| 868 | Y11652 | Homo sapiens | phosphate cyclase | 238 | 100 |
| 869 | AF192968 | Homo sapiens | high-glucose-regulated protein 8 | 3041 | 99 |
| 870 | AB020648 | Homo sapiens | KIAA0841 protein | 3237 | 99 |
| 871 | AL031427 | Homo sapiens | dJ167A19.1 (novel protein) | 1608 | 100 |
| 872 | AF151534 | Homo sapiens | core histone macroH2A2.2 | 1866 | 100 |
| 873 | AL021331 | Homo sapiens | dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein) | 1129 | 100 |
| 874 | X14608 | Homo sapiens | propionyl-CoA carboxylase | 3579 | 100 |
| 875 | AL117334 | Homo sapiens | dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249)) | 306 | 100 |
| 876 | X79489 | Saccharomyces cerevisiae | E-925 protein | 446 | 35 |
| 877 | Y53001 | Homo sapiens | Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8. | 811 | 100 |
| 878 | AF281064 | Homo sapiens | CHMP1.5 | 957 | 100 |
| 879 | X79417 | Sus scrofa | 40S ribosomal protein S12 | 687 | 100 |
| 880 | AF001317 | Saccharomyces cerevisiae | Soilp | 478 | 28 |
| 881 | Y87275 | Homo sapiens | Human signal peptide containing protein HSPP-52 SEQ ID NO:52. | 2547 | 100 |
| 882 | M14036 | Homo sapiens | C1-inhibitor | 598 | 77 |
| 883 | AB041261 | Homo sapiens | calcium-independent phospholipase A2 | 2903 | 100 |
| 884 | AF020313 | Mus musculus | proline-rich protein 48 | 999 | 84 |
| 885 | Y10936 | Homo sapiens | hypothetical protein | 1104 | 99 |
| 886 | AF073997 | Mus musculus | myotubularin related protein 1 | 866 | 36 |
| 887 | Y57893 | Homo sapiens | Human transmembrane protein HTPN-17. | 1099 | 94 |
| 888 | AL117635 | Homo sapiens | hypothetical protein | 929 | 99 |
| 889 | AF210317 | Homo sapiens | facilitative glucose transporter family member GLUT9 | 2046 | 99 |
| 890 | Y36031 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 416. | 583 | 100 |
| 891 | Y36031 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 416. | 192 | 57 |
| 892 | AF237631 | Homo sapiens | ubiquitous tropomodulin U-Tmod | 1798 | 100 |
| 893 | AF090929 | Homo sapiens | PRO0477p | 653 | 99 |
| 894 | AL031228 | Homo sapiens | dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)) | 3196 | 100 |
| 895 | AL031228 | Homo sapiens | dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)) | 2825 | 96 |
| 896 | AF171102 | Homo sapiens | retinal degeneration B beta | 1302 | 95 |
| 897 | AE003551 | Drosophila melanogaster | CG18176 gene product | 633 | 33 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--|---|----------------------|------------|
| 898 | AJ237946 | Homo sapiens | DEAD Box Protein 5 | 2443 | 100 |
| 899 | Z97184 | Homo sapiens | HKE2 | 624 | 100 |
| 900 | Z97184 | Homo sapiens | HKE2 | 409 | 98 |
| 901 | AJ245587 | Homo sapiens | Kruppel-type zinc finger | 1942 | 100 |
| 902 | AF091034 | Homo sapiens | GTP-binding protein RAE22A | 1011 | 100 |
| 903 | R95953 | Homo sapiens | Eukaryotic cell growth inhibiting factor. | 414 | 96 |
| 904 | L04733 | Homo sapiens | kinesin light chain | 1936 | 72 |
| 905 | AE003540 | Drosophila melanogaster | CG10984 gene product | 446 | 33 |
| 906 | M55542 | Homo sapiens | guanylate binding protein isoform I | 2993 | 98 |
| 907 | M55542 | Homo sapiens | guanylate binding protein isoform I | 2901 | 96 |
| 908 | W84085 | Homo sapiens | Human membrane fusion protein WDProl. | 1889 | 100 |
| 909 | AF168676 | Homo sapiens | TNF intracellular domain-interacting protein | 647 | 100 |
| 910 | AB029150 | Homo sapiens | KRAB zinc finger protein HFB101L | 2196 | 100 |
| 911 | G02871 | Homo sapiens | Human secreted protein, SEQ ID NO: 6952. | 521 | 100 |
| 912 | G03162 | Homo sapiens | Human secreted protein, SEQ ID NO: 7243. | 387 | 87 |
| 913 | AJ243721 | Homo sapiens >Y92508 Y92508 13- APR-2000 06- OCT-1998 Human OXRE- 5. [Homo sapiens | dTDP-4-keto-6-deoxy-D-glucose 4-reductase | 1710 | 100 |
| 914 | U24189 | Caenorhabditis elegans | hypothetical protein 1207-1; Method: conceptual translation supplied by authors | 244 | 41 |
| 915 | Y02591 | Homo sapiens | A human progesterone receptor complex p23-like protein. | 843 | 99 |
| 916 | AE000984 | Archaeoglobus fulgidus | dinitrogenase reductase activating glycohydrolase (draG) | 171 | 26 |
| 918 | M23159 | Cricetus cricetus | DHFR-coamplified protein | 163 | 30 |
| 919 | L12018 | Caenorhabditis elegans | putative | 1232 | 41 |
| 920 | AF102177 | Homo sapiens | tumor antigen SLP-8p | 1260 | 97 |
| 921 | AL096712 | Homo sapiens | dJ744I24.2 (similar to a novel human gene mapping to Activator) | 1017 | 78 |
| 922 | AL161495 | Arabidopsis thaliana | putative WD-repeat protein | 866 | 42 |
| 923 | AL161495 | Arabidopsis thaliana | putative WD-repeat protein | 442 | 36 |
| 924 | U97001 | Caenorhabditis elegans | similar to Schizosaccharomyces pombe | 605 | 51 |
| 925 | X71978 | Mus musculus | Fif | 1503 | 95 |
| 926 | M92288 | Drosophila melanogaster | beta-spectrin | 290 | 51 |
| 927 | Y27575 | Homo sapiens | Human secreted protein encoded by gene No. 9. | 1392 | 100 |
| 928 | Y22499 | Homo sapiens | Human secreted protein sequence clone mh703_1. | 2249 | 100 |
| 930 | AJ224326 | Homo sapiens | ribulose-5-phosphate-epimerase | 912 | 100 |
| 931 | U28991 | Caenorhabditis | coded for by C. elegans cDNA | 660 | 55 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|--|----------------------|------------|
| | | is elegans | cm21c7 | | |
| 932 | AL080065 | Homo sapiens | hypothetical protein | 210 | 25 |
| 933 | G01884 | Homo sapiens | Human secreted protein, SEQ ID NO: 5965. | 767 | 98 |
| 934 | AJ276485 | Homo sapiens | integral membrane transporter protein | 1200 | 100 |
| 935 | AL035681 | Homo sapiens | dJ756G23.3 (novel protein similar to drosophila transcriptional repressor) | 1142 | 80 |
| 936 | AB026808 | Mus musculus | synaptotagmin XI | 2142 | 95 |
| 937 | AB015345 | Homo sapiens | HRIHFB2216 | 2601 | 99 |
| 938 | X65724 | Homo sapiens | ORF2 | 498 | 100 |
| 939 | W89024 | Homo sapiens | Polypeptide fragment encoded by gene 156. | 1487 | 100 |
| 940 | G04047 | Homo sapiens | Human secreted protein, SEQ ID NO: 8128. | 117 | 100 |
| 941 | AF094583 | Homo sapiens | putative HIV-1 infection related protein | 452 | 100 |
| 942 | AC024200 | Caenorhabditis elegans | contains similarity to several zinc finger proteins but not to the zinc finger domains | 350 | 69 |
| 943 | AF129756 | Homo sapiens | G5c | 273 | 100 |
| 944 | M23765 | Rattus norvegicus | alpha-tropomyosin | 133 | 96 |
| 945 | AC009917 | Arabidopsis thaliana | Contains similarity to | 583 | 47 |
| 946 | AF223468 | Homo sapiens | AD021 protein | 551 | 44 |
| 947 | AF055473 | Homo sapiens | GAGE-8 | 273 | 51 |
| 948 | X75756 | Homo sapiens | protein kinase C mu | 2019 | 68 |
| 949 | AF143956 | Mus musculus | coronin-2 | 2300 | 93 |
| 950 | Y36729 | Homo sapiens | Human PGI protein sequence. | 1861 | 99 |
| 951 | W49041 | Homo sapiens | Human low density lipoprotein binding protein LBP-2. | 282 | 67 |
| 952 | AB016881 | Arabidopsis thaliana | gene_id:MXC17.7- | 203 | 46 |
| 953 | Y01785 | Homo sapiens | Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL-1999 12-AUG-1998 Human NCE-2 protein. | 365 | 100 |
| 954 | AF145615 | Drosophila melanogaster | BcDNA.GH03377 | 823 | 46 |
| 955 | U09410 | Homo sapiens | zinc finger protein ZNF131 | 2483 | 99 |
| 956 | U09410 | Homo sapiens | zinc finger protein ZNF131 | 1853 | 99 |
| 957 | AF195623 | Homo sapiens | cholinephosphotransferase 1 alpha | 2126 | 99 |
| 958 | X94917 | Drosophila melanogaster | head-elevated expression in 0.9 kb | 155 | 32 |
| 959 | U54807 | Rattus norvegicus | GTP-binding protein | 1167 | 97 |
| 960 | AF058807 | Bos taurus | GTP-binding protein rah | 606 | 97 |
| 961 | G03244 | Homo sapiens | Human secreted protein, SEQ ID NO: 7325. | 471 | 100 |
| 962 | AF078850 | Homo sapiens | steroid dehydrogenase homolog | 583 | 40 |
| 963 | AP001754 | Homo sapiens | transient receptor potential-related channel 7, a novel putative Ca2+ channel protein | 317 | 30 |
| 964 | AL035419 | Homo sapiens | dJ1100H13.1 (putative novel protein) | 1129 | 100 |
| 965 | X61381 | Rattus rattus | interferon-induced protein | 202 | 46 |
| 966 | D38169 | Homo sapiens | inositol 1,4,5-trisphosphate 3-kinase isoenzyme | 3278 | 100 |
| 967 | AL031432 | Homo sapiens | dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) | 893 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 968 | U79275 | Homo sapiens | unknown | 611 | 100 |
| 969 | AJ011306 | Homo sapiens | guanine nucleotide exchange factor (long isoform) | 2752 | 99 |
| 970 | AF281134 | Homo sapiens | exosome component Rrp46 | 1186 | 100 |
| 971 | U53336 | Caenorhabditis elegans | weak similarity over a short region to myosin heavy chain | 536 | 23 |
| 972 | AC018749 | Leishmania major | L8840.12 | 589 | 53 |
| 973 | AF188504 | Mus musculus | LNV | 544 | 85 |
| 974 | U25801 | Homo sapiens | Tax1 binding protein | 852 | 98 |
| 975 | AP049523 | Homo sapiens | huntingtin-interacting protein HYPA/FBP11 | 1390 | 97 |
| 976 | AF161530 | Homo sapiens | HSPC182 | 1040 | 100 |
| 977 | G04020 | Homo sapiens | Human secreted protein, SEQ ID NO: 8101. | 626 | 100 |
| 978 | AF164797 | Homo sapiens | ribosomal protein L17 isolog | 908 | 100 |
| 979 | U94991 | Xenopus laevis | transcription factor XLM01 | 795 | 97 |
| 980 | S73775 | Homo sapiens | calmitine; calsequestrine | 2029 | 100 |
| 981 | Y94888 | Homo sapiens | Human protein clone HP01462. | 2501 | 100 |
| 982 | AJ243191 | Homo sapiens | heat shock protein | 827 | 96 |
| 983 | X65020 | Bos taurus | PSST subunit of the NADH: ubiquinone oxidoreductase complex | 964 | 85 |
| 984 | AJ249207 | Rhodococcus sp. AD45 | putative racemase | 351 | 43 |
| 985 | Z30093 | Homo sapiens | basic transcription factor 2, 35 kD subunit | 1576 | 99 |
| 986 | AB030835 | Homo sapiens | contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3) | 4697 | 99 |
| 987 | AF227258 | Bos taurus | RPGR-interacting protein-1 | 1262 | 38 |
| 988 | AL022238 | Homo sapiens | dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) | 4048 | 99 |
| 989 | AL022238 | Homo sapiens | dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) | 2321 | 99 |
| 990 | AF161426 | Homo sapiens | HSPC308 | 448 | 92 |
| 991 | AF161426 | Homo sapiens | HSPC308 | 448 | 92 |
| 992 | AF161426 | Homo sapiens | HSPC308 | 453 | 92 |
| 993 | AL023859 | Schizosaccharomyces pombe | trna-splicing endonuclease subunit | 172 | 42 |
| 994 | AL049631 | Homo sapiens | dJ513M9.1 (novel Homeobox domain protein) | 241 | 47 |
| 995 | AC005253 | Homo sapiens | R26445_1 | 902 | 100 |
| 996 | AF265206 | Homo sapiens | MOG1 isoform A | 974 | 100 |
| 997 | AJ248285 | Pyrococcus abyssi | sarcosine oxidase, subunit beta (soxB) | 195 | 28 |
| 998 | AE003641 | Drosophila melanogaster | BG:DS00941.3 gene product | 218 | 58 |
| 999 | W69343 | Homo sapiens | Secreted protein of clone CR930_1. | 1340 | 98 |
| 1000 | AY007135 | Homo sapiens | similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1 | 1543 | 100 |
| 1001 | Y73381 | Homo sapiens | HTRM clone 1877278 protein sequence. | 1668 | 100 |
| 1002 | AF208844 | Homo sapiens | BM-002 | 428 | 100 |
| 1003 | AE004944 | Pseudomonas aeruginosa | hypothetical protein | 134 | 35 |
| 1004 | AL031431 | Homo sapiens | dJ462023.2 (novel protein) | 2058 | 100 |
| 1005 | S45367 | Canis familiaris | centractin | 1949 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 1006 | S45367 | Canis familiaris | centractin | 1315 | 98 |
| 1007 | AB022158 | Mus musculus | chaperonin containing TCP-1 epsilon subunit | 2649 | 96 |
| 1008 | Y76332 | Homo sapiens | Fragment of human secreted protein encoded by gene 38. | 1282 | 97 |
| 1009 | AB011414 | Homo sapiens | Kruppel-type zinc finger protein | 1671 | 58 |
| 1010 | Z68218 | Caenorhabditis elegans | K01H12.1 | 269 | 67 |
| 1011 | AB011414 | Homo sapiens | Kruppel-type zinc finger protein | 1671 | 58 |
| 1012 | Z14000 | Homo sapiens | RING1 | 2017 | 100 |
| 1013 | G02841 | Homo sapiens | Human secreted protein, SEQ ID NO: 6922. | 332 | 93 |
| 1014 | AF145659 | Drosophila melanogaster | BcDNA.GH10333 | 1244 | 52 |
| 1015 | Y02860 | Homo sapiens | Fragment of human secreted protein encoded by gene 65. | 664 | 67 |
| 1016 | Y02591 | Homo sapiens | A human progesterone receptor complex p23-like protein. | 772 | 97 |
| 1017 | Y99448 | Homo sapiens | Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374. | 2323 | 100 |
| 1018 | X67250 | Rattus norvegicus | n-chimaerin | 1710 | 97 |
| 1019 | AF183417 | Homo sapiens | microtubule-associated proteins 1A/1B light chain 3 | 631 | 100 |
| 1020 | AF164795 | Homo sapiens | sex-regulated protein janus-a | 674 | 100 |
| 1021 | AF190625 | Coturnix coturnix | qdg1-1 | 638 | 96 |
| 1022 | AL133363 | Arabidopsis thaliana | putative protein | 155 | 37 |
| 1023 | AB034912 | Homo sapiens | WD-repeat like sequence | 2483 | 100 |
| 1024 | AY007091 | Homo sapiens | similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge | 2243 | 100 |
| 1025 | X69910 | Homo sapiens | P63 protein | 2958 | 99 |
| 1026 | U80736 | Homo sapiens | CAGF9 | 1657 | 100 |
| 1027 | AB029333 | Halocynthia roretzi | HrPET-1 | 1048 | 54 |
| 1028 | AB032931 | Homo sapiens | ubiquitin-conjugating enzyme isolog | 1045 | 100 |
| 1029 | G01797 | Homo sapiens | Human secreted protein, SEQ ID NO: 5878. | 749 | 98 |
| 1030 | G01797 | Homo sapiens | Human secreted protein, SEQ ID NO: 5878. | 749 | 98 |
| 1031 | AF193795 | Homo sapiens | vacuolar sorting protein VPS29/PEP11 | 960 | 100 |
| 1032 | AJ222968 | Mus musculus | L-periaxin | 120 | 30 |
| 1033 | Z81317 | Schizosaccharomyces pombe | DNA2-NAM7 helicase family protein | 685 | 31 |
| 1034 | Y41519 | Homo sapiens | Fragment of human secreted protein encoded by gene 75. | 1321 | 99 |
| 1035 | AJ276004 | Mus musculus | Paxneb protein | 1709 | 77 |
| 1036 | AF025459 | Caenorhabditis elegans | H14A12.3 gene product | 190 | 30 |
| 1037 | U37251 | Homo sapiens | Description: KRAB zinc finger protein; this is a splicing supplied by author | 196 | 43 |
| 1038 | W74580 | Homo sapiens | Human membrane protein BA0306. | 1921 | 97 |
| 1039 | U88173 | Caenorhabditis elegans | weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 | 331 | 80 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------------|---|----------------------|------------|
| 1040 | AF290204 | Homo sapiens | blood group carrier molecule DOK1 | 1637 | 99 |
| 1041 | Y96730 | Homo sapiens | PRO539, a Costal-2 homologue. | 162 | 22 |
| 1042 | AF140683 | Mus musculus | F-box protein FWD2 | 2397 | 98 |
| 1043 | AF151023 | Homo sapiens | HSPC189 | 1104 | 100 |
| 1044 | AF181631 | Drosophila melanogaster | BcDNA.GH04929 | 204 | 37 |
| 1045 | Y77985 | Homo sapiens | Human collectin amino acid sequence. | 1940 | 100 |
| 1046 | AJ243972 | Homo sapiens | 6-phosphogluconolactonase | 1317 | 100 |
| 1047 | AB035863 | Homo sapiens | ATP specific succinyl CoA synthetase beta subunit precursor | 2324 | 99 |
| 1048 | AL034550 | Homo sapiens | dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP)) | 981 | 92 |
| 1049 | AF163825 | Homo sapiens | pre-B lymphocyte protein 3 | 634 | 100 |
| 1050 | AF201949 | Homo sapiens | 60S ribosomal protein L30 isolog | 868 | 100 |
| 1051 | AF190624 | Mus musculus | mdg1-1 | 236 | 85 |
| 1052 | AE003529 | Drosophila melanogaster | CG6151 gene product | 160 | 44 |
| 1053 | G01191 | Homo sapiens | Human secreted protein, SEQ ID NO: 5272. | 646 | 98 |
| 1054 | AL162756 | Neisseria meningitidis | Glu-tRNA(Gln) amidotransferase subunit A | 682 | 44 |
| 1055 | AF181856 | Rattus norvegicus | tRNA selenocysteine associated protein | 1525 | 99 |
| 1056 | U89649 | Chlamydomonas reinhardtii | Mr19,000 outer arm dynein light chain | 244 | 34 |
| 1057 | AF159141 | Homo sapiens | breast cancer metastasis-suppressor 1 | 663 | 53 |
| 1058 | AF230929 | Homo sapiens | keratinocyte annexin-like protein pemphaxin | 1710 | 99 |
| 1059 | AJ270952 | Homo sapiens | putative membrane protein | 1363 | 100 |
| 1060 | AF224263 | Heterodontus francisci | HoxD8 | 742 | 83 |
| 1061 | X63417 | Homo sapiens | IRLB | 1037 | 100 |
| 1062 | AL079345 | Streptomyces coelicolor A3(2) | hypothetical protein | 143 | 27 |
| 1063 | Y71112 | Homo sapiens | Human Hydrolase protein-10 (HYDRL-10). | 2547 | 100 |
| 1064 | AF263614 | Homo sapiens | acetyl-CoA synthetase | 3493 | 99 |
| 1065 | Y13356 | Homo sapiens | Amino acid sequence of protein PRO221. | 1363 | 100 |
| 1066 | AC006153 | Homo sapiens | similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292) | 662 | 98 |
| 1067 | Y18930 | Sulfolobus solfataricus | hypothetical protein | 162 | 29 |
| 1068 | R65969 | Homo sapiens T98G | Glioblastoma-derived polypeptide. | 887 | 100 |
| 1069 | Y07964 | Homo sapiens | Human secreted protein fragment | 863 | 96 |
| 1070 | AF177476 | Rattus norvegicus | CDK5 activator-binding protein | 1995 | 86 |
| 1071 | AF245505 | Homo sapiens | adlcan | 3109 | 99 |
| 1072 | U92794 | Mus musculus | alpha glucosidase II, beta subunit | 147 | 36 |
| 1073 | G03889 | Homo sapiens | Human secreted protein, SEQ ID NO: 7970. | 698 | 98 |
| 1074 | U15779 | Homo sapiens | p70 | 380 | 28 |
| 1075 | Y13392 | Homo sapiens | Amino acid sequence of | 1271 | 91 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| | | | protein PRO328. | | |
| 1076 | AF161457 | Homo sapiens | HSPC339 | 571 | 100 |
| 1077 | Y79509 | Homo sapiens | Human carbohydrate-associated protein CRBAP-5. | 2151 | 98 |
| 1078 | AF223466 | Homo sapiens | HT015 protein | 831 | 66 |
| 1079 | AL132965 | Arabidopsis thaliana | putative WD-40 repeat-protein | 286 | 29 |
| 1080 | AB024937 | Homo sapiens | LUNX | 1284 | 100 |
| 1081 | Y14768 | Homo sapiens | V-ATPase G-subunit like protein | 579 | 100 |
| 1082 | AF016416 | Caenorhabditis elegans | F29A7.4 gene product | 141 | 31 |
| 1083 | L13291 | Homo sapiens | ADP-ribosylarginine hydrolase | 802 | 45 |
| 1084 | AB041541 | Mus musculus | unnamed protein product | 151 | 44 |
| 1085 | G01922 | Homo sapiens | Human secreted protein, SEQ ID NO: 6003. | 202 | 97 |
| 1086 | AB030814 | Homo sapiens | H-REV107 protein homolog | 833 | 100 |
| 1087 | AF151638 | Homo sapiens | phosphatidylcholine transfer protein | 1142 | 100 |
| 1088 | Y84432 | Homo sapiens | Amino acid sequence of a human RNA-associated protein. | 2783 | 100 |
| 1089 | Y94867 | Homo sapiens | Human protein clone HP10563. | 613 | 100 |
| 1090 | AK023982 | Homo sapiens | unnamed protein product | 130 | 49 |
| 1091 | AB041586 | Mus musculus | unnamed protein product | 1103 | 81 |
| 1092 | Y71277 | Homo sapiens | Human Zlipo3 protein. | 606 | 100 |
| 1093 | U34973 | Mus musculus | protein tyrosine phosphatase-like | 1131 | 95 |
| 1094 | Y66677 | Homo sapiens | Membrane-bound protein PRO828. | 522 | 56 |
| 1095 | Y87276 | Homo sapiens | Human signal peptide containing protein HSPP-53 SEQ ID NO:53. | 1029 | 99 |
| 1096 | Y87276 | Homo sapiens | Human signal peptide containing protein HSPP-53 SEQ ID NO:53. | 863 | 98 |
| 1097 | AF161455 | Homo sapiens | HSPC337 | 742 | 98 |
| 1098 | U80029 | Caenorhabditis elegans | similar to thioredoxin | 242 | 39 |
| 1099 | AJ005866 | Homo sapiens | Sqv-7-like protein | 1321 | 99 |
| 1100 | AJ005866 | Homo sapiens | Sqv-7-like protein | 1118 | 99 |
| 1101 | AJ005866 | Homo sapiens | Sqv-7-like protein | 891 | 99 |
| 1102 | AJ005866 | Homo sapiens | Sqv-7-like protein | 1016 | 99 |
| 1103 | AL110244 | Homo sapiens | hypothetical protein | 299 | 31 |
| 1104 | AF242194 | Drosophila melanogaster | brakeless-B | 147 | 52 |
| 1105 | AL031010 | Homo sapiens | dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5) | 968 | 100 |
| 1106 | U28016 | Mus musculus | parathion hydrolase (phosphotriesterase)-related protein | 1624 | 87 |
| 1107 | AJ278150 | Homo sapiens | putative lipid kinase | 2207 | 99 |
| 1108 | G03733 | Homo sapiens | Human secreted protein, SEQ ID NO: 7814. | 495 | 98 |
| 1109 | AF217287 | Drosophila melanogaster | G protein RhoBTB | 834 | 54 |
| 1110 | Y28921 | Homo sapiens | Human regulatory protein HRGP-7. | 941 | 48 |
| 1111 | Y28921 | Homo sapiens | Human regulatory protein HRGP-7. | 1331 | 51 |
| 1112 | AF176704 | Homo sapiens | F-box protein FBX9 | 2027 | 99 |
| 1113 | AF182076 | Homo sapiens | glioma tumor suppressor candidate region protein 2 | 2418 | 100 |
| 1114 | G04039 | Homo sapiens | Human secreted protein, SEQ | 475 | 96 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH- WATERMAN SCORE | % IDENTITY |
|------------------|---------------------|----------------------------------|---|-----------------------------|---------------|
| | | | ID NO: 8120. | | |
| 1115 | AF229439 | Mus musculus | zinc finger protein 289 | 1697 | 91 |
| 1116 | L40357 | Homo sapiens | thyroid receptor interactor | 509 | 100 |
| 1117 | L40357 | Homo sapiens | thyroid receptor interactor | 404 | 85 |
| 1118 | A12155 | Homo sapiens | Human X5L cDNA. | 1673 | 100 |
| 1119 | AL161542 | Arabidopsis thaliana | isomerase like protein | 607 | 53 |
| 1120 | AL023754 | Homo sapiens | dJ272L16.1 (Rat Ca ²⁺ /Calmodulin dependent Protein Kinase LIKE protein) | 2341 | 98 |
| 1121 | Y57901 | Homo sapiens | Human transmembrane protein HTMPN-25. | 321 | 36 |
| 1122 | Z14122 | Xenopus laevis | XLCL2 | 455 | 77 |
| 1123 | AF225418 | Homo sapiens | lipase | 1531 | 97 |
| 1124 | Y06518 | Homo sapiens | Zen GTPase interacting protein ZIP. | 3227 | 100 |
| 1125 | AL035690 | Homo sapiens | dJ202I21.1 (novel protein) | 952 | 100 |
| 1126 | AJ000217 | Homo sapiens | CLIC2 | 1286 | 99 |
| 1127 | AB030505 | Mus musculus | UBE-1c2 | 1069 | 79 |
| 1128 | Y73375 | Homo sapiens | HTRM clone 1427838 protein sequence. | 874 | 100 |
| 1129 | Y78941 | Homo sapiens | Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence. | 877 | 100 |
| 1130 | AL023553 | Homo sapiens | dJ347H13.4 (novel protein) | 557 | 100 |
| 1131 | Y91945 | Homo sapiens | Human chaperone protein 6 (HCHP-6). | 1408 | 100 |
| 1132 | Z68197 | Schizosaccha romyces pombe | putative nuclear pore protein | 596 | 39 |
| 1133 | Z68197 | Schizosaccha romyces pombe | putative nuclear pore protein | 389 | 35 |
| 1134 | AF180681 | Homo sapiens | guanine nucleotide exchange factor | 3597 | 100 |
| 1135 | AF079765 | Mus musculus | enhancer of polycomb | 264 | 41 |
| 1136 | M62419 | Mus musculus | clathrin-associated protein | 2189 | 99 |
| 1137 | AJ006219 | Drosophila melanogaster | clathrin-associated protein | 1254 | 78 |
| 1138 | Y76218 | Homo sapiens | Human secreted protein encoded by gene 95. | 440 | 98 |
| 1139 | W88104 | Homo sapiens | A Rab protein designated HRAB-2. | 1065 | 99 |
| 1140 | Y13401 | Homo sapiens | Amino acid sequence of protein PRO339. | 3979 | 98 |
| 1141 | W85026 | Chimeric - Homo sapiens | Green fluorescent protein- Zap70 fusion product. | 3309 | 100 |
| 1142 | Y13402 | Homo sapiens | Amino acid sequence of protein PRO310. | 1694 | 99 |
| 1143 | G03875 | Homo sapiens | Human secreted protein, SEQ ID NO: 7956. | 660 | 99 |
| 1144 | Y12917 | Homo sapiens | Amino acid sequence of a human secreted peptide. | 750 | 98 |
| 1145 | Y12917 | Homo sapiens | Amino acid sequence of a human secreted peptide. | 1096 | 100 |
| 1146 | AL022157 | Homo sapiens | SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34)) | 1233 | 100 |
| 1147 | AL022157 | Homo sapiens | SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34)) | 1233 | 100 |
| 1148 | G02548 | Homo sapiens | Human secreted protein, SEQ ID NO: 6629. | 370 | 98 |
| 1149 | Y73338 | Homo sapiens | HTRM clone 2019742 protein sequence. | 1492 | 100 |
| 1150 | W74841 | Homo sapiens | Human secreted protein encoded by gene 113 clone | 228 | 55 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
| | | | HEAAR60. | | |
| 1151 | AF044201 | Rattus norvegicus | neural membrane protein 35; NMP35 | 1570 | 92 |
| 1152 | AF156774 | Homo sapiens | lysophosphatidic acid acyltransferase-gamma1 | 1855 | 99 |
| 1153 | AL118501 | Homo sapiens | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 872 | 64 |
| 1154 | AF131852 | Homo sapiens | Unknown | 473 | 100 |
| 1155 | Y41705 | Homo sapiens | Human PR0352 protein sequence. | 1381 | 97 |
| 1156 | G04036 | Homo sapiens | Human secreted protein, SEQ ID NO: 8117. | 607 | 99 |
| 1157 | AF112444 | Lupinus luteus | L-asparaginase | 287 | 43 |
| 1158 | AF151848 | Homo sapiens | CGI-90 protein | 232 | 32 |
| 1159 | AJ272267 | Homo sapiens | choline dehydrogenase | 2449 | 100 |
| 1160 | AB001773 | Clona savignyi | PEM-6 | 196 | 33 |
| 1161 | Y87330 | Homo sapiens | Human signal peptide containing protein HSPP-107 SEQ ID NO:107. | 746 | 83 |
| 1162 | Y87330 | Homo sapiens | Human signal peptide containing protein HSPP-107 SEQ ID NO:107. | 746 | 83 |
| 1163 | AF113534 | Homo sapiens | HP1-BP74 protein | 2723 | 96 |
| 1164 | AF232226 | Danio rerio | Deddl | 191 | 41 |
| 1165 | AL118501 | Homo sapiens | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 1051 | 71 |
| 1166 | AL118501 | Homo sapiens | dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069)) | 945 | 76 |
| 1167 | AF187733 | Homo sapiens | syntaphilin | 831 | 42 |
| 1168 | AB019435 | Homo sapiens | phospholipase | 951 | 55 |
| 1169 | AF064604 | Homo sapiens | KE03 protein | 324 | 33 |
| 1170 | Y01164 | Homo sapiens | Polypeptide fragment encoded by gene 6. | 1191 | 100 |
| 1171 | L03188 | Saccharomyces cerevisiae | putative | 180 | 22 |
| 1172 | AF113751 | Mus musculus | nuclear pore membrane glycoprotein POM210 | 3941 | 81 |
| 1173 | AJ245417 | Homo sapiens | G5b protein | 794 | 100 |
| 1174 | AL022238 | Homo sapiens | dJ1042K10.3 (novel protein) | 1285 | 100 |
| 1175 | U41278 | Caenorhabditis elegans | F33G12.3 gene product | 332 | 28 |
| 1176 | M35617 | Homo sapiens | T-cell receptor V-alpha-J-alpha region | 284 | 83 |
| 1177 | AC012680 | Arabidopsis thaliana | putative protein phosphatase 2C; 55455-56414 | 209 | 37 |
| 1178 | G01345 | Homo sapiens | Human secreted protein, SEQ ID NO: 5426. | 692 | 99 |
| 1179 | AL096767 | Homo sapiens | dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins) | 1342 | 100 |
| 1180 | AF039716 | Caenorhabditis elegans | similar to ATP synthase B chain | 496 | 55 |
| 1181 | Y11710 | Homo sapiens | collagen type XIV | 1048 | 97 |
| 1182 | X82240 | Homo sapiens >R94974 R94974 09-MAY-1996 27-OCT-1994 Human TCL-1 polypeptide. | T cell leukemia/lymphoma 1 | 617 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| | | [Homo sapiens | | | |
| 1183 | U42841 | Caenorhabditis elegans | short region of weak similarity to collagen | 161 | 33 |
| 1185 | AJ131613 | Homo sapiens | dicarboxylate carrier protein | 1470 | 99 |
| 1186 | L27645 | Danio rerio | growth-associated protein | 130 | 36 |
| 1187 | Y02738 | Homo sapiens | Human secreted protein encoded by gene 89 clone HLHFP03. | 636 | 100 |
| 1188 | AF217544 | Xenopus laevis | ornithine decarboxylase-2 | 1459 | 60 |
| 1189 | AL136307 | Homo sapiens | dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth) | 182 | 33 |
| 1190 | X89602 | Homo sapiens | rTSbeta | 197 | 100 |
| 1191 | U32828 | Haemophilus influenzae Rd | ribosomal protein S6 modification protein (rimK) | 268 | 31 |
| 1192 | AF154831 | Rattus norvegicus | PV-1 | 1403 | 60 |
| 1193 | Y50926 | Homo sapiens | Human fetal brain cDNA clone vcl6.1 derived protein. | 918 | 100 |
| 1194 | AF026530 | Rattus norvegicus | stathmin-like-protein splice variant RB3'' | 1093 | 97 |
| 1195 | U35244 | Rattus norvegicus | vacuolar protein sorting homolog r-vps33a | 2981 | 96 |
| 1196 | Y70470 | Homo sapiens | Human p53 target molecule, PRG3 protein. | 1680 | 100 |
| 1197 | AF157318 | Homo sapiens | AD-017 protein | 912 | 47 |
| 1198 | AF125443 | Caenorhabditis elegans | contains similarity to S. pombe phosphatidyl synthase (GB:228295) | 460 | 39 |
| 1199 | AF201934 | Homo sapiens | DC12 | 1649 | 88 |
| 1200 | AL031775 | Homo sapiens | dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4) | 1902 | 100 |
| 1201 | M21103 | Ovis aries | BIIIIB4 high-sulfur keratin | 484 | 82 |
| 1202 | Z85986 | Homo sapiens | dJ108K11.3 (similar to yeast suppressor protein SRP40) | 1143 | 75 |
| 1203 | U18762 | Rattus norvegicus | retinol dehydrogenase type I | 890 | 52 |
| 1204 | U35730 | Mus musculus | jerky | 2235 | 76 |
| 1205 | AB002327 | Homo sapiens | KIAA0329 | 151 | 24 |
| 1206 | AB019233 | Arabidopsis thaliana | ubiquinone/menaquinone biosynthesis methyltransferase-like | 762 | 56 |
| 1207 | AL136307 | Homo sapiens | dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth) | 742 | 100 |
| 1208 | AF207989 | Homo sapiens | orphan G-protein coupled receptor | 2326 | 100 |
| 1209 | Z97630 | Homo sapiens | dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G))) | 181 | 44 |
| 1210 | U21549 | Mus musculus | Ac39/physophilin | 1280 | 68 |
| 1211 | Y27700 | Homo sapiens | Human secreted protein encoded by gene No. 12. | 1267 | 100 |
| 1212 | AF117814 | Mus musculus | odd-skipped related 1 protein | 945 | 66 |
| 1213 | AF277233 | Naegleria fowleri | calcineurin B | 222 | 39 |
| 1214 | D14849 | Mus musculus | meiosis-specific nuclear structural protein 1 | 1950 | 77 |
| 1215 | G03022 | Homo sapiens | Human secreted protein, SEQ ID NO: 7103. | 590 | 100 |
| 1216 | Z72510 | Caenorhabditis | similarity to yeast UTR3 | 634 | 49 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------------|--|----------------------|------------|
| | | <i>is elegans</i> | protein (Swiss Prot accession yk677h11.5 comes from this gene | | |
| 1217 | Z49703 | <i>Saccharomyces cerevisiae</i> | unknown | 134 | 22 |
| 1218 | AC013430 | <i>Arabidopsis thaliana</i> | F3F9.18 | 199 | 29 |
| 1219 | L10910 | <i>Homo sapiens</i> | splicing factor | 1026 | 71 |
| 1220 | Z70750 | <i>Caenorhabditis elegans</i> | similar to vanadate resistance protein transmembranous comes from this gene | 965 | 58 |
| 1221 | AL163815 | <i>Arabidopsis thaliana</i> | putative protein | 653 | 61 |
| 1222 | AF155100 | <i>Homo sapiens</i> | zinc finger protein NY-REN-21 antigen | 2261 | 100 |
| 1223 | J05071 | <i>Bos taurus</i> | GTP-binding regulatory protein gamma-6 subunit | 356 | 100 |
| 1224 | Y73364 | <i>Homo sapiens</i> | HTRM clone 2765991 protein sequence. | 1169 | 99 |
| 1225 | AL050170 | <i>Homo sapiens</i> | hypothetical protein | 714 | 100 |
| 1226 | X64002 | <i>Homo sapiens</i> | RAP74 | 2661 | 99 |
| 1227 | X04085 | <i>Homo sapiens</i> | catalase | 2846 | 100 |
| 1228 | AJ005620 | <i>Mus musculus</i> | skeletal muscle-specific gene | 1416 | 90 |
| 1229 | AF045564 | <i>Rattus norvegicus</i> | development-related protein | 1715 | 93 |
| 1230 | X97571 | <i>Mus musculus</i> | HCMV-interacting protein | 479 | 96 |
| 1231 | L08239 | <i>Homo sapiens</i> | located at OATL1 | 2274 | 100 |
| 1232 | AF121863 | <i>Homo sapiens</i> | sorting nexin 14 | 1964 | 100 |
| 1233 | AF121863 | <i>Homo sapiens</i> | sorting nexin 14 | 1203 | 84 |
| 1234 | AC024805 | <i>Caenorhabditis elegans</i> | contains similarity to TR:004595 | 744 | 31 |
| 1235 | AC006634 | <i>Caenorhabditis elegans</i> | contains similarity to <i>Saccharomyces cerevisiae</i> probable membrane protein YLR418c (GB:U20162) | 357 | 33 |
| 1236 | Y18101 | <i>Mus musculus</i> | macrophage actin-associated-tyrosine-phosphorylated protein | 1559 | 87 |
| 1237 | AB042646 | <i>Homo sapiens</i> | TGIF2 | 1224 | 100 |
| 1238 | AB026264 | <i>Homo sapiens</i> | IMPACT | 1694 | 100 |
| 1239 | AB026264 | <i>Homo sapiens</i> | IMPACT | 1123 | 100 |
| 1240 | G00429 | <i>Homo sapiens</i> | Human secreted protein, SEQ ID NO: 4510. | 324 | 100 |
| 1241 | Y76144 | <i>Homo sapiens</i> | Human secreted protein encoded by gene 21. | 1363 | 53 |
| 1242 | AL035602 | <i>Arabidopsis thaliana</i> | putative protein | 499 | 28 |
| 1243 | X76483 | <i>Gallus gallus</i> | Yes-associated protein (65kDa) | 574 | 48 |
| 1244 | AF220186 | <i>Homo sapiens</i> | uncharacterized hypothalamus protein HT012 | 503 | 100 |
| 1245 | AL021453 | <i>Homo sapiens</i> | dJ821D11.3 (PUTATIVE protein) | 856 | 100 |
| 1246 | AJ276003 | <i>Homo sapiens</i> | GAR1 protein | 1216 | 100 |
| 1247 | Y57910 | <i>Homo sapiens</i> | Human transmembrane protein HTPN-34. | 1369 | 98 |
| 1248 | AC004874 | <i>Homo sapiens</i> | similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) | 957 | 100 |
| 1249 | AF199597 | <i>Homo sapiens</i> | A-type potassium channel modulatory protein 1 | 1139 | 100 |
| 1250 | Y13148 | <i>Rattus norvegicus</i> | PAG608 | 1350 | 88 |
| 1251 | M24852 | <i>Rattus norvegicus</i> | neuron-specific protein PEP-19 | 124 | 46 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 1252 | AF146738 | Rattus norvegicus | testis specific protein | 771 | 83 |
| 1253 | G02725 | Homo sapiens | Human secreted protein, SEQ ID NO: 6806. | 419 | 97 |
| 1254 | W44375 | Homo sapiens | Human ubiquitin-conjugating enzyme polypeptide. | 1045 | 99 |
| 1255 | AC006538 | Homo sapiens | BC41195_1 | 831 | 78 |
| 1256 | AB004316 | Bos taurus | mitochondrial methionyl-tRNA transformylase | 1556 | 88 |
| 1257 | Z35094 | Homo sapiens | SURF-2 | 1354 | 97 |
| 1258 | Y13362 | Homo sapiens | Amino acid sequence of protein PRO214. | 2383 | 100 |
| 1259 | AC006014 | Homo sapiens | similar to RFP transforming protein; similar to P14373 (PID:g132517) | 1299 | 100 |
| 1260 | AC005099 | Homo sapiens | match to AI222572 (NID:g3804775) | 469 | 100 |
| 1261 | V00507 | Homo sapiens | coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon) | 984 | 100 |
| 1262 | X15443 | Rattus sp. | gamma-glutamyltranspeptidase (AA 1-568) | 697 | 32 |
| 1263 | AF173871 | Mus musculus | neuronal PAS3 | 977 | 94 |
| 1264 | AF178983 | Homo sapiens | Ras-associated protein Rap1 | 433 | 97 |
| 1265 | Y70473 | Homo sapiens | Human cyclic nucleotide-associated protein-1 (CNAP-1). | 2785 | 99 |
| 1266 | Y41738 | Homo sapiens | Human PRO541 protein sequence. | 1622 | 100 |
| 1267 | AF061346 | Mus musculus | Edp1 protein | 1077 | 64 |
| 1268 | U97006 | Caenorhabditis elegans | C13F10.4 gene product | 154 | 23 |
| 1269 | AF233582 | Mus musculus | GTPase Rab37 | 942 | 95 |
| 1270 | AF195951 | Homo sapiens | signal recognition particle 68 | 3127 | 98 |
| 1271 | AL031177 | Homo sapiens | dJ889M15.3 (novel protein) | 1150 | 55 |
| 1272 | AF201933 | Homo sapiens | DC11 | 650 | 100 |
| 1273 | AF201933 | Homo sapiens | DC11 | 346 | 98 |
| 1274 | AL021710 | Arabidopsis thaliana | putative protein | 348 | 49 |
| 1275 | AC004449 | Homo sapiens | R33683_3 | 556 | 100 |
| 1276 | Y86295 | Homo sapiens | Human secreted protein HL2AG87, SEQ ID NO:210. | 1920 | 100 |
| 1277 | Y71111 | Homo sapiens | Human Hydrolase protein-9 (HYDRL-9). | 1576 | 99 |
| 1278 | S94421 | Homo sapiens | T cell receptor eta-exon | 478 | 100 |
| 1279 | Y66695 | Homo sapiens | Membrane-bound protein PRO1344. | 1909 | 100 |
| 1280 | AF161380 | Homo sapiens | HSPC262 | 772 | 100 |
| 1281 | Y48610 | Homo sapiens | Human breast tumour-associated protein 71. | 779 | 100 |
| 1282 | AC015446 | Arabidopsis thaliana | Similar to AIG1 protein | 406 | 35 |
| 1283 | AK024432 | Homo sapiens | FLJ00022 protein | 403 | 35 |
| 1284 | W96153 | Homo sapiens | Human FADD-interacting protein (FIP). | 1825 | 81 |
| 1285 | AJ001019 | Homo sapiens | ring finger protein | 1301 | 100 |
| 1286 | AE003823 | Drosophila melanogaster | CG13178 gene product | 195 | 29 |
| 1287 | AF178632 | Homo sapiens | FEM-1-like death receptor binding protein | 3261 | 100 |
| 1288 | AC006033 | Homo sapiens | similar to MLN 64; similar to I38027 (PID:g2135214) | 1195 | 100 |
| 1289 | AC006033 | Homo sapiens | similar to MLN 64; similar to I38027 (PID:g2135214) | 668 | 93 |
| 1290 | AB023811 | Homo sapiens | TU3A | 351 | 54 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---|--|----------------------|------------|
| 1291 | Z73424 | Caenorhabditis elegans | C44B9.1 | 235 | 36 |
| 1292 | Y94871 | Homo sapiens | Human protein clone HP02551. | 1222 | 100 |
| 1293 | AF180425 | Homo sapiens | retinoblastoma-associated protein RAP140 | 489 | 29 |
| 1294 | G03856 | Homo sapiens | Human secreted protein, SEQ ID NO: 7937. | 538 | 99 |
| 1295 | AF133670 | Mus musculus | ARL-6 interacting protein-2 | 367 | 51 |
| 1296 | AJ249735 | Homo sapiens | claudin-6 | 1142 | 100 |
| 1297 | X57560 | Escherichia coli | pspE protein | 535 | 100 |
| 1298 | AF169284 | Homo sapiens | LIM and cysteine-rich domains protein 1 | 1997 | 100 |
| 1299 | U41023 | Caenorhabditis elegans | coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5 | 324 | 29 |
| 1300 | AB024523 | Homo sapiens | basic kruppel like factor | 1206 | 100 |
| 1301 | X55989 | Homo sapiens | eosinophil cationic-related protein | 737 | 99 |
| 1302 | AF007151 | Homo sapiens | unknown | 1481 | 100 |
| 1303 | X52904 | Escherichia coli | open reading frame (AA 1-65) | 359 | 100 |
| 1304 | U19577 | Escherichia coli | galactonate dehydratase | 242 | 93 |
| 1305 | AF266508 | Mus musculus | NELF protein | 1409 | 97 |
| 1306 | Y57901 | Homo sapiens | Human transmembrane protein HTPN-25. | 932 | 100 |
| 1307 | U58750 | Caenorhabditis elegans | similar to the mitochondrial carrier family | 365 | 54 |
| 1308 | AF044774 | Homo sapiens | breakpoint cluster region protein 2 | 2681 | 99 |
| 1309 | AL078593 | Homo sapiens | dJ210B1.1 (KIAA0680) | 267 | 34 |
| 1310 | X82693 | Homo sapiens | E48 antigen | 620 | 96 |
| 1311 | Z82263 | Caenorhabditis elegans | C47A4.1 | 283 | 35 |
| 1312 | AF131218 | Homo sapiens | chromosome 16 open reading frame 5 | 1493 | 100 |
| 1313 | Y41763 | Homo sapiens | Human PR0938 protein sequence. | 1636 | 100 |
| 1314 | AF196972 | Homo sapiens | JM24 protein | 2239 | 100 |
| 1315 | AF053356 | Homo sapiens | insulin receptor substrate like protein | 228 | 97 |
| 1316 | Y66695 | Homo sapiens | Membrane-bound protein PRO1344. | 1909 | 100 |
| 1317 | AF153127 | Gallus gallus | SAPK interacting protein | 2442 | 89 |
| 1318 | AF153127 | Gallus gallus | SAPK interacting protein | 1477 | 83 |
| 1319 | AF153127 | Gallus gallus | SAPK interacting protein | 1651 | 86 |
| 1320 | X56932 | Homo sapiens | 23 kD highly basic protein | 1044 | 100 |
| 1321 | AF174605 | Homo sapiens >Y83086 Y83086 09-MAR-2000 28-AUG-1998 F-box protein FBP-18. [Homo sapiens] | F-box protein Fbx25 | 467 | 70 |
| 1322 | M61732 | Trypanosoma cruzi | neuraminidase | 214 | 24 |
| 1323 | Y17013 | porcine endogenous | pol | 304 | 64 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------------------|--|----------------------|------------|
| | | retrovirus | | | |
| 1324 | AL138655 | Arabidopsis thaliana | putative protein | 1174 | 37 |
| 1325 | AL138655 | Arabidopsis thaliana | putative protein | 946 | 35 |
| 1326 | AL133215 | Homo sapiens | bA108L7.2 (novel protein similar to rat tricarboxylate carrier) | 1322 | 99 |
| 1327 | AF161541 | Homo sapiens | HSPC056 | 1357 | 99 |
| 1328 | Y73346 | Homo sapiens | HTRM clone 619699 protein sequence. | 785 | 96 |
| 1329 | L10910 | Homo sapiens | splicing factor | 912 | 82 |
| 1330 | AF146568 | Homo sapiens | MIL1 protein | 1936 | 100 |
| 1331 | W87772 | Homo sapiens | Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide. | 232 | 39 |
| 1332 | Y41741 | Homo sapiens | Human PR0704 protein sequence. | 1860 | 100 |
| 1333 | AF295096 | Homo sapiens | zinc-finger protein ZBRK1 | 411 | 91 |
| 1334 | Z82271 | Caenorhabditis elegans | Similarity to Mouse kinesin-like protein KIF4 comes from this gene | 578 | 44 |
| 1335 | AE000810 | Methanobacterium thermoautotrophicum | conserved protein | 290 | 43 |
| 1336 | Y68779 | Homo sapiens | Amino acid sequence of a human phosphorylation effector PHSP-11. | 1019 | 91 |
| 1337 | AE027003 | Mus musculus | protein phosphatase | 378 | 84 |
| 1338 | U64856 | Caenorhabditis elegans | weak similarity to TPR domains | 215 | 40 |
| 1339 | AE001394 | Plasmodium falciparum | protein of the YMR7 family | 170 | 29 |
| 1340 | X76717 | Homo sapiens | MT-11 protein | 204 | 89 |
| 1341 | AC011914 | Arabidopsis thaliana | putative-mutT protein; 68398-67881 | 289 | 45 |
| 1342 | AJ276171 | Homo sapiens | ASPIC | 2122 | 100 |
| 1343 | AF187016 | Homo sapiens | myosin regulatory light chain interacting protein MIR | 2303 | 99 |
| 1344 | AC006963 | Homo sapiens | similar to Kelch proteins; similar to BAA77027 (PID:g4650844) | 894 | 35 |
| 1345 | AF257466 | Homo sapiens | N-acetylneuraminic acid phosphate synthase | 1880 | 99 |
| 1346 | Y25896 | Homo sapiens | Human secreted protein fragment encoded from gene 64. | 1148 | 100 |
| 1347 | AJ272073 | Torpedo marmorata | male sterility protein 2-like protein | 1664 | 58 |
| 1348 | AF161548 | Homo sapiens | HSPC063 | 1018 | 98 |
| 1349 | W78128 | Homo sapiens | Human secreted protein encoded by gene 3 clone HOSBI96. | 1117 | 100 |
| 1351 | G02144 | Homo sapiens | Human secreted protein, SEQ ID NO: 6225. | 418 | 100 |
| 1352 | D90869 | Escherichia coli | similar to | 2047 | 100 |
| 1353 | A12029 | Homo sapiens | MRP-14 | 613 | 100 |
| 1354 | AC005328 | Homo sapiens | R26660_1, partial CDS | 870 | 74 |
| 1355 | AC024876 | Caenorhabditis elegans | contains similarity to SW:RPB1_CRIGR | 829 | 61 |
| 1356 | AF077226 | Homo sapiens | copine III | 1876 | 64 |
| 1359 | AF217188 | Mus musculus | YIP1B | 801 | 63 |
| 1360 | AC074331 | Homo sapiens | ZNF234 | 3869 | 100 |
| 1361 | AL163279 | Homo sapiens | homolog to cAMP response | 5035 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|--------------------------|--|----------------------|------------|
| | | | element binding and beta transducin family proteins | | |
| 1362 | Z48475 | Homo sapiens | glucokinase regulator | 3160 | 99 |
| 1363 | Z48475 | Homo sapiens | glucokinase regulator | 2682 | 97 |
| 1364 | AF195764 | Homo sapiens | megakaryocyte-enhanced gene transcript 1 protein; MEGT1 protein | 2055 | 99 |
| 1365 | AF116609 | Homo sapiens | PRO0915 | 581 | 100 |
| 1366 | AF116609 | Homo sapiens | PRO0915 | 581 | 100 |
| 1367 | AL117352 | Homo sapiens | dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557)) | 2581 | 99 |
| 1368 | Y34124 | Homo sapiens | Human potassium channel K+Hnov15. | 1342 | 100 |
| 1369 | AJ245621 | Homo sapiens | CTL2 protein | 3728 | 99 |
| 1370 | AF008220 | Bacillus subtilis | YtaG | 429 | 45 |
| 1371 | X05562 | Homo sapiens | alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon) | 5908 | 99 |
| 1372 | Z98048 | Homo sapiens | dJ408N23.4 (novel DnaJ domain protein) | 1296 | 99 |
| 1373 | AF154415 | Homo sapiens | FLASH | 10253 | 100 |
| 1374 | U20286 | Rattus norvegicus | lamina associated polypeptide 1C | 1567 | 69 |
| 1375 | U53445 | Homo sapiens | DOC1 | 1645 | 46 |
| 1376 | AL117337 | Homo sapiens | ba393J16.1 (zinc finger protein 33a (KOX 31)) | 250 | 60 |
| 1377 | AC005328 | Homo sapiens | R26660_1, partial CDS | 1126 | 100 |
| 1378 | U35113 | Homo sapiens | metastasis-associated gene | 1823 | 69 |
| 1379 | L15313 | Caenorhabditis elegans | putative | 858 | 58 |
| 1380 | Y25756 | Homo sapiens | Human secreted protein encoded from gene 46. | 1508 | 100 |
| 1381 | AB037360 | Homo sapiens | ANKHZN | 5734 | 95 |
| 1382 | AB037360 | Homo sapiens | ANKHZN | 959 | 97 |
| 1383 | AF237676 | Mus musculus | G beta-like protein GBL | 1721 | 96 |
| 1384 | AF237676 | Mus musculus | G beta-like protein GBL | 1043 | 70 |
| 1385 | Y58793 | Homo sapiens | Human calcium regulatory protein CaREG-1. | 715 | 100 |
| 1386 | AF212162 | Homo sapiens | ninein | 10369 | 99 |
| 1387 | AL031685 | Homo sapiens | dJ963K23.2 (novel protein) | 337 | 33 |
| 1388 | AC004890 | Homo sapiens | similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein. | 542 | 86 |
| 1389 | AF187989 | Homo sapiens | zinc finger protein ZNF223 | 2665 | 99 |
| 1390 | AC035150 | Homo sapiens | Zinc finger protein ZNF221 | 3459 | 100 |
| 1391 | AF287894 | Homo sapiens | PIST | 1410 | 97 |
| 1392 | AF282265 | Homo sapiens | inner centromere protein INCENP | 1794 | 99 |
| 1393 | X90840 | Homo sapiens | axonal transporter of synaptic vesicles | 4584 | 99 |
| 1394 | AF076249 | Homo sapiens | zinc finger protein SBBIZ1 | 3208 | 99 |
| 1395 | G02224 | Homo sapiens | Human secreted protein, SEQ ID NO: 6305. | 299 | 75 |
| 1396 | AC004809 | Arabidopsis thaliana | Similar to | 130 | 34 |
| 1398 | AF242519 | Homo sapiens | zinc finger protein SBZF3 | 181 | 66 |
| 1399 | AL133396 | Homo sapiens | dJ1066H6.4 (prion protein like protein doppel) | 962 | 100 |
| 1400 | Y48611 | Homo sapiens | Human breast tumour-associated protein 72. | 817 | 99 |
| 1401 | AC004472 | Homo sapiens | Pl.11659_5 | 280 | 54 |
| 1402 | X91489 | Saccharomyces cerevisiae | putative HMG box | 164 | 27 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------|---|----------------------|------------|
| 1403 | Y79222 | Homo sapiens | Human transferase TRNSFS-14. | 2842 | 100 |
| 1404 | X81058 | Mus musculus | tex261 | 1010 | 99 |
| 1405 | AB012084 | Mus musculus | ITM | 194 | 29 |
| 1406 | AB030251 | Homo sapiens | GTPase activating protein | 3233 | 99 |
| 1407 | AJ010585 | Rattus rattus | PTB-like protein | 2684 | 99 |
| 1408 | X75760 | Drosophila melanogaster | LRR47 | 364 | 29 |
| 1409 | U76618 | Mus musculus | N-RAP | 804 | 48 |
| 1410 | AC005578 | Homo sapiens | P20887_1, partial CDS | 835 | 63 |
| 1411 | AE000284 | Escherichia coli | orf, hypothetical protein | 360 | 100 |
| 1412 | X01563 | Escherichia coli | L5 (rp1E) (aa 1-179) | 911 | 100 |
| 1413 | W78279 | Homo sapiens | Fragment of human secreted protein encoded by gene 33. | 1264 | 99 |
| 1414 | AB031051 | Homo sapiens | organic anion transporter OATP-E | 3832 | 100 |
| 1415 | M17466 | Homo sapiens | coagulation factor XII | 3455 | 100 |
| 1416 | AF097994 | Homo sapiens | L-kynurenine/alpha-amino adipate aminotransferase | 2202 | 99 |
| 1417 | AF151077 | Homo sapiens | HSPC243 | 1262 | 99 |
| 1418 | Y09945 | Rattus norvegicus | putative integral membrane transport protein | 1098 | 61 |
| 1419 | U13152 | Mesocricetus auratus | guanine nucleotide-binding protein beta 5 | 2179 | 76 |
| 1420 | AL162458 | Homo sapiens | BA465L10.5 (KIAA1176 (novel protein, presumed ortholog of mouse K-Cl cotransporter KCC2)) | 5696 | 100 |
| 1421 | Y99426 | Homo sapiens | Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308. | 152 | 29 |
| 1422 | Y94923 | Homo sapiens | Human secreted protein clone qs14.3 protein sequence SEQ ID NO:52. | 4039 | 99 |
| 1423 | AF177388 | Homo sapiens | cancer-amplified transcriptional coactivator ASC-2 | 10748 | 99 |
| 1424 | Y48517 | Homo sapiens | Human breast tumour-associated protein 62. | 1851 | 99 |
| 1425 | AF208848 | Homo sapiens | BM-006 | 1454 | 89 |
| 1426 | AF208848 | Homo sapiens | BM-006 | 853 | 79 |
| 1427 | AF112886 | Bos taurus | differentiation enhancing factor 1 | 4693 | 95 |
| 1428 | U41387 | Homo sapiens | Gu protein | 1372 | 63 |
| 1429 | AF161534 | Homo sapiens | HSPC049 | 2853 | 78 |
| 1430 | AF125043 | Mus musculus | bisphosphate 3'-nucleotidase | 275 | 30 |
| 1431 | Y66718 | Homo sapiens | Membrane-bound protein PRO1106. | 1886 | 100 |
| 1432 | AF193613 | Homo sapiens | cell recognition molecule Caspr2 | 568 | 100 |
| 1433 | AB044560 | Mus musculus | Gliacolin | 192 | 34 |
| 1434 | R99800 | Homo sapiens | NTII-1 nerve protein, facilitates regeneration of nerve cells. | 707 | 51 |
| 1435 | AF220530 | Homo sapiens | myo-inositol 1-phosphate synthase A1 | 2904 | 100 |
| 1436 | X70944 | Homo sapiens | PTB-associated splicing factor | 1261 | 72 |
| 1437 | AF271732 | Homo sapiens | bridging integrator-3 | 1282 | 100 |
| 1438 | Y30811 | Homo sapiens | Human secreted protein encoded from gene 1. | 595 | 98 |
| 1439 | AJ293659 | Homo sapiens | mucolipidin | 628 | 97 |
| 1440 | AF219138 | Homo sapiens | GGA3 long isoform | 3083 | 100 |
| 1441 | AF219138 | Homo sapiens | GGA3 long isoform | 3346 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|---|----------------------|------------|
| 1442 | AB039669 | Homo sapiens | ALEX3 | 1944 | 100 |
| 1443 | AF237711 | Drosophila melanogaster | Diablo | 191 | 27 |
| 1444 | AJ011896 | Homo sapiens | Naf1 beta protein | 439 | 39 |
| 1445 | X73874 | Homo sapiens | phosphorylase kinase | 6233 | 98 |
| 1446 | AF214114 | Homo sapiens | breast carcinoma-associated antigen BCAA | 3999 | 99 |
| 1447 | AF003924 | Homo sapiens | ANC_2H01 | 2645 | 99 |
| 1448 | AF003136 | Caenorhabditis elegans | contains weak similarity to an AMP-binding motif | 2843 | 52 |
| 1449 | AF155112 | Homo sapiens | NY-REN-50 antigen | 1184 | 89 |
| 1450 | Y95004 | Homo sapiens | Human secreted protein vc54_1, SEQ ID NO:48. | 985 | 100 |
| 1451 | AF107203 | Homo sapiens | ataxin 2-binding protein | 688 | 57 |
| 1452 | AF107203 | Homo sapiens | ataxin 2-binding protein | 456 | 78 |
| 1453 | Z38011 | Mus musculus | DMR-N9 | 882 | 56 |
| 1454 | X90568 | Homo sapiens | Protein sequence and annotation available soon via LABELIT@EMBL-Heidelberg.DE | 510 | 28 |
| 1455 | AL035409 | Homo sapiens | dJ564M11.3 (similar to sialyltransferase) | 1356 | 100 |
| 1456 | D44480 | Mus musculus | MATH-2 protein | 272 | 100 |
| 1458 | AF141326 | Homo sapiens | RNA helicase HDB/DICE1 | 478 | 45 |
| 1459 | AF242552 | Gallus gallus | retinovin | 945 | 34 |
| 1460 | U11036 | Homo sapiens | Ibd1 | 724 | 84 |
| 1461 | AB025258 | Mus musculus | granuphilin-a | 545 | 39 |
| 1462 | Y08134 | Homo sapiens | acid sphingomyelinase-like phosphodiesterase | 2428 | 99 |
| 1463 | AC004997 | Homo sapiens | match to ESTs 243979 (NID:g573097), R19699 (NID:g774333) | 869 | 98 |
| 1464 | AC004997 | Homo sapiens | match to ESTs 243979 (NID:g573097), R19699 (NID:g774333) | 869 | 98 |
| 1465 | U32743 | Haemophilus influenzae Rd | fucose operon protein (fucU) | 315 | 50 |
| 1466 | Y09022 | Homo sapiens | Not56-like protein | 2342 | 100 |
| 1467 | AC003034 | Homo sapiens | Homolog of rat kidney-specific (KS) gene | 1072 | 99 |
| 1468 | AF071544 | Spinacia oleracea | ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I | 333 | 26 |
| 1469 | Y57930 | Homo sapiens | Human transmembrane protein HTPN-54. | 1053 | 100 |
| 1470 | AF032666 | Rattus norvegicus | rsec5 | 4504 | 93 |
| 1471 | Y70467 | Homo sapiens | Human membrane channel protein-17 (MECHP-17). | 452 | 74 |
| 1472 | AL031033 | Homo sapiens | C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) | 1694 | 100 |
| 1473 | AF177292 | Homo sapiens | genethonin 3 | 4026 | 98 |
| 1474 | S45936 | Homo sapiens | HTS1 | 1101 | 50 |
| 1475 | Y86241 | Homo sapiens | Human secreted protein HOABR60, SEQ ID NO:156. | 1879 | 98 |
| 1476 | AJ010317 | Fugu rubripes | Sand | 1278 | 68 |
| 1477 | U42831 | Caenorhabditis elegans | coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) | 846 | 44 |
| 1478 | X62447 | Homo sapiens | PR 264 | 543 | 61 |
| 1479 | X82209 | Homo sapiens | MN1 | 7116 | 100 |
| 1480 | U10536 | Pan paniscus | MHC class I A | 675 | 84 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| 1481 | AL078599 | Homo sapiens | dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086)) | 1274 | 65 |
| 1482 | Z98977 | Schizosaccharomyces pombe | putative vacuolar protein | 256 | 29 |
| 1483 | AB005662 | Mus musculus | JNK/SAPK-associated protein-1 | 4968 | 92 |
| 1484 | AL050120 | Homo sapiens | hypothetical protein | 716 | 100 |
| 1485 | M27878 | Homo sapiens | DNA binding protein | 1006 | 53 |
| 1486 | Y69161 | Homo sapiens | Amino acid sequence of a partial protein kinase. | 575 | 99 |
| 1487 | X84156 | Saccharomyces cerevisiae | ATH1 | 341 | 29 |
| 1488 | AF038963 | Homo sapiens | RNA helicase | 446 | 34 |
| 1489 | U56966 | Caenorhabditis elegans | coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 | 620 | 42 |
| 1490 | AE000989 | Archaeoglobus fulgidus | enoyl-CoA hydratase (fad-4) | 533 | 46 |
| 1491 | M80633 | Rattus norvegicus | adenylyl cyclase type IV | 707 | 95 |
| 1492 | Y73342 | Homo sapiens | HTRM clone 2709055 protein sequence. | 3513 | 99 |
| 1493 | Y17220 | Homo sapiens | Human secreted protein (clone fj283-11). | 462 | 37 |
| 1494 | AF133670 | Mus musculus | ARL-6 interacting protein-2 | 701 | 97 |
| 1495 | Y94697 | Homo sapiens | Human protein clone HP10574. | 1371 | 100 |
| 1496 | AL049699 | Homo sapiens | dJ747H23.2 (novel protein) | 1550 | 100 |
| 1497 | AF037447 | Homo sapiens | ribosomal S6 protein kinase | 2427 | 100 |
| 1498 | AL445067 | Thermoplasma acidophilum | putative target YPL207w of the HAP2 transcriptional complex related protein | 269 | 35 |
| 1499 | AB039947 | Homo sapiens | X11L-binding protein 51 | 227 | 36 |
| 1500 | AJ277750 | Homo sapiens | UBASH3A protein | 3509 | 100 |
| 1501 | AL050333 | Homo sapiens | dJ93K22.1 (novel protein (contains DKFZP564B116)) | 2439 | 100 |
| 1502 | AF179896 | Homo sapiens | TAL1 homeobox protein Meis2b | 1140 | 100 |
| 1503 | AF178948 | Homo sapiens | TAL1 homeobox protein Meis2a | 1177 | 100 |
| 1504 | Y53005 | Homo sapiens | Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16. | 1442 | 99 |
| 1505 | X82494 | Homo sapiens | fibulin-2 | 3580 | 99 |
| 1506 | X98296 | Homo sapiens | ubiquitin hydrolase | 783 | 42 |
| 1507 | AL034548 | Homo sapiens | dJ1103G7.6 (novel protein) | 1098 | 100 |
| 1508 | Y76144 | Homo sapiens | Human secreted protein encoded by gene 21. | 1736 | 100 |
| 1509 | AF220182 | Homo sapiens | uncharacterized hypothalamus protein HT008 | 1181 | 98 |
| 1510 | U64601 | Caenorhabditis elegans | Gene probably begins in the next cosmid | 415 | 58 |
| 1511 | AL356192 | Neurospora crassa | related to MDM1 protein | 196 | 29 |
| 1512 | D17629 | Homo sapiens | N-acetylgalactosamine 6-sulfate sulfatase (GALNS) | 1829 | 100 |
| 1513 | AF168717 | Homo sapiens | x 009 protein | 694 | 99 |
| 1514 | AJ243531 | Homo sapiens | nm15 protein | 735 | 100 |
| 1515 | AC003672 | Arabidopsis thaliana | putative C3HC4-type RING zinc finger protein | 407 | 30 |
| 1516 | AF115435 | Rattus norvegicus | syntaxin 17 | 1374 | 90 |
| 1517 | AF003140 | Caenorhabditis elegans | C44E4.5 gene product | 274 | 31 |
| 1518 | AB002584 | Rattus norvegicus | beta-alanine-pyruvate aminotransferase | 2238 | 82 |
| 1519 | AL121764 | Schizosaccharomyces | yeast atp12 protein precursor | 270 | 30 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| | | romyces pombe | homolog | | |
| 1520 | AF255910 | Homo sapiens | vascular endothelial junction-associated molecule | 547 | 100 |
| 1521 | D31764 | Homo sapiens | KIAA0064 | 170 | 27 |
| 1522 | Y66634 | Homo sapiens | Membrane-bound protein PRO190. | 985 | 100 |
| 1523 | Y94450 | Homo sapiens | Human inflammation associated protein | 250 | 43 |
| 1524 | AC000107 | Arabidopsis thaliana | F17F8.22 | 277 | 37 |
| 1525 | AF109377 | Mus musculus | IdlBp | 1277 | 83 |
| 1526 | AL031427 | Homo sapiens | dJ167A19.4 (novel protein) | 1432 | 99 |
| 1527 | Y08135 | Mus musculus | acid sphingomyelinase-like phosphodiesterase | 1496 | 79 |
| 1528 | AK024423 | Homo sapiens | FLJ00012 protein | 611 | 100 |
| 1529 | AF154502 | Homo sapiens | quiescent cell proline dipeptidase | 679 | 100 |
| 1530 | AF205598 | Homo sapiens | transposase-like protein | 1368 | 100 |
| 1531 | AF251039 | Homo sapiens | putative zinc finger protein | 1420 | 50 |
| 1532 | W74805 | Homo sapiens | Human secreted protein encoded by gene 77 clone HOEAS24. | 493 | 57 |
| 1533 | AF039023 | Homo sapiens | Ran-GTP binding protein; RanBP6 | 5707 | 99 |
| 1534 | AC007190 | Arabidopsis thaliana | F23N19.9 | 374 | 37 |
| 1535 | AB027564 | Homo sapiens | DINB1 | 4482 | 100 |
| 1536 | Y36178 | Homo sapiens | Human secreted protein | 377 | 87 |
| 1537 | Y50907 | Homo sapiens | Human fetal brain cDNA clone vb3_1 derived protein. | 3693 | 99 |
| 1538 | AF017368 | Mus musculus | faciogenital dysplasia protein 2 | 177 | 47 |
| 1539 | AF266756 | Homo sapiens | sphingosine kinase | 2011 | 99 |
| 1540 | Z48804 | Homo sapiens | OA1 | 2238 | 100 |
| 1541 | AF000195 | Caenorhabditis elegans | Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1 | 379 | 42 |
| 1542 | Y71159 | Homo sapiens | Human phosphodiesterase interacting protein, myomegalin. | 9415 | 99 |
| 1543 | X76092 | Homo sapiens | DNA binding protein RFX3 | 3327 | 100 |
| 1544 | AB015330 | Homo sapiens | HRIHFB2007 | 631 | 50 |
| 1545 | AF198487 | Homo sapiens | transcription factor LBP-1b | 2822 | 100 |
| 1546 | AF016417 | Caenorhabditis elegans | Similar to BZIP transcription factor | 518 | 42 |
| 1547 | X55885 | Homo sapiens | KDEL receptor | 1106 | 100 |
| 1548 | AB035495 | Carassius auratus | ubiquitin-activating enzyme E1 | 836 | 42 |
| 1549 | AL021707 | Homo sapiens | dJ508I15.4 (KIAA0668) | 3688 | 100 |
| 1550 | AJ223978 | Bacillus subtilis | YvqK protein | 292 | 42 |
| 1551 | AF145615 | Drosophila melanogaster | BcDNA.GH03377 | 822 | 44 |
| 1552 | AL157734 | Schizosaccharomyces pombe | putative mannosyltransferase involved in N-glycosylation | 435 | 37 |
| 1553 | AF079527 | Mus musculus | IER5 | 691 | 63 |
| 1554 | AB026291 | Rattus norvegicus | acetoacetyl-CoA synthetase | 1099 | 88 |
| 1555 | Y44722 | Homo sapiens | Human immune system molecule, ISMO-3. | 1780 | 99 |
| 1556 | AF116553 | Drosophila melanogaster | antennal-specific short-chain dehydrogenase/reductase | 277 | 32 |
| 1557 | Y71056 | Homo sapiens | Human membrane transport | 1975 | 99 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------------------|--|----------------------|------------|
| | | | protein, MTRP-1. | | |
| 1558 | Y71056 | Homo sapiens | Human membrane transport protein, MTRP-1. | 1975 | 99 |
| 1559 | Y71056 | Homo sapiens | Human membrane transport protein, MTRP-1. | 1894 | 97 |
| 1560 | AF092050 | Mus musculus | beta-1,3-N-acetylglucosaminyltransferase | 262 | 44 |
| 1561 | AL109827 | Homo sapiens | dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4))) | 1607 | 97 |
| 1562 | AJ131890 | Homo sapiens | DNA polymerase lambda | 3002 | 100 |
| 1563 | AL035424 | Homo sapiens | dA22D12.1 (novel protein similar to Drosophila Kelch proteins) | 3015 | 100 |
| 1564 | AC002400 | Homo sapiens | Gene product with similarity to Ubiquitin binding enzyme | 2790 | 100 |
| 1565 | AC005306 | Homo sapiens | R27216_1 | 919 | 82 |
| 1566 | AF000195 | Caenorhabditis elegans | Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1 | 550 | 45 |
| 1567 | AB033281 | Homo sapiens | F-box and WD-repeats protein beta-TRCP2 isoform C | 2879 | 100 |
| 1568 | D49473 | Mus musculus | truncated form of Sox17 | 1047 | 78 |
| 1569 | AK025270 | Homo sapiens | unnamed protein product | 210 | 91 |
| 1570 | X75756 | Homo sapiens | protein kinase C mu | 4797 | 99 |
| 1571 | AF145713 | Homo sapiens | SCHIP-1 | 2388 | 100 |
| 1572 | AE003831 | Drosophila melanogaster | CG18445 gene product | 180 | 31 |
| 1573 | AF074603 | Streptomyces griseus subsp. griseus | NonF | 205 | 38 |
| 1574 | U28993 | Caenorhabditis elegans | F22D3.3 gene product | 144 | 27 |
| 1575 | AF129507 | Homo sapiens | transcription factor ICBP90 | 287 | 68 |
| 1576 | X64878 | Homo sapiens | oxytocin receptor | 2002 | 100 |
| 1577 | AF237711 | Drosophila melanogaster | Diablo | 421 | 54 |
| 1578 | G00975 | Homo sapiens | Human secreted protein, SEQ ID NO: 5056. | 480 | 100 |
| 1579 | AF248744 | Cryptosporidium parvum | thrombospondin-related adhesive protein | 123 | 33 |
| 1580 | AL121782 | Homo sapiens | dJ585114.2 (novel protein (translation of cDNA Em:AK000219)) | 663 | 100 |
| 1581 | AF041853 | Homo sapiens | kinesin family member protein KIF3A | 345 | 33 |
| 1582 | AF025441 | Homo sapiens | Opa-interacting protein OIP5 | 1198 | 100 |
| 1583 | AE001803 | Thermotoga maritima | glycerate kinase, putative | 349 | 34 |
| 1584 | AF252283 | Homo sapiens | Kelch-like 1 protein | 3973 | 100 |
| 1585 | AF169675 | Homo sapiens | leucine-rich repeat transmembrane protein FLRT1 | 3494 | 99 |
| 1586 | AF118274 | Homo sapiens | DNB-5 | 2628 | 97 |
| 1587 | X79440 | Homo sapiens | NADP+-dependent malic enzyme | 3167 | 99 |
| 1588 | X99802 | Homo sapiens | ZYG homologue | 3966 | 99 |
| 1589 | AF169803 | Homo sapiens | flavohemoprotein b5+b5R | 2563 | 100 |
| 1590 | Y29861 | Homo sapiens | Human secreted protein clone cb98_4. | 181 | 47 |
| 1591 | Z25535 | Homo sapiens | nuclear pore complex protein hnup153 | 7567 | 99 |
| 1592 | X13293 | Homo sapiens | B-myb protein (AA 1-700) | 3678 | 99 |
| 1593 | M74027 | Homo sapiens | mucin | 242 | 27 |
| 1594 | AL139314 | Schizosaccharomyces | hypothetical protein | 235 | 54 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|---------------------------|--|----------------------|------------|
| | | pombe | | | |
| 1595 | W78324 | Homo sapiens | Fragment of human secreted protein encoded by gene 81. | 1318 | 98 |
| 1596 | Y94906 | Homo sapiens | Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18. | 2236 | 98 |
| 1597 | AF174605 | Homo sapiens | F-box protein Fbx25 | 1408 | 99 |
| 1598 | AB032254 | Homo sapiens | bromodomain adjacent to zinc finger domain 2A | 9676 | 98 |
| 1599 | X73114 | Homo sapiens | slow MyBP-C | 5568 | 95 |
| 1600 | X82200 | Homo sapiens | gpStaf50 | 2305 | 100 |
| 1601 | Y00876 | Homo sapiens | Human LAPH-1 protein sequence. | 1149 | 98 |
| 1602 | AJ223351 | Homo sapiens | HIRA-interacting protein 3 | 2821 | 99 |
| 1603 | AJ222801 | Homo sapiens | neutral sphingomyelinase | 2268 | 99 |
| 1604 | AJ222801 | Homo sapiens | neutral sphingomyelinase | 1601 | 99 |
| 1605 | AF185576 | Mus musculus | POZ/zinc finger transcription factor ODA-8 | 3435 | 97 |
| 1606 | AF093744 | Homo sapiens | unknown | 131 | 100 |
| 1607 | A12142 | synthetic construct | IFN-pseudo-omega 2 | 800 | 98 |
| 1608 | Y57949 | Homo sapiens | Human transmembrane protein HTMPN-73. | 1868 | 100 |
| 1609 | AF151044 | Homo sapiens | HSPC210 | 681 | 97 |
| 1610 | X15218 | Homo sapiens | ski protein (AA 1 - 728) | 3765 | 100 |
| 1611 | Y08200 | Homo sapiens | rab geranylgeranyl transferase | 2976 | 100 |
| 1612 | AF220560 | Homo sapiens | B/K protein | 2486 | 99 |
| 1613 | AC004481 | Arabidopsis thaliana | nodulin-like protein | 371 | 26 |
| 1614 | Y09501 | Homo sapiens | NADH-cytochrome-b5 reductase | 1607 | 100 |
| 1615 | Y15521 | Homo sapiens | start position 1 | 3150 | 97 |
| 1616 | AJ010750 | Rattus norvegicus | Castration induced prostatic apoptosis related protein-1, (CIPAR-1) | 890 | 62 |
| 1617 | X58079 | Homo sapiens | S100 alpha protein | 481 | 100 |
| 1618 | Y66678 | Homo sapiens | Membrane-bound protein PRO1009. | 967 | 100 |
| 1619 | AJ242973 | Homo sapiens | peptide methionine sulfoxide reductase | 929 | 100 |
| 1620 | AF150733 | Homo sapiens | AD-014 protein | 288 | 100 |
| 1621 | AJ007509 | Homo sapiens | ElB-55kDa-associated protein | 4646 | 98 |
| 1622 | X64177 | Homo sapiens | metallothionein | 380 | 100 |
| 1623 | AE001045 | Archaeoglobus fulgidus | A. fulgidus predicted coding region AF0859 | 240 | 36 |
| 1624 | AL355013 | Schizosaccharomyces pombe | mitochondrial carrier protein | 403 | 34 |
| 1625 | Y66746 | Homo sapiens | Membrane-bound protein PRO1198. | 1184 | 100 |
| 1626 | D90053 | Sus scrofa | destrin | 863 | 100 |
| 1627 | Y35954 | Homo sapiens | Extended human secreted protein sequence, SEQ ID NO. 203. | 756 | 100 |
| 1628 | AL031775 | Homo sapiens | dJ30M3.2 (novel protein) | 470 | 100 |
| 1629 | AF132484 | Mus musculus | unknown | 286 | 68 |
| 1630 | AF017096 | Drosophila melanogaster | similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c | 493 | 61 |
| 1631 | X03077 | Homo sapiens | lactate dehydrogenase-A | 1704 | 100 |
| 1632 | AF151084 | Homo sapiens | HSPC250 | 763 | 100 |
| 1633 | AJ001874 | Homo sapiens | orf | 255 | 97 |
| 1634 | AC012187 | Arabidopsis thaliana | Contains weak similarity to GATA-6 DNA-binding protein gb H36135, gb Z26200 come from this gene. | 143 | 38 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | IDENTITY |
|------------|------------------|--|---|----------------------|----------|
| 1635 | AF026246 | Homo sapiens | HERV-E integrase | 411 | 90 |
| 1636 | Y50943 | Homo sapiens | Human adult brain cDNA clone ve8_1 derived protein. | 1126 | 95 |
| 1637 | AF134593 | Homo sapiens | L-pipecolic acid oxidase | 2068 | 99 |
| 1638 | AJ238247 | Mus musculus | putative phosphatase subunit | 1948 | 96 |
| 1639 | Y94942 | Homo sapiens | Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90. | 1320 | 100 |
| 1640 | AF235030 | Homo sapiens | BM88 antigen | 766 | 99 |
| 1641 | AF233288 | Drosophila melanogaster | WDS | 358 | 26 |
| 1642 | M19351 | Mus musculus | immunoglobulin heavy chain binding protein | 145 | 34 |
| 1643 | Y70452 | Homo sapiens | Human membrane channel protein-2 (MECHP-2). | 1352 | 100 |
| 1644 | AF176520 | Mus musculus | WD repeat-containing F-box protein FBW5 | 2676 | 88 |
| 1645 | W67816 | Homo sapiens | Human secreted protein encoded by gene 10 clone HCEMU42. | 1156 | 100 |
| 1646 | X67155 | Homo sapiens | mitotic kinase-like protein-1 | 4456 | 99 |
| 1647 | M63180 | Homo sapiens | threonyl-tRNA synthetase | 1040 | 61 |
| 1648 | Y87342 | Homo sapiens | Human signal peptide containing protein HSPP-119 SEQ ID NO:119. | 1566 | 93 |
| 1649 | R95332 | Homo sapiens | Tumor necrosis factor receptor 1 death domain ligand (clone 3TW). | 4137 | 100 |
| 1650 | AC007136 | Homo sapiens | Putative map kinase interacting kinase | 856 | 99 |
| 1651 | AB015346 | Homo sapiens | Eps15R | 4464 | 99 |
| 1652 | AL161576 | Arabidopsis thaliana | putative protein | 1341 | 48 |
| 1653 | AC005313 | Arabidopsis thaliana | putative calmodulin | 288 | 28 |
| 1654 | AL031428 | Homo sapiens | dJ184J9.1 (KIAA0601 protein) | 3526 | 100 |
| 1655 | AL031428 | Homo sapiens | dJ184J9.1 (KIAA0601 protein) | 3526 | 100 |
| 1656 | AB017910 | Dictyostellium discoideum | myoM | 297 | 32 |
| 1657 | Y28919 | Homo sapiens | Human regulatory protein HRGP-5. | 2251 | 99 |
| 1658 | AF056191 | Homo sapiens | TPA inducible protein | 2744 | 98 |
| 1659 | U76846 | Arabidopsis thaliana | ubiquitin-specific protease | 137 | 35 |
| 1660 | AL078627 | Schizosaccharomyces pombe | actin-like protein; (2 actin domains) | 320 | 34 |
| 1662 | X52022 | Homo sapiens | collagen type VI, alpha 3 chain | 16274 | 99 |
| 1663 | AF300648 | Homo sapiens | guanine nucleotide binding protein beta subunit 4 | 1811 | 100 |
| 1664 | AF214736 | Homo sapiens | EH domain containing protein 2 | 2774 | 100 |
| 1665 | Z48613 | Saccharomyces cerevisiae | unknown | 138 | 26 |
| 1666 | AF177385 | Homo sapiens | cytochrome c oxidase assembly protein isoform 2 | 1395 | 99 |
| 1667 | AC007842 | Homo sapiens | BC331191_1 | 1581 | 47 |
| 1668 | S67513 | Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Peptide, 370 | p40 | 397 | 43 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH- WATERMAN SCORE | % IDENTITY |
|------------------|---------------------|---------------------------|--|-----------------------------|---------------|
| | | aa | | | |
| 1669 | Z99753 | Schizosaccharomyces pombe | putative NOL1-NOP2-sun family nucleolar protein | 569 | 47 |
| 1670 | G03130 | Homo sapiens | Human secreted protein, SEQ ID NO: 7211. | 427 | 97 |
| 1671 | M96625 | Gallus gallus | cardiac muscle tensin | 1185 | 54 |
| 1672 | AF174482 | Homo sapiens | polycomb 3 | 2005 | 99 |
| 1673 | Y51846 | Homo sapiens | Human 18.1 homolog protein fragment. | 233 | 29 |
| 1674 | AF255334 | Homo sapiens | EXP35 | 152 | 29 |
| 1675 | Y94867 | Homo sapiens | Human protein clone HP10563. | 109 | 30 |
| 1676 | Y25712 | Homo sapiens | Human secreted protein encoded from gene 2. | 3043 | 99 |
| 1677 | Y25712 | Homo sapiens | Human secreted protein encoded from gene 2. | 1580 | 91 |
| 1678 | AF163151 | Homo sapiens | dentin sialophosphoprotein precursor | 170 | 17 |
| 1679 | AF163151 | Homo sapiens | dentin sialophosphoprotein precursor | 170 | 17 |
| 1680 | AK024453 | Homo sapiens | FLJ00045 protein | 1349 | 100 |
| 1681 | AF019236 | Dictyostellium discoideum | TipD | 613 | 34 |
| 1682 | AJ243459 | Leishmania major | proteophosphoglycan | 153 | 26 |
| 1683 | Z69369 | Schizosaccharomyces pombe | putative GTP-binding protein | 560 | 46 |
| 1684 | X94910 | Homo sapiens | ERp28 | 1334 | 100 |
| 1685 | AF286475 | Takifugu rubripes | retinitis pigmentosa GTPase regulator-like protein | 196 | 19 |
| 1686 | AF191298 | Homo sapiens | vacuolar sorting protein 35 | 4087 | 100 |
| 1687 | AJ275986 | Homo sapiens | transcription factor | 2958 | 100 |
| 1688 | AJ275986 | Homo sapiens | transcription factor | 1886 | 88 |
| 1689 | X07311 | Drosophila melanogaster | heat shock protein | 138 | 43 |
| 1690 | AF240463 | Rattus norvegicus | LIS1-interacting protein NUDE1 | 1383 | 83 |
| 1691 | AJ272078 | Homo sapiens | APOBEC-1 stimulating protein | 1256 | 68 |
| 1692 | AJ272079 | Homo sapiens | APOBEC-1 stimulating protein | 1336 | 60 |
| 1693 | AF177942 | Xenopus laevis | katanin p60 | 1664 | 66 |
| 1694 | AF263539 | Homo sapiens | arginine N-methyltransferase | 1774 | 100 |
| 1695 | AF222689 | Homo sapiens | protein arginine N-methyltransferase 1-variant 2 | 1182 | 81 |
| 1696 | AK000193 | Homo sapiens | unnamed protein product | 1060 | 100 |
| 1697 | AB041035 | Homo sapiens | kidney superoxide-producing NADPH oxidase | 3122 | 100 |
| 1698 | AB041035 | Homo sapiens | kidney superoxide-producing NADPH oxidase | 2181 | 100 |
| 1699 | AF025772 | Homo sapiens | C2H2 zinc finger protein | 488 | 54 |
| 1700 | Y44676 | Homo sapiens | Human ARF-Related Protein-1 (HARP-1). | 938 | 97 |
| 1701 | AK022407 | Homo sapiens | unnamed protein product | 315 | 98 |
| 1702 | AB024574 | Homo sapiens | GTP-binding like protein 2 | 1172 | 100 |
| 1703 | AF055078 | Homo sapiens | zinc finger protein 42 | 421 | 52 |
| 1704 | AF198092 | Mus musculus | RP42 | 1057 | 77 |
| 1705 | AE003573 | Drosophila melanogaster | CG12474 gene product | 161 | 33 |
| 1706 | AB036345 | Drosophila melanogaster | aquaporin | 164 | 24 |
| 1707 | Y55927 | Homo sapiens | Human STLK2 protein. | 2146 | 100 |
| 1708 | U27121 | Danio rerio | G12 | 212 | 47 |
| 1709 | AL391710 | Arabidopsis | putative protein | 505 | 50 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | % IDENTITY |
|------------|------------------|-------------------------------|--|----------------------|------------|
| | | <i>thaliana</i> | | | |
| 1710 | B01311 | <i>Homo sapiens</i> | Human PRO241 polypeptide. | 1649 | 97 |
| 1711 | U40750 | <i>Mus musculus</i> | formin binding protein 30 | 4561 | 85 |
| 1712 | AJ011118 | <i>Mus musculus</i> | skeletal muscle and cardiac protein | 1490 | 89 |
| 1713 | AF255303 | <i>Homo sapiens</i> | membrane-associated nucleic acid binding protein | 4416 | 99 |
| 1714 | AF255303 | <i>Homo sapiens</i> | membrane-associated nucleic acid binding protein | 2960 | 100 |
| 1715 | U08227 | <i>Rattus norvegicus</i> | Ras-related protein | 511 | 51 |
| 1716 | AF168795 | <i>Rattus norvegicus</i> | schlafen-4 | 1129 | 44 |
| 1717 | AF196304 | <i>Homo sapiens</i> | SUMO-1-specific protease | 5804 | 99 |
| 1718 | AL355737 | <i>Homo sapiens</i> | HMG20A | 1782 | 100 |
| 1719 | AB029333 | <i>Halocynthia roretzi</i> | HrPET-1 | 1069 | 46 |
| 1720 | AF071317 | <i>Mus musculus</i> | COP9 complex subunit 7b | 1297 | 97 |
| 1721 | AJ272215 | <i>Homo sapiens</i> | HEYL protein | 1681 | 99 |
| 1722 | G01982 | <i>Homo sapiens</i> | Human secreted protein, SEQ ID NO: 6063. | 718 | 100 |
| 1723 | AL032643 | <i>Caenorhabditis elegans</i> | similar to Uncharacterized protein family UPF0034, | 825 | 41 |
| 1724 | G01972 | <i>Homo sapiens</i> | Human secreted protein, SEQ ID NO: 6053. | 586 | 92 |
| 1725 | Y94441 | <i>Homo sapiens</i> | Human Adipose Specific Protein 1. | 1231 | 100 |
| 1726 | AF255443 | <i>Homo sapiens</i> | CGI-201 protein | 4397 | 99 |
| 1727 | AF183426 | <i>Homo sapiens</i> | HT004 protein | 1810 | 99 |
| 1728 | D10884 | <i>Bos taurus</i> | neurocalcin | 1002 | 99 |
| 1729 | Z18529 | <i>Gallus gallus</i> | tensin | 1411 | 84 |
| 1730 | Z73423 | <i>Caenorhabditis elegans</i> | cdna EST EMBL:Z14908 comes from this gene-cDNA EST this gene | 233 | 41 |
| 1732 | AF090891 | <i>Homo sapiens</i> | PRO0105 | 470 | 30 |
| 1733 | AJ277724 | <i>Homo sapiens</i> | histone deacetylase 8 | 2015 | 100 |
| 1734 | G04050 | <i>Homo sapiens</i> | Human secreted protein, SEQ ID NO: 8131. | 503 | 95 |
| 1735 | D45913 | <i>Mus musculus</i> | leucine-rich-repeat protein | 3531 | 94 |
| 1736 | AF096709 | <i>Drosophila virilis</i> | failed axon connections protein | 276 | 32 |
| 1737 | AF195120 | <i>Homo sapiens</i> | dynactin p62 subunit | 2417 | 99 |
| 1738 | L15314 | <i>Caenorhabditis elegans</i> | contains similarity to Pfam family PF01772 N=1 | 206 | 37 |
| 1739 | X54618 | <i>Listeria monocytogenes</i> | phosphatidylinositol specific phospholipase C | 134 | 27 |
| 1740 | AL031658 | <i>Homo sapiens</i> | dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins) | 123 | 31 |
| 1741 | Y35924 | <i>Homo sapiens</i> | Extended human secreted protein sequence, SEQ ID NO. 173. | 1013 | 99 |
| 1742 | AC013354 | <i>Arabidopsis thaliana</i> | F15H18.15 | 202 | 32 |
| 1743 | W75771 | <i>Homo sapiens</i> | Human GTP binding protein APD08. | 1932 | 59 |
| 1744 | W75771 | <i>Homo sapiens</i> | Human GTP binding protein APD08. | 1854 | 61 |
| 1745 | AF221098 | <i>Homo sapiens</i> | Ral guanine nucleotide exchange factor RalGPS1A | 1224 | 70 |
| 1746 | Y99372 | <i>Homo sapiens</i> | Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116. | 1332 | 99 |
| 1747 | Y94294 | <i>Homo sapiens</i> | Human coenzyme A-utilising | 842 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH-WATERMAN SCORE | IDENTITY |
|------------|------------------|--------------------------------------|--|----------------------|----------|
| | | | enzyme CoAEN-2. | | |
| 1748 | AK024436 | Homo sapiens | FLJ00026 protein | 1619 | 100 |
| 1749 | AE000877 | Methanobacterium thermoautotrophicum | conserved protein | 231 | 36 |
| 1750 | AF101361 | Drosophila melanogaster | Abnormal X segregation | 193 | 33 |
| 1751 | Y15067 | Homo sapiens | ZNF232 | 889 | 100 |
| 1752 | AF251038 | Homo sapiens | GAP-like protein | 822 | 100 |
| 1753 | AC003093 | Homo sapiens | OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308) | 352 | 57 |
| 1754 | X69089 | Homo sapiens | 165kD protein | 5703 | 99 |
| 1755 | AL049795 | Homo sapiens | dJ622L5.3 (novel protein) | 1039 | 100 |
| 1756 | AL031393 | Homo sapiens | dJ733D15.1 (Zinc-finger protein) | 2765 | 100 |
| 1757 | AB040672 | Homo sapiens | UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase | 2020 | 99 |
| 1758 | AL022238 | Homo sapiens | dJ1042K10.4 (novel protein) | 776 | 43 |
| 1759 | AF117653 | Homo sapiens | double homeobox protein | 375 | 54 |
| 1760 | Y12065 | Homo sapiens | hNop56 | 2959 | 99 |
| 1761 | AL049712 | Homo sapiens | dJ686C3.2 (nucleolar protein hNop56) | 2595 | 99 |
| 1762 | AC002394 | Homo sapiens | Gene product with similarity to dynein beta subunit | 1542 | 51 |
| 1763 | AF169017 | Homo sapiens | formiminotransferase cyclodeaminase | 877 | 100 |
| 1764 | U91541 | Homo sapiens | human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end | 596 | 100 |
| 1765 | AB013365 | Bacillus halodurans | YlqF | 350 | 34 |
| 1766 | Y38421 | Homo sapiens | Human secreted protein encoded by gene No. 36. | 145 | 71 |
| 1767 | AC009176 | Arabidopsis thaliana | putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I | 216 | 27 |
| 1768 | AK000647 | Homo sapiens | unnamed protein product | 737 | 99 |
| 1769 | AJ238982 | Homo sapiens | VNN3 protein | 2665 | 99 |
| 1770 | U73522 | Homo sapiens | AMSH | 1214 | 56 |
| 1771 | U89435 | Mus musculus | unknown | 829 | 86 |
| 1772 | S70011 | Rattus sp. | tricarboxylate carrier | 1604 | 95 |
| 1773 | AL035086 | Homo sapiens | dJ44A20.2 (novel protein) | 2036 | 100 |
| 1774 | Y99426 | Homo sapiens | Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308. | 1057 | 99 |
| 1775 | AF110330 | Homo sapiens | glutaminase | 3146 | 100 |
| 1776 | AJ269529 | Homo sapiens | glycerol 3-phosphate permease | 2787 | 100 |
| 1777 | Z81579 | Caenorhabditis elegans | cDNA EST yk76f1.5 comes from this gene | 232 | 31 |
| 1778 | AY007239 | Homo sapiens | monooxygenase X | 1875 | 99 |
| 1779 | AL109608 | Schizosaccharomyces pombe | oxysterol-binding protein family | 644 | 38 |
| 1780 | AF254260 | Homo sapiens | tuftelin 1 | 1729 | 100 |
| 1781 | L07924 | Mus musculus | guanine nucleotide dissociation stimulator | 247 | 50 |
| 1782 | AF295773 | Homo sapiens | ral guanine nucleotide dissociation stimulator | 142 | 49 |
| 1783 | AK024475 | Homo sapiens | FLJ00068 protein | 4333 | 100 |
| 1784 | AK024475 | Homo sapiens | FLJ00068 protein | 3996 | 93 |
| 1785 | G03933 | Homo sapiens | Human secreted protein, SEQ ID NO: 8014. | 570 | 100 |
| 1786 | S82637 | Homo sapiens | Ig lambda-like gene/beta- | 247 | 100 |

TABLE 2

| SEQ ID NO: | ACCESSION NUMBER | SPECIES | DESCRIPTION | SMITH- WATERMAN SCORE | % IDENTITY |
|------------------|---------------------|---------|-------------------------------|-----------------------------|---------------|
| | | | glucuronidase exon 11 homolog | | |

TRADOC5:1416280.1(%CT4011).DOC)

TABLE 3

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| 2 | BL00240 | Receptor tyrosine kinase class III proteins. | BL00240B 24.70 8.250e-12 157-181 |
| 3 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109D 17.04 8.085e-13 358-381 |
| 4 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 9.400e-10 1129-1146 BL00028 16.07 1.257e-09 820-837 |
| 5 | BL00023 | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390 |
| 6 | BL00023 | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390 |
| 7 | BL00023 | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390 |
| 8 | BL00023 | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390 |
| 9 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 5.119e-09 863-917 |
| 10 | PR00464 | E-CLASS P450 GROUP II SIGNATURE | PR00464D 17.40 6.182e-12 294-312 PR00464G 12.41 4.231e-11 377-393 |
| 11 | PR00734 | GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE | PR00734I 11.46 4.296e-09 502-520 |
| 12 | PF00023 | Ank repeat proteins. | PF00023B 14.20 6.500e-10 89-99 PF00023B 14.20 2.636e-09 56-66 |
| 14 | DM00031 | IMMUNOGLOBULIN V REGION. | DM00031B 15.41 3.848e-09 79-113 |
| 15 | PRO0208 | GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE | PRO0208A 12.59 9.868e-10 517-535 PRO0208A 12.59 2.233e-09 520-538 |
| 17 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 8.200e-14 282-295 PD00066 13.92 9.400e-14 477-490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e-13 254-267 PD00066 13.92 1.429e-12 393-406 PD00066 13.92 6.571e-12 421-434 |
| 18 | BL00845 | CAP-Gly domain proteins. | BL00845 16.43 2.200e-25 55-80 |
| 20 | BL00487 | IMP dehydrogenase / GMP reductase proteins. | BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 287-329 |
| 21 | BL00487 | IMP dehydrogenase / GMP reductase proteins. | BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 348-390 |
| 22 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 3.250e-26 302-333 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| 23 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 3.250e-26 302-333 |
| 25 | BL00115 | Eukaryotic RNA polymerase II heptapeptide repeat proteins. | BL00115T 8.45 7.273e-29 1208-1242 BL00115Q 18.08 2.776e-21 953-983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e-16 731-774 BL00115H 14.34 9.392e-16 463-496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e-14 983-1010 BL00115J 16.71 9.289e-14 591-617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e-13 662-694 BL00115G 11.65 6.011e-13 435-463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e-10 863-913 BL00115P 11.54 7.538e-10 913-953 BL00115S 18.24 7.968e-10 1010-1052 BL00115U 10.34 4.475e-09 1242-1265 |
| 26 | BL00420 | Speract receptor repeat proteins domain proteins. | BL00420A 20.42 4.109e-11 81-110 BL00420A 20.42 8.820e-10 84-113 |
| 27 | BL00050 | Ribosomal protein L23 proteins. | BL00050A 23.71 9.250e-27 94-127 BL00050B 14.81 8.125e-12 133-147 |
| 28 | PR00925 | NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE | PR00925B 3.73 3.089e-10 41-54 |
| 29 | PF00756 | Putative esterase. | PF00756C 14.12 1.108e-09 486-516 |
| 32 | BL00557 | FMN-dependent alpha-hydroxy acid dehydrogenases proteins. | BL00557D 17.76 5.065e-37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e-28 227-257 BL00557B 21.27 8.898e-22 130-169 |
| 34 | PR00629 | SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE | PR00629E 9.90 5.886e-35 299-328 PR00629F 10.95 8.364e-32 334-361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e-21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e-11 276-286 |
| 35 | PD01270 | RECEPTOR FC IMMUNOGLOBULIN AFFIN. | PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166 |
| 36 | PD01270 | RECEPTOR FC IMMUNOGLOBULIN AFFIN. | PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | | PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166 |
| 37 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412C 10.28 9.241e-10 264-298 |
| 38 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412C 10.28 9.241e-10 264-298 |
| 39 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412C 10.28 9.241e-10 264-298 |
| 40 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380B 12.64 7.366e-14 342-360 PR00380C 13.18 6.927e-13 375-394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e-12 143-165 |
| 44 | BL00345 | Ets-domain proteins. | BL00345B 21.28 1.000e-40 239-290 BL00345A 13.96 2.452e-14 204-223 |
| 45 | BL00345 | Ets-domain proteins. | BL00345B 21.28 1.000e-40 215-266 BL00345A 13.96 2.452e-14 180-199 |
| 46 | DM01551 | kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER. | DM01551A 15.63 3.538e-26 172-202 DM01551C 14.62 3.571e-17 232-252 DM01551B 8.84 4.750e-11 214-226 |
| 47 | PR00876 | NEMATODE METALLOTHIONEIN SIGNATURE | PR00876B 7.66 9.328e-11 246-260 |
| 48 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 4.231e-33 6-45 |
| 50 | BL00972 | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 7.750e-19 994-1019 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312 |
| 51 | BL00972 | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 7.750e-19 990-1015 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312 |
| 52 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 3.063e-14 10-54 |
| 53 | PR00988 | URIDINE KINASE SIGNATURE | PR00988A 6.39 8.500e-17 20-38 PR00988F 12.23 7.828e-15 196-210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e-11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e-09 57-69 |
| 55 | PR00762 | CHLORIDE CHANNEL SIGNATURE | PR00762C 9.29 4.682e-21 294-314 PR00762D 11.29 4.103e-19 509-530 PR00762A 14.22 9.333e-18 199-217 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | PR00762F 15.12 3.100e-16 563-583 PR00762B 12.12 6.063e-16 230-250 PR00762E 12.07 2.286e-15 545-562 PR00762G 14.13 6.276e-13 601-616 |
| 56 | BL00216 | Sugar transport proteins. | BL00216B 27.64 8.800e-10 153-203 |
| 58 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 2.049e-10 1080-1135 |
| 59 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 2.049e-10 1062-1117 |
| 61 | PD01929 | KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM. | PD01929E 10.76 9.018e-09 206-221 |
| 68 | PR00360 | C2 DOMAIN SIGNATURE | PR00360A 14.59 7.395e-09 680-693 |
| 69 | PR00360 | C2 DOMAIN SIGNATURE | PR00360A 14.59 7.395e-09 670-683 |
| 70 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 8.714e-10 51-64 |
| 72 | DM00179 | w KINASE ALPHA ADHESION T-CELL. | DM00179 13.97 5.304e-09 108-118 |
| 73 | BL00239 | Receptor tyrosine kinase class II proteins. | BL00239B 25.15 7.075e-12 118-166 |
| 74 | BL00790 | Receptor tyrosine kinase class V proteins. | BL00790N 13.25 6.116e-10 93-120 |
| 76 | DM00471 | 0 PROKARYOTIC DNA TOPOISOMERASE I. | DM00471A 11.73 9.357e-13 53-66 DM00471B 8.45 4.857e-12 70-81 |
| 80 | PD02876 | DECARBOXYLASE PHOSPHATIDYLSERINE. | PD02876C 8.80 2.723e-13 223-236 PD02876D 12.13 2.588e-12 334-351 |
| 81 | PD02876 | DECARBOXYLASE PHOSPHATIDYLSERINE. | PD02876C 8.80 2.723e-13 282-295 PD02876D 12.13 2.588e-12 393-410 |
| 83 | BL00708 | Prolyl endopeptidase family serine proteins. | BL00708B 24.91 7.197e-12 570-601 |
| 84 | PR00014 | FIBRONECTIN TYPE III REPEAT SIGNATURE | PR00014C 15.44 8.043e-09 985-1004 |
| 86 | PR00678 | PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE | PR00678H 9.13 1.379e-09 246-269 |
| 89 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 8.200e-09 264-279 PR00320B 12.19 8.650e-09 264-279 |
| 93 | BL00455 | Putative AMP-binding domain proteins. | BL00455 13.31 2.588e-14 316-332 |
| 95 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 4.000e-10 123-154 |
| 96 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 4.000e-10 212-243 |
| 97 | PR00081 | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE | PR00081B 10.38 6.318e-13 134-146 PR00081A 10.53 2.500e-12 54-72 |
| 98 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 5.500e-24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e-16 529-547 PR00380C 13.18 2.756e-13 560-579 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| 102 | PR00300 | ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE | PR00300A 9.56 7.545e-14 289-308 |
| 104 | BL00479 | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 6.786e-18 298-314 BL00479A 19.86 4.913e-16 155-178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e-12 181-197 |
| 106 | BL01019 | ADP-ribosylation factors family proteins. | BL01019A 13.20 8.013e-12 43-83 |
| 107 | DM01970 | 0 kw 2K632.12 YDR313C ENDOSOMAL III. | DM01970B 8.60 5.000e-16 403-416 |
| 108 | BL00191 | Cytochrome b5 family, heme-binding domain proteins. | BL00191K 17.38 4.951e-27 238-282 BL00191J 11.37 6.447e-17 182-204 |
| 109 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 4.938e-37 8-47 |
| 110 | BL01138 | Scorpion short toxins proteins. | BL01138A 10.96 8.297e-10 38-50 |
| 113 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 5.800e-23 156-187 BL00107B 13.31 9.100e-14 225-241 |
| 117 | BL00214 | Cytosolic fatty-acid binding proteins. | BL00214B 26.51 1.000e-17 46-91 BL00214A 21.17 7.052e-11 5-31 |
| 118 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 8.560e-13 36-67 |
| 119 | PR00529 | GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE | PR00529C 11.03 7.506e-10 158-177 |
| 120 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 9.400e-09 80-95 |
| 121 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 9.400e-09 80-95 |
| 127 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 7.158e-13 216-241 |
| 128 | BL01032 | Protein phosphatase 2C proteins. | BL01032C 6.14 3.195e-12 147-157 BL01032H 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e-09 379-389 |
| 129 | BL01310 | ATP1G1 / PLM / MAT8 family proteins. | BL01310 14.74 6.694e-26 28-64 |
| 130 | PR00990 | RIBOKINASE SIGNATURE | PR00990B 12.32 9.534e-15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-09 119-133 |
| 133 | BL00880 | Acyl-CoA-binding protein. | BL00880 17.52 5.576e-26 72-122 |
| 134 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 9.308e-14 18-37 |
| 135 | PR00215 | NEUROMODULIN SIGNATURE | PR00215C 13.98 6.779e-10 475-496 |
| 136 | BL01310 | ATP1G1 / PLM / MAT8 family proteins. | BL01310 14.74 2.432e-29 71-107 |
| 140 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.882e-14 214-231 BL00028 16.07 9.471e-14 102-119 BL00028 16.07 2.800e-13 18-35 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | BL00028 16.07 5.500e-13 74-91 BL00028 16.07 9.100e-13 186-203 BL00028 16.07 8.043e-12 46-63 BL00028 16.07 8.435e-12 130-147 BL00028 16.07 9.217e-12 270-287 BL00028 16.07 6.192e-11 242-259 BL00028 16.07 4.000e-10 158-175 |
| 141 | BL00501 | Signal peptidases I serine proteins. | BL00501D 16.69 9.538e-14 113-133 BL00501C 9.61 8.688e-10 89-101 |
| 143 | BL01020 | SAR1 family proteins. | BL01020C 15.35 7.722e-20 79-130 |
| 146 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 6.400e-25 335-374 |
| 149 | BL00126 | 3'5'-cyclic nucleotide phosphodiesterases proteins. | BL00126C 22.07 1.450e-25 509-550 BL00126E 35.22 3.951e-16 654-709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e-11 483-495 BL00126A 27.56 8.269e-11 442-479 |
| 151 | BL00632 | Ribosomal protein S4 proteins. | BL00632 23.79 5.271e-20 106-149 |
| 154 | BL00559 | Eukaryotic molybdopterin oxidoreductases proteins. | BL00559I 13.63 5.304e-19 29-58 BL00559K 13.17 2.957e-18 172-199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e-12 241-259 |
| 155 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 1.692e-13 13-35 |
| 157 | BL00406 | Actins proteins. | BL00406D 12.58 2.547e-18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e-12 69-124 BL00406C 6.75 9.682e-12 128-183 |
| 160 | BL00132 | Zinc carboxypeptidases, zinc-binding region 1 proteins. | BL00132A 26.07 7.000e-14 22-63 BL00132C 21.35 3.466e-12 104-145 |
| 165 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109B 12.27 9.043e-13 139-158 |
| 168 | BL00362 | Ribosomal protein S15 proteins. | BL00362 24.67 9.700e-15 129-172 |
| 169 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 1.000e-35 640-686 BL00039A 18.44 1.964e-13 212-251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-12 465-489 |
| 175 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 3.721e-12 14-36 |
| 178 | BL01310 | ATP1G1 / PLM / MAT8 family proteins. | BL01310 14.74 2.432e-29 133-169 |
| 179 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL- | PD01066 19.43 9.455e-36 6-45 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | BINDING NU. | |
| 180 | PR00007 | COMPLEMENT C1Q DOMAIN SIGNATURE | PR00007B 14.16 7.429e-20 160-180 PR00007A 19.33 4.938e-19 133-160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-11 238-249 |
| 181 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 9.526e-24 280-323 |
| 182 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 9.526e-24 263-306 |
| 183 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 9.526e-24 280-323 |
| 184 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 9.526e-24 263-306 |
| 188 | PR00929 | AT-HOOK-LIKE DOMAIN SIGNATURE | PR00929C 5.26 3.328e-09 460-471 |
| 189 | PR00929 | AT-HOOK-LIKE DOMAIN SIGNATURE | PR00929C 5.26 3.328e-09 440-451 |
| 190 | BL00383 | Tyrosine specific protein phosphatases proteins. | BL00383F 15.51 7.188e-17 666-682 BL00383A 13.34 8.714e-17 162-177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e-14 628-639 BL00383F 15.51 1.720e-13 371-387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e-13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e-09 509-520 BL00383D 11.92 4.000e-09 589-602 BL00383B 7.61 8.000e-09 479-488 |
| 191 | PR00450 | RECOVERIN FAMILY SIGNATURE | PR00450C 12.22 7.911e-15 83-105 PR00450C 12.22 6.286e-13 47-69 |
| 193 | PF00564 | Octicosapeptide repeat proteins. | PF00564B 24.74 6.164e-16 227-278 |
| 194 | PR00503 | BROMODOMAIN SIGNATURE | PR00503D 20.81 9.156e-15 204-224 PR00503B 9.96 9.571e-13 170-187 |
| 195 | BL00901 | Cysteine synthase/cystathionine beta-synthase P-phosphate att. | BL00901C 20.63 3.429e-18 67-117 |
| 197 | BL00636 | Nt-dnaJ domain proteins. | BL00636A 8.07 6.211e-17 40-57 BL00636B 15.11 2.000e-13 67-88 |
| 198 | PR00690 | ADHESIN FAMILY SIGNATURE | PR00690A 10.86 9.866e-09 463-482 |
| 199 | BL01131 | Ribosomal RNA adenine dimethylases proteins. | BL01131A 26.62 2.343e-12 84-130 |
| 201 | PR00910 | LUTEOVIRUS ORF6 PROTEIN SIGNATURE | PR00910A 2.51 8.352e-12 509-522 |
| 203 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 2.286e-10 39-72 |
| 206 | PR00261 | LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE | PR00261A 11.02 4.462e-19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e-18 65-87 PR00261B 14.12 4.000e-18 143-165 PR00261A 11.02 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 4.833e-18 143-165 PR00261D 12.47 7.500e-18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e-16 143-165 PR00261F 11.57 4.938e-13 143-165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e-13 65-87 PR00261E 11.08 1.643e-11 143-165 |
| 209 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 6.143e-13 118-173 PF00791C 20.98 7.680e-10 132-171 |
| 211 | PR00007 | COMPLEMENT C1Q DOMAIN SIGNATURE | PR00007A 19.33 5.781e-19 131-158 PR00007B 14.16 4.115e-18 158-178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e-11 233-244 |
| 212 | BL00183 | Ubiquitin-conjugating enzymes proteins. | BL00183 28.97 1.545e-30 43-91 |
| 213 | BL00183 | Ubiquitin-conjugating enzymes proteins. | BL00183 28.97 1.545e-30 43-91 |
| 215 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 1.900e-29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e-11 364-388 BL00039B 19.19 4.064e-11 277-303 |
| 217 | BL00100 | Chloramphenicol acetyltransferase proteins. | BL00100D 17.22 8.484e-09 68-106 |
| 219 | PR00213 | MYELIN P0 PROTEIN SIGNATURE | PR00213C 15.94 3.969e-11 199-227 |
| 222 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 1.947e-09 144-155 |
| 224 | PR00875 | MOLLUSC METALLOTHIONEIN SIGNATURE | PR00875A 5.83 1.000e-09 901-913 |
| 225 | BL00636 | Nt-dnaJ domain proteins. | BL00636B 15.11 8.200e-19 18-39 |
| 226 | BL00636 | Nt-dnaJ domain proteins. | BL00636A 8.07 1.000e-21 21-38 BL00636B 15.11 8.200e-19 45-66 |
| 229 | PR00301 | 70 KD HEAT SHOCK PROTEIN SIGNATURE | PR00301F 13.98 7.563e-13 329-346 PR00301G 13.78 4.300e-12 361-382 |
| 230 | BL00460 | Glutathione peroxidases selenocysteine proteins. | BL00460A 28.67 8.773e-20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e-12 111-134 BL00460D 16.89 8.773e-11 140-160 |
| 231 | PR00647 | SENR ORPHAN RECEPTOR SIGNATURE | PR00647B 10.19 8.522e-09 273-287 |
| 233 | BL00292 | Cyclins proteins. | BL00292B 20.31 7.429e-27 244-275 BL00292A 22.87 7.750e-27 201-235 |
| 234 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 6.308e-13 7-29 PR00449C |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | 17.27 4.462e-11 47-70 PR00449D 10.79 7.120e-11 109-123 |
| 235 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 7.300e-10 251-265 PR00019B 11.36 5.320e-09 119-133 PR00019B 11.36 1.000e-08 229-243 |
| 236 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 7.300e-10 245-259 PR00019B 11.36 5.320e-09 113-127 PR00019B 11.36 1.000e-08 223-237 |
| 237 | PD00289 | PROTEIN SH3 DOMAIN REPEAT PRESVNA. | PD00289 9.97 8.448e-09 67-81 |
| 240 | PR00011 | TYPE III EGF-LIKE SIGNATURE | PR00011D 14.03 3.492e-10 616-635 |
| 241 | PR00011 | TYPE III EGF-LIKE SIGNATURE | PR00011D 14.03 3.492e-10 616-635 |
| 244 | BL00903 | Cytidine and deoxycytidylate deaminases zinc-binding region s. | BL00903 12.93 8.941e-12 54-64 |
| 245 | DM00179 | w KINASE ALPHA ADHESION T-CELL. | DM00179 13.97 8.043e-09 124-134 |
| 248 | BL00246 | Wnt-1 family proteins. | BL00246D 23.97 1.000e-40 186-239 BL00246E 20.32 1.000e-40 305-351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e-24 70-90 BL00246C 15.56 4.857e-22 150-175 |
| 250 | PR00927 | ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE | PR00927E 14.93 5.114e-10 253-275 |
| 254 | BL00674 | AAA-protein family proteins. | BL00674B 4.46 1.000e-09 223-245 |
| 255 | PD01796 | PROTEIN TRANSMEMBRANE COBALT ZINC CADMIUM. | PD01796 15.01 6.045e-09 61-88 |
| 256 | BL50002 | Src homology 3 (SH3) domain proteins profile. | BL50002B 15.18 2.800e-10 421-435 |
| 258 | PR00094 | ADENYLATE KINASE SIGNATURE | PR00094C 12.94 2.200e-18 87-104 PR00094D 12.52 2.731e-14 161-177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e-13 39-54 PR00094E 11.25 7.333e-13 178-193 |
| 259 | BL00892 | HIT family proteins. | BL00892A 18.17 5.500e-13 60-91 |
| 262 | BL00388 | Proteasome A-type subunits proteins. | BL00388A 23.14 1.000e-40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e-21 153-184 BL00388C 18.79 8.147e-16 126-148 |
| 264 | BL00903 | Cytidine and deoxycytidylate deaminases zinc-binding region s. | BL00903 12.93 5.821e-09 91-101 |
| 267 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107B 13.31 1.529e-09 241-257 |
| 270 | BL00226 | Intermediate filaments proteins. | BL00226D 19.10 1.000e-37 362-409 BL00226B |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 23.86 8.043e-35 196-244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e-15 96-111 |
| 271 | PD02952 | KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI. | PD02952C 15.76 9.731e-16 235-265 PD02952B 15.57 5.625e-09 215-229 |
| 272 | PD02929 | ADHESION GLYCOPROTEIN PRECURSOR I. | PD02929A 28.27 1.000e-40 106-160 PD02929B 18.36 8.800e-17 179-199 |
| 274 | BL01027 | Glycosyl hydrolases family 39 proteins. | BL01027B 15.34 3.486e-09 213-250 |
| 275 | PR00424 | ADENOSINE RECEPTOR SIGNATURE | PR00424D 14.32 6.451e-11 39-59 |
| 277 | BL00052 | Ribosomal protein S7 proteins. | BL00052A 27.85 6.000e-13 137-184 BL00052B 15.17 5.143e-12 208-235 |
| 279 | BL00790 | Receptor tyrosine kinase class V proteins. | BL00790N 13.25 5.659e-13 267-294 |
| 280 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e-21 51-68 PR00319B 11.47 8.200e-19 70-85 |
| 281 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319D 11.64 6.625e-23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e-21 38-55 PR00319B 11.47 8.200e-19 57-72 |
| 287 | PF00929 | Exonuclease. | PF00929D 16.17 7.366e-09 149-163 |
| 291 | BL00326 | Tropomyosins proteins. | BL00326A 14.01 2.360e-09 93-127 |
| 292 | BL00326 | Tropomyosins proteins. | BL00326A 14.01 2.360e-09 93-127 |
| 294 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 8.714e-12 203-216 |
| 295 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 5.500e-15 322-339 BL00028 16.07 9.471e-14 433-450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e-13 760-777 BL00028 16.07 9.550e-13 788-805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e-12 461-478 BL00028 16.07 8.435e-12 844-861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e-11 211-228 BL00028 16.07 5.154e-11 732-749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e-11 816-833 BL00028 16.07 7.231e-11 676-693 BL00028 16.07 9.654e-11 564-581 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | BL00028 16.07 4.086e-09 517-534 BL00028 16.07 7.429e-09 489-506 |
| 296 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 8.333e-16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e-11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-10 205-230 |
| 302 | PF00953 | Glycosyl transferase. | PF00953C 19.70 8.773e-34 236-269 PF00953A 19.68 5.000e-25 102-129 PF00953B 6.17 1.000e-13 182-194 |
| 304 | PF00152 | tRNA synthetases class II. | PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67 |
| 305 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 8.250e-35 37-76 |
| 306 | PD02784 | PROTEIN NUCLEAR RIBONUCLEOPROTEIN. | PD02784B 26.46 5.840e-09 92-135 |
| 307 | PR00454 | ETS DOMAIN SIGNATURE | PR00454C 11.24 7.808e-09 1167-1186 |
| 308 | PR00237 | RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE | PR00237E 13.03 5.091e-13 188-212 PR00237G 19.63 7.207e-13 268-295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e-10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e-10 230-255 PR00237B 13.50 9.438e-10 57-79 |
| 309 | BL00522 | DNA polymerase family X proteins. | BL00522C 11.90 7.577e-24 315-339 BL00522F 14.90 1.310e-15 470-494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e-14 430-460 BL00522B 27.30 9.625e-12 267-313 |
| 310 | BL00326 | Tropomyosins proteins. | BL00326D 8.76 5.235e-10 856-897 |
| 312 | BL00290 | Immunoglobulins and major histocompatibility complex proteins. | BL00290A 20.89 4.706e-14 151-174 BL00290B 13.17 9.000e-12 211-229 |
| 313 | BL00345 | Ets-domain proteins. | BL00345B 21.28 1.000e-40 34-85 BL00345A 13.96 9.217e-16 1-20 |
| 315 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 5.091e-15 63-76 |
| 317 | BL01020 | SARI family proteins. | BL01020C 15.35 3.198e-17 79-130 |
| 318 | BL00216 | Sugar transport proteins. | BL00216B 27.64 4.696e-11 164-214 |
| 320 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN | PR00109B 12.27 4.814e-10 216-235 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | SIGNATURE | |
| 321 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 5.688e-10 329-372 |
| 322 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109B 12.27 8.765e-12 558-577 |
| 324 | BL01241 | Link domain proteins. | BL01241 35.81 8.313e-30 183-236 BL01241 35.81 3.222e-13 282-335 |
| 326 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 4.000e-12 515-566 BL00412D 16.54 5.705e-11 516-567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e-09 514-565 BL00412D 16.54 1.918e-09 513-564 BL00412D 16.54 2.102e-09 520-571 |
| 328 | BL00232 | Cadherins extracellular repeat proteins domain proteins. | BL00232B 32.79 9.557e-20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e-18 370-418 BL00232B 32.79 5.500e-16 258-306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e-12 256-274 BL00232C 10.65 4.326e-11 368-386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-11 39-57 |
| 330 | PR00454 | ETS DOMAIN SIGNATURE | PR00454C 11.24 7.808e-09 1167-1186 |
| 331 | BL00598 | Chromo domain proteins. | BL00598 14.45 8.393e-18 27-49 |
| 333 | BL01016 | Glycoprotease family proteins. | BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93 8.855e-09 38-50 |
| 339 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 5.500e-11 17-61 |
| 340 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 1.231e-33 10-49 |
| 341 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 5.042e-09 55-109 |
| 342 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 2.400e-30 16-55 |
| 343 | DM00031 | IMMUNOGLOBULIN V REGION. | DM00031A 16.80 1.000e-40 20-68 |
| 346 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109B 12.27 4.764e-11 135-154 |
| 347 | PR00109 | TYROSINE KINASE | PR00109B 12.27 4.764e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | CATALYTIC DOMAIN SIGNATURE | 11 135-154 |
| 351 | BL01187 | Calcium-binding EGF-like domain proteins pattern proteins. | BL01187B 12.04 1.783e-13 100-116 BL01187B 12.04 8.435e-13 276-292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e-10 54-70 BL01187B 12.04 5.725e-09 231-247 BL01187A 9.98 7.000e-09 255-267 |
| 352 | PD00078 | REPEAT PROTEIN ANK NUCLEAR ANKYR. | PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181 |
| 354 | BL00380 | Rhodanese proteins. | BL00380F 9.76 6.694e-11 542-553 |
| 355 | PF00628 | PHD-finger. | PF00628 15.84 1.000e-11 116-131 |
| 356 | PR00587 | SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE | PR00587A 8.06 9.700e-09 17-37 |
| 359 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 4.462e-15 261-274 PD00066 13.92 6.500e-13 233-246 PD00066 13.92 4.300e-09 289-302 |
| 361 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 9.604e-13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e-09 71-126 PF00791B 28.49 7.440e-09 184-239 |
| 362 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 2.273e-11 279-334 |
| 363 | PR00450 | RECOVERIN FAMILY SIGNATURE | PR00450C 12.22 5.080e-10 73-95 PR00450C 12.22 3.278e-09 109-131 |
| 364 | PF00242 | DNA polymerase (viral) N-terminal domain proteins. | PF00242Q 13.51 2.328e-09 22-68 |
| 365 | PF00242 | DNA polymerase (viral) N-terminal domain proteins. | PF00242Q 13.51 2.328e-09 22-68 |
| 366 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 6.644e-09 1038-1092 |
| 367 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 1.360e-09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e-09 370-384 |
| 368 | PR00011 | TYPE III EGF-LIKE SIGNATURE | PR00011D 14.03 9.000e-15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e-14 30-49 PR00011C 24.25 5.143e-09 6-35 |
| 369 | BL01032 | Protein phosphatase 2C proteins. | BL01032H 11.25 4.150e-09 417-430 |
| 372 | BL00478 | LIM domain proteins. | BL00478B 14.79 7.750e-12 410-425 |
| 373 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 9.757e-34 26-65 |
| 376 | PR00170 | SODIUM CHANNEL SIGNATURE | PR00170E 6.48 2.739e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 10 88-118 |
| 380 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 1.000e-23 276-307 BL00107B 13.31 1.692e-12 342-358 |
| 381 | BL00455 | Putative AMP-binding domain proteins. | BL00455 13.31 5.714e-12 50-66 |
| 382 | PR00624 | HISTONE H5 SIGNATURE | PR00624G 4.08 4.900e-09 524-544 |
| 384 | PD00078 | REPEAT PROTEIN ANK NUCLEAR ANKYR. | PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181 |
| 385 | PR00511 | TEKTIN SIGNATURE | PR00511D 7.11 5.371e-09 67-80 |
| 386 | PD02870 | RECEPTOR INTERLEUKIN-1 PRECURSOR. | PD02870B 18.83 6.000e-10 97-130 |
| 388 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 5.000e-13 516-529 |
| 389 | BL00290 | Immunoglobulins and major histocompatibility complex proteins. | BL00290A 20.89 7.667e-09 151-174 |
| 390 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 5.200e-15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e-11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e-09 272-285 BL00215B 10.44 8.500e-09 165-178 |
| 394 | BL00674 | AAA-protein family proteins. | BL00674B 4.46 2.723e-16 299-321 |
| 397 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 8.579e-11 141-155 |
| 398 | PR00761 | BINDIN PRECURSOR SIGNATURE | PR00761B 9.93 6.764e-09 55-74 |
| 399 | BL00240 | Receptor tyrosine kinase class III proteins. | BL00240B 24.70 7.907e-10 118-142 |
| 401 | PF00676 | Dehydrogenase E1 component. | PF00676B 24.71 8.071e-18 331-369 PF00676D 14.40 3.854e-15 486-506 PF00676C 16.88 9.182e-14 454-478 |
| 402 | BL00514 | Fibrinogen beta and gamma chains C-terminal domain proteins. | BL00514C 17.41 4.673e-28 4432-4469 BL00514G 15.98 6.092e-14 4555-4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e-10 4519-4534 BL00514H 14.95 4.955e-10 4584-4609 |
| 403 | PF00992 | Troponin. | PF00992A 16.67 5.974e-09 105-140 |
| 404 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 1.450e-10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e-09 50-64 PR00019B 11.36 1.000e-09 96-110 |
| 405 | BL00232 | Cadherins extracellular repeat proteins domain proteins. | BL00232B 32.79 9.557e-20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e-18 358-406 BL00232B 32.79 5.500e-16 246- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 294 BL00232B 32.79 9.384e-15 463-511 BL00232C 10.65 2.537e-12 244-262 BL00232C 10.65 4.326e-11 356-374 BL00232C 10.65 7.261e-11 461-479 BL00232C 10.65 7.457e-11 27-45 |
| 407 | PF00426 | Outer Capsid protein VP4 (Hemagglutinin). | PF00426S 15.67 5.634e-09 902-940 |
| 409 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 9.695e-09 126-180 |
| 410 | BL00741 | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 2.731e-09 252-275 |
| 411 | PF00646 | F-box domain proteins. | PF00646A 14.37 6.344e-09 86-100 |
| 412 | BL00603 | Thymidine kinase cellular-type proteins. | BL00603B 11.39 8.500e-09 542-557 |
| 415 | BL00866 | Carbamoyl-phosphate synthase subdomain proteins. | BL00866B 36.29 3.571e-31 245-291 BL00866C 23.26 9.000e-25 331-366 |
| 418 | PR00239 | MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE | PR00239E 1.58 6.114e-09 590-602 |
| 421 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 7.955e-14 23-78 PF00791B 28.49 3.653e-12 273-328 PF00791B 28.49 4.273e-11 156-211 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e-09 37-76 PF00791C 20.98 5.235e-09 170-209 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e-09 189-244 PF00791B 28.49 7.028e-09 435-490 PF00791B 28.49 8.679e-09 367-422 |
| 424 | DM00892 | 3 RETROVIRAL PROTEINASE. | DM00892C 23.55 7.207e-28 1645-1679 |
| 425 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109D 17.04 5.881e-10 228-251 |
| 429 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 4.600e-11 31-40 |
| 431 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 1.844e-34 490-536 BL00039A 18.44 5.615e-19 205-244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e-15 333-357 |
| 432 | PR00452 | SH3 DOMAIN SIGNATURE | PR00452B 11.65 7.652e-12 169-185 |
| 433 | PR00828 | FORMIN SIGNATURE | PR00828B 5.23 8.210e-10 382-405 |
| 436 | BL00415 | Synapsins proteins. | BL00415N 4.29 8.643e-11 195-239 BL00415N 4.29 3.036e-09 809-853 |
| 443 | PR00834 | HTRA/DEGQ PROTEASE FAMILY SIGNATURE | PR00834F 10.91 6.040e-11 221-234 |
| 446 | PF01140 | Matrix protein (MA), | PF01140D 15.54 9.663e- |

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|------------|---------------|---|---|
| | | p15. | 10 183-218 PF01140D 15.54 3.093e-09 246-281 |
| 449 | PR00568 | DOPAMINE D3 RECEPTOR SIGNATURE | PR00568G 13.95 5.551e-09 39-53 |
| 451 | PF00084 | Sushi domain proteins (SCR repeat proteins. | PF00084B 9.45 3.813e-10 47-59 |
| 452 | BL00790 | Receptor tyrosine kinase class V proteins. | BL00790I 20.01 2.821e-09 618-649 |
| 456 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 1.000e-25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e-17 230-249 PR00380B 12.64 4.724e-16 194-212 |
| 457 | PR00253 | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE | PR00253A 9.15 9.143e-24 246-267 PR00253B 13.47 2.000e-23 272-294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e-21 452-473 |
| 467 | PR00849 | GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE | PR00849D 9.77 9.236e-09 910-937 |
| 471 | BL00678 | Trp-Asp (WD) repeat proteins. | BL00678 9.67 8.200e-12 33-44 |
| 472 | BL00226 | Intermediate filaments proteins. | BL00226B 23.86 3.721e-09 282-330 |
| 473 | BL00344 | GATA-type zinc finger domain proteins. | BL00344 17.99 7.000e-12 814-852 |
| 474 | BL00481 | Thiol-activated cytolytic proteins. | BL00481E 13.07 8.909e-09 173-199 |
| 479 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319B 11.47 2.571e-09 393-408 |
| 480 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 1.900e-38 8-47 |
| 481 | PR00405 | HIV REV INTERACTING PROTEIN SIGNATURE | PR00405C 19.41 1.000e-19 451-473 PR00405B 11.83 4.333e-18 430-448 PR00405A 17.71 4.971e-18 411-431 |
| 482 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 9.286e-10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e-09 937-952 PR00049D 0.00 8.322e-09 939-954 |
| 486 | PR00007 | COMPLEMENT C1Q DOMAIN SIGNATURE | PR00007B 14.16 8.615e-23 653-673 PR00007A 19.33 6.192e-22 626-653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e-13 732-743 |
| 487 | PD00567 | PROTEIN RNA-BINDING RNA REPEAT HYD. | PD00567B 18.23 2.853e-09 200-214 |
| 488 | PR00988 | URIDINE KINASE SIGNATURE | PR00988A 6.39 4.569e-12 3-21 |
| 489 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 4.882e-27 30-69 PD01066 19.43 3.430e-10 71-110 |
| 490 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 7.864e-09 663-678 |
| 492 | BL01128 | Shikimate kinase proteins. | BL01128A 18.84 6.464e-17 58-92 |
| 497 | PF00429 | ENV polyprotein (coat | PF00429 31.08 7.171e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | polyprotein). | 15 21-71 |
| 498 | BL00120 | Lipases, serine proteins. | BL00120B 11.37 7.923e-09 185-200 |
| 500 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 7.353e-11 299-318 |
| 501 | BL01159 | WW/rsp5/WWP domain proteins. | BL01159 13.85 8.579e-12 131-146 |
| 505 | BL00021 | Kringle domain proteins. | BL00021B 13.33 3.739e-17 492-510 |
| 508 | PR00120 | H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE | PR00120C 9.90 5.800e-19 705-722 |
| 509 | DM01417 | 6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04. | DM01417E 20.62 2.938e-16 362-395 DM01417D 11.08 3.800e-13 322-338 |
| 510 | PF00534 | Glycosyl transferases group 1. | PF00534B 14.47 6.625e-09 346-370 |
| 511 | PF00534 | Glycosyl transferases group 1. | PF00534B 14.47 6.625e-09 293-317 |
| 512 | PF00534 | Glycosyl transferases group 1. | PF00534B 14.47 6.625e-09 366-390 |
| 513 | PD01841 | PHOSPHORYLASE KINASE ALPHA MUSCL. | PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591 |
| 514 | PR00153 | CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE | PR00153C 11.01 7.188e-13 95-111 PR00153E 9.10 4.150e-12 122-138 |
| 515 | BL00740 | MAM domain proteins. | BL00740A 13.87 7.188e-12 410-423 |
| 516 | DM00892 | 3 RETROVIRAL PROTEINASE. | DM00892C 23.55 6.087e-12 1018-1052 |
| 517 | BL00242 | Integrins alpha chain proteins. | BL00242C 16.86 8.320e-09 12-42 |
| 523 | DM00031 | IMMUNOGLOBULIN V REGION. | DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 1.000e-25 84-118 |
| 525 | BL00319 | Amyloidogenic glycoprotein extracellular domain proteins. | BL00319C 17.12 8.375e-10 61-95 |
| 526 | PF00789 | Domain present in ubiquitin-regulatory proteins. | PF00789B 19.70 3.308e-12 322-343 PF00789C 20.98 5.269e-09 367-392 |
| 528 | BL01162 | Quinone oxidoreductase / zeta-crystallin proteins. | BL01162C 22.80 1.500e-16 120-164 |

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|------------|---------------|--|---|
| 529 | PR00910 | LUTEOVIRUS ORF6 PROTEIN SIGNATURE | PR00910A 2.51 3.893e-09 60-73 |
| 532 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 123-148 |
| 533 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 97-122 |
| 534 | BL00098 | Thiolases acyl-enzyme intermediate proteins. | BL00098C 21.65 2.800e-38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-35 245-288 BL00098E 22.12 1.000e-34 314-352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-11 38-50 |
| 535 | PR00370 | FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE | PR00370E 11.96 7.429e-22 321-340 PR00370D 16.33 6.143e-21 185-204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e-21 27-46 PR00370C 12.72 3.500e-20 140-157 PR00370A 3.35 6.442e-17 4-20 |
| 536 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.429e-16 285-302 BL00028 16.07 6.294e-14 341-358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e-11 397-414 BL00028 16.07 4.462e-11 453-470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-10 313-330 |
| 537 | BL00762 | WHEP-TRS domain proteins. | BL00762A 23.43 9.419e-15 844-881 |
| 538 | BL00762 | WHEP-TRS domain proteins. | BL00762A 23.43 9.419e-15 819-856 |
| 539 | BL00762 | WHEP-TRS domain proteins. | BL00762A 23.43 9.419e-15 822-859 |
| 540 | PR00985 | LEUCYL-TRNA SYNTHETASE SIGNATURE | PR00985A 12.10 9.000e-10 357-375 |
| 541 | PD02102 | SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. | PD02102A 16.74 1.000e-40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146 |
| 543 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 1.000e-10 48-65 BL00028 16.07 6.400e-10 193-210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e-09 78-95 |
| 545 | BL00250 | TGF-beta family proteins. | BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390 |
| 547 | PR00319 | BETA G-PROTEIN | PR00319B 11.47 2.714e- |

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|------------|---------------|--|--|
| | | (TRANSDUCIN) SIGNATURE | 09 186-201 PR00319A 15.27 7.344e-09 210-227 |
| 548 | BL01204 | NF-kappa-B/Rel/dorsal domain proteins. | BL01204A 17.74 1.000e-40 8-56 BL01204D 16.42 1.000e-40 177-221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e-22 141-160 BL01204B 15.41 4.333e-16 102-116 |
| 549 | PR00326 | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE | PR00326A 8.75 8.364e-15 255-276 |
| 551 | PF00632 | HECT-domain (ubiquitin-transferase). | PF00632C 20.66 3.302e-23 1569-1601 PF00632B 18.45 3.700e-21 1515-1543 |
| 554 | BL00290 | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 1.600e-14 187-205 BL00290A 20.89 2.059e-14 130-153 |
| 557 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 6.339e-09 846-879 |
| 559 | DM01111 | 4 kw PHOSPHATASE TRANSFORMING 61K PDF1. | DM01111L 11.93 3.762e-09 7-35 |
| 562 | PF00658 | Poly-adenylate binding protein, unique domain proteins. | PF00658C 16.33 9.455e-32 118-155 |
| 564 | BL00141 | Eukaryotic and viral aspartyl proteases proteins. | BL00141A 12.10 4.150e-10 472-488 |
| 566 | PF00855 | PWWP domain proteins. | PF00855 13.75 5.667e-15 272-289 |
| 567 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 4.977e-13 229-268 |
| 569 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199 |
| 570 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199 |
| 572 | PR00193 | MYOSIN HEAVY CHAIN SIGNATURE | PR00193D 14.36 1.857e-34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 508-537 |
| 573 | PR00193 | MYOSIN HEAVY CHAIN SIGNATURE | PR00193D 14.36 1.857e-34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 524-553 |
| 575 | BL00752 | XPA protein. | BL00752B 19.17 9.703e-10 885-929 |
| 576 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 7.000e-09 276-295 |
| 577 | BL00116 | DNA polymerase family B | BL00116A 12.81 5.737e- |

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|------------|---------------|--|--|
| | | proteins. | 13 864-877 BL00116B 11.82 1.529e-12 952-965 |
| 578 | BL00195 | Glutaredoxin proteins. | BL00195B 15.31 7.158e-09 121-141 |
| 579 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 9.000e-11 217-231 PR00019B 11.36 1.360e-09 386-400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e-09 363-377 |
| 580 | PR00253 | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE | PR00253A 9.15 2.125e-25 275-296 PR00253B 13.47 7.923e-24 301-323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e-20 335-357 |
| 583 | PR00343 | SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE | PR00343C 16.85 2.286e-11 1233-1252 PR00343C 16.85 5.500e-11 333-352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e-10 1491-1510 PR00343C 16.85 8.230e-10 1686-1705 |
| 584 | DM01537 | kw SKI2W SKI2 NUCLEOLAR HELICASE. | DM01537B 21.63 1.878e-37 79-126 DM01537B 21.63 9.491e-30 916-963 DM01537A 15.14 3.186e-11 784-804 |
| 586 | PF00013 | KH domain proteins family of RNA binding proteins. | PF00013 5.78 1.450e-09 124-136 |
| 587 | DM00892 | 3 RETROVIRAL PROTEINASE. | DM00892C 23.55 4.409e-13 262-296 |
| 589 | BL00478 | LIM domain proteins. | BL00478B 14.79 1.643e-13 261-276 BL00478B 14.79 7.709e-09 321-336 |
| 590 | PF00855 | PWWP domain proteins. | PF00855 13.75 8.000e-15 931-948 |
| 591 | PF00855 | PWWP domain proteins. | PF00855 13.75 8.000e-15 1062-1079 |
| 593 | PF00628 | PHD-finger. | PF00628 15.84 3.455e-12 424-439 |
| 594 | PR00205 | CADHERIN SIGNATURE | PR00205B 11.39 2.241e-16 558-576 PR00205A 14.73 9.308e-13 542-558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-10 336-354 |
| 596 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 4.789e-18 307-338 |
| 598 | PD01675 | GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3. | PD01675C 19.89 2.330e-10 55-89 |
| 600 | BL00242 | Integrins alpha chain proteins. | BL00242E 9.03 9.591e-27 985-1014 BL00242C 16.86 4.115e-26 286-316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e-12 189-199 BL00242D 13.57 3.455e-11 421-446 BL00242A 13.80 |

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|------------|---------------|--|--|
| | | | 5.000e-11 61-73 BL00242D 13.57 4.986e-10 291-316 |
| 601 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320A 16.74 5.610e-09 198-213 |
| 602 | PR00278 | PANCREATIC HORMONE SIGNATURE | PR00278A 12.43 4.569e-10 331-348 |
| 603 | BL00479 | Phorbol esters / diacylglycerol binding domain proteins. | BL00479C 12.01 3.250e-12 170-183 |
| 604 | BL00315 | Dehydrins proteins. | BL00315A 9.35 1.672e-09 424-452 |
| 605 | BL00415 | Synapsins proteins. | BL00415N 4.29 9.794e-10 295-339 |
| 606 | PR00926 | MITOCHONDRIAL CARRIER PROTEIN SIGNATURE | PR00926F 17.75 1.000e-13 335-358 |
| 608 | PF00855 | PWWP domain proteins. | PF00855 13.75 5.167e-15 265-282 |
| 609 | PF00855 | PWWP domain proteins. | PF00855 13.75 5.167e-15 211-228 |
| 612 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 7.411e-10 877-897 DM01206B 10.69 8.027e-10 861-881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10.69 1.456e-09 859-879 DM01206B 10.69 1.797e-09 879-899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-09 898-918 DM01206B 10.69 7.949e-09 871-891 DM01206B 10.69 8.291e-09 767-787 |
| 615 | PD02699 | PROTEIN DNA-BINDING BINDING DNA. | PD02699A 8.91 2.023e-28 129-158 PD02699C 24.84 1.000e-27 317-364 PD02699B 18.28 1.000e-17 158-182 |
| 616 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455 |
| 617 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455 |
| 618 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 5.143e-12 531-551 DM01206B 10.69 2.603e-10 535-555 |
| 621 | PR00700 | PROTEIN TYROSINE PHOSPHATASE SIGNATURE | PR00700B 16.80 3.160e-21 561-582 |
| 622 | BL00239 | Receptor tyrosine kinase class II proteins. | BL00239F 28.15 3.222e-10 647-692 BL00239C 18.75 8.304e-10 543-566 |
| 623 | PR00407 | EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE | PR00407K 9.94 8.448e-09 326-339 |
| 624 | BL00641 | Respiratory-chain NADH dehydrogenase 75 Kd | BL00641C 21.10 1.000e-40 157-202 BL00641E |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | subunit proteins. | 24.37 1.000e-40 255-308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-37 48-80 BL00641B 12.62 5.846e-34 113-139 BL00641D 13.23 9.308e-29 216-240 |
| 627 | PR00103 | CAMP-DEPENDENT PROTEIN KINASE SIGNATURE | PR00103E 17.80 2.500e-18 367-380 PR00103B 13.39 2.080e-14 297-312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e-12 346-358 PR00103C 15.68 1.000e-11 334-344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-10 160-175 |
| 630 | PR00081 | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE | PR00081A 10.53 6.211e-16 4-22 |
| 631 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 8.500e-14 37-50 |
| 632 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 2.233e-10 1324-1344 DM01206B 10.69 4.822e-10 1276-1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e-10 1280-1300 DM01206B 10.69 4.532e-09 1320-1340 DM01206B 10.69 7.266e-09 1326-1346 |
| 635 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 7.600e-23 145-176 BL00107B 13.31 2.636e-13 211-227 |
| 636 | BL00657 | Fork head domain proteins. | BL00657A 19.39 1.545e-30 101-143 BL00657B 22.27 7.750e-26 149-192 |
| 637 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107B 13.31 1.000e-10 607-623 |
| 643 | BL00018 | EF-hand calcium-binding domain proteins. | BL00018 7.41 4.913e-09 199-212 |
| 647 | PF00628 | PHD-finger. | PF00628 15.84 2.350e-13 385-400 PF00628 15.84 3.455e-12 464-479 |
| 648 | BL01129 | Hypothetical yabO/yceC/sfhB family proteins. | BL01129E 13.25 4.000e-25 332-357 BL01129C 25.56 8.200e-23 236-279 BL01129B 12.51 6.118e-13 191-212 |
| 649 | BL01228 | Hypothetical cof family proteins. | BL01228D 17.44 3.908e-10 455-480 |
| 650 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 6.684e-13 771-814 |
| 651 | BL50002 | Src homology 3 (SH3) domain proteins profile. | BL50002A 14.19 1.750e-12 1026-1045 |
| 653 | PR00253 | GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE | PR00253A 9.15 4.000e-24 253-274 PR00253C 13.85 8.800e-24 313-335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 20 422-443 |
| 654 | PD01719 | PRECURSOR GLYCOPROTEIN SIGNAL RE. | PD01719A 12.89 4.452e-11 969-997 PD01719A 12.89 3.961e-10 128-156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-09 1220-1248 |
| 657 | BL00354 | HMG-I and HMG-Y DNA-binding domain proteins (Ahook). | BL00354C 6.61 8.397e-09 563-578 |
| 658 | BL00354 | HMG-I and HMG-Y DNA-binding domain proteins (Ahook). | BL00354C 6.61 8.397e-09 580-595 |
| 659 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 2.174e-13 539-572 DM00215 19.43 4.750e-12 549-582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e-10 548-581 DM00215 19.43 4.054e-10 550-583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e-10 544-577 |
| 660 | PR00688 | XYLOSE ISOMERASE SIGNATURE | PR00688I 13.78 9.518e-09 224-236 |
| 661 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 5.950e-23 249-292 |
| 662 | PR00360 | C2 DOMAIN SIGNATURE | PR00360B 13.61 7.158e-10 596-610 |
| 663 | PR00360 | C2 DOMAIN SIGNATURE | PR00360B 13.61 7.158e-10 596-610 |
| 664 | PR00360 | C2 DOMAIN SIGNATURE | PR00360B 13.61 7.158e-10 596-610 |
| 666 | PR00819 | CBXX/CFQX SUPERFAMILY SIGNATURE | PR00819B 10.83 8.988e-10 704-720 |
| 667 | BL50040 | Elongation factor 1 gamma chain profile. | BL50040C 22.62 2.143e-16 135-178 |
| 668 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019B 11.36 1.360e-09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-09 163-177 |
| 670 | BL00018 | EF-hand calcium-binding domain proteins. | BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730 |
| 672 | PD00131 | ATP-BINDING TRANSPORT TRANSMEMBR. | PD00131B 34.97 1.000e-34 356-410 PD00131C 19.59 1.346e-26 504-542 |
| 673 | PR00667 | RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE | PR00667G 15.33 7.557e-10 106-123 |
| 674 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320A 16.74 4.857e-13 593-608 PR00320B 12.19 4.115e-12 635-650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e-10 635-650 PR00320C 13.01 6.400e-10 593-608 PR00320B 12.19 3.250e-09 593-608 |
| 675 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320A 16.74 4.857e-13 572-587 PR00320B 12.19 4.115e-12 614- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | 629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572- 587 PR00320B 12.19 3.250e-09 572-587 |
| 676 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 9.667e- 09 249-263 |
| 679 | PF00642 | Zinc finger C-x8-C-x5-C- x3-H type (and similar). | PF00642 11.59 3.700e- 16 225-236 PF00642 11.59 7.900e-12 187- 198 |
| 680 | PR00308 | TYPE I ANTIFREEZE PROTEIN SIGNATURE | PR00308C 3.83 8.754e- 10 286-296 |
| 681 | BL00019 | Actinin-type actin- binding domain proteins. | BL00019D 15.33 4.200e- 19 227-257 |
| 682 | PR00700 | PROTEIN TYROSINE PHOSPHATASE SIGNATURE | PR00700D 12.47 4.000e- 09 99-118 |
| 687 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 8.500e- 10 538-553 |
| 689 | BL01024 | Protein phosphatase 2A regulatory subunit PR55 proteins. | BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442 |
| 691 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 8.071e- 31 152-195 |
| 692 | BL00211 | ABC transporters family proteins. | BL00211A 12.23 5.050e- 09 45-57 |
| 693 | BL00211 | ABC transporters family proteins. | BL00211A 12.23 5.050e- 09 45-57 |
| 694 | BL00211 | ABC transporters family proteins. | BL00211A 12.23 5.050e- 09 58-70 |
| 696 | BL00680 | Methionine aminopeptidase subfamily 1 proteins. | BL00680 14.37 5.304e- 17 173-195 |
| 697 | BL00741 | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 3.418e- 11 242-265 |
| 698 | DM01930 | 2 kw FINGER SMCK SMCY YDR096W. | DM01930E 15.41 1.367e- 37 170-215 DM01930F 14.16 8.232e-28 267- 303 DM01930B 19.86 9.163e-10 37-71 |
| 700 | PR00869 | DNA-POLYMERASE FAMILY X SIGNATURE | PR00869A 12.80 1.281e- 16 245-263 |
| 701 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e- 09 161-175 |
| 702 | BL00523 | Sulfatases proteins. | BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137- |

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|------------|---------------|--|--|
| | | | 148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e-10 513-523 BL00523F 10.85 6.351e-09 413-424 |
| 703 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 8.412e-12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-09 364-374 |
| 707 | PD00787 | SYNTHASE BIOSYNTHESIS TRANSFERASE. | PD00787A 14.84 8.941e-14 66-82 |
| 708 | PR00761 | BINDIN PRECURSOR SIGNATURE | PR00761E 14.32 8.500e-10 822-841 |
| 712 | DM01354 | kw TRANSCRIPTASE REVERSE II ORF2. | DM01354Y 10.69 4.977e-38 425-465 DM01354X 13.86 7.300e-34 376-415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e-10 356-376 |
| 713 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 7.545e-27 450-496 BL00039A 18.44 2.537e-18 147-186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-13 194-220 |
| 715 | BL00383 | Tyrosine specific protein phosphatases proteins. | BL00383E 10.35 4.981e-10 150-161 |
| 717 | PF00777 | Sialyltransferase family. | PF00777C 18.60 4.035e-21 106-161 |
| 718 | DM00031 | IMMUNOGLOBULIN V REGION. | DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e-12 131-142 |
| 719 | BL00243 | Integrins beta chain cysteine-rich domain proteins. | BL00243B 17.54 1.000e-40 131-172 BL00243C 16.42 1.000e-40 172-208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e-40 314-358 BL00243I 31.77 6.571e-39 607-650 BL00243E 16.70 3.077e-35 274-304 BL00243G 21.38 3.625e-34 358-400 BL00243H 17.53 5.235e-29 567-593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e-16 477-503 BL00243H 17.53 2.304e-11 524-550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-09 610-653 |
| 720 | PR00217 | 43 KD POSTSYNAPTIC PROTEIN SIGNATURE | PR00217C 10.91 8.022e-09 20-36 |
| 722 | PR00704 | CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE | PR00704D 11.05 5.909e-34 135-161 PR00704F 13.61 7.000e-26 190-218 PR00704E 12.55 8.071e-26 165-189 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | PR00704B 17.94 2.241e-23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-18 99-116 |
| 725 | PR00194 | TROPOMYOSIN SIGNATURE | PR00194A 7.86 7.652e-09 169-187 |
| 726 | PR00194 | TROPOMYOSIN SIGNATURE | PR00194A 7.86 7.652e-09 169-187 |
| 727 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 2.125e-13 277-292 PR00320A 16.74 1.310e-11 277-292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e-11 323-338 PR00320B 12.19 4.343e-10 323-338 PR00320B 12.19 6.914e-10 277-292 |
| 731 | PR00195 | DYNAMIN SIGNATURE | PR00195A 11.94 8.627e-16 288-307 PR00195E 9.82 3.912e-11 457-474 |
| 733 | PF00642 | Zinc finger C-x8-C-x5-C-x3-H type (and similar). | PF00642 11.59 9.082e-10 787-798 |
| 738 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039A 18.44 2.565e-28 26-65 BL00039D 21.67 2.105e-20 338-384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e-11 73-99 |
| 739 | BL01289 | TSC-22 / dip / bun family proteins. | BL01289A 12.18 8.909e-31 326-353 BL01289B 10.45 9.571e-17 353-383 |
| 742 | BL01019 | ADP-ribosylation factors family proteins. | BL01019A 13.20 7.078e-12 41-81 |
| 743 | BL00965 | Phosphomannose isomerase type I proteins. | BL00965C 23.78 1.000e-40 256-305 BL00965B 17.77 1.600e-25 126-153 BL00965A 10.57 6.400e-19 94-113 |
| 747 | BL00021 | Kringle domain proteins. | BL00021D 24.56 4.563e-25 231-273 BL00021B 13.33 5.345e-21 60-78 |
| 748 | BL00612 | Osteonectin domain proteins. | BL00612B 11.35 2.034e-11 93-126 |
| 749 | PR00450 | RECOVERIN FAMILY SIGNATURE | PR00450C 12.22 6.880e-10 135-157 |
| 752 | BL00795 | Involucrin proteins. | BL00795C 17.06 6.000e-11 384-429 BL00795C 17.06 9.444e-11 370-415 |
| 754 | BL00051 | Ribosomal protein L39e proteins. | BL00051 20.92 1.935e-16 4-50 |
| 755 | DM01970 | 0 kw ZK632.12 YDR313C ENDOSOMAL III. | DM01970B 8.60 7.723e-09 171-184 |
| 760 | BL01020 | SAR1 family proteins. | BL01020C 15.35 9.020e-12 99-150 |
| 762 | BL00046 | Histone H2A proteins. | BL00046 12.95 1.000e-40 33-88 |
| 763 | PD02411 | PROTEIN TRANSCRIPTION REGULATION NUCLEAR. | PD02411 21.89 9.137e-10 206-240 |
| 764 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 8.800e-29 417-460 |
| 767 | BL01208 | VWFC domain proteins. | BL01208B 15.83 6.063e-10 309-324 BL01208B 15.83 8.031e-10 165- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | | 180 BL01208B 15.83 4.162e-09 85-100 |
| 770 | BL00031 | Nuclear hormones receptors DNA-binding region proteins. | BL00031A 19.55 9.571e-32 208-241 BL00031B 22.25 5.500e-27 242-274 |
| 772 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 1.450e-18 4-26 PR00449E 13.50 3.520e-14 142-165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e-13 107-121 PR00449B 14.34 3.455e-11 27-44 |
| 773 | BL00523 | Sulfatases proteins. | BL00523E 19.27 9.333e-23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-10 141-152 BL00523F 10.85 5.821e-10 373-384 |
| 775 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.686e-09 568-585 |
| 776 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.686e-09 621-638 |
| 777 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.686e-09 595-612 |
| 778 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 8.412e-11 322-341 BL00030A 14.39 7.000e-10 220-239 |
| 779 | PR00079 | GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE | PR00079B 12.98 2.929e-26 193-222 PR00079E 16.65 4.150e-23 348-375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e-16 264-281 PR00079A 16.12 6.769e-13 169-183 |
| 781 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 9.250e-17 10-35 BL00215A 15.82 6.000e-16 221-246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e-11 168-181 |
| 783 | PD00289 | PROTEIN SH3 DOMAIN REPEAT PRESNA. | PD00289 9.97 6.276e-09 159-173 |
| 785 | BL00690 | DEAH-box subfamily ATP-dependent helicases proteins. | BL00690B 13.38 1.000e-12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-09 218-228 |
| 786 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449C 17.27 8.500e-16 50-73 PR00449A 13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-11 150-173 PR00449D 10.79 1.545e-09 111-125 |
| 788 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 8.767e-10 1-21 |
| 790 | BL00915 | Phosphatidylinositol 3- and 4-kinases proteins. | BL00915C 22.43 9.182e-39 725-764 BL00915B |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | 22.78 5.050e-33 633-671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e-13 395-407 |
| 791 | PR00208 | GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE | PR00208A 12.59 6.294e-10 120-138 PR00208A 12.59 6.294e-10 121-139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-10 123-141 PR00208A 12.59 6.294e-10 124-142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e-10 126-144 PR00208A 12.59 6.294e-10 127-145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e-10 129-147 PR00208A 12.59 7.411e-09 130-148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e-09 132-150 PR00208A 12.59 8.274e-09 118-136 PR00208A 12.59 8.274e-09 119-137 |
| 795 | PR00205 | CADHERIN SIGNATURE | PR00205B 11.39 5.034e-16 302-320 PR00205A 14.73 1.257e-11 284-300 PR00205C 13.65 1.333e-11 337-352 |
| 796 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 4.000e-12 196-247 BL00412D 16.54 5.705e-11 197-248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e-09 195-246 BL00412D 16.54 1.918e-09 194-245 BL00412D 16.54 2.102e-09 201-252 |
| 797 | BL00021 | Kringle domain proteins. | BL00021B 13.33 6.339e-13 40-58 |
| 799 | BL01052 | Calponin family repeat proteins. | BL01052C 18.51 1.000e-40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-25 52-78 BL01052D 10.26 5.737e-25 174-194 |
| 800 | BL00348 | p53 tumor antigen proteins. | BL00348F 23.19 3.714e-09 197-240 |
| 801 | BL00309 | Vertebrate galactoside-binding lectin proteins. | BL00309C 18.65 1.621e-09 62-87 |
| 802 | PR00245 | OLFACTORY RECEPTOR SIGNATURE | PR00245D 10.47 5.224e-09 187-199 |
| 804 | PF00774 | Dihydropyridine sensitive L-type calcium channel (Beta subuni. | PF00774A 16.47 8.457e-10 110-156 |
| 808 | PR00667 | RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE | PR00667C 11.71 9.875e-09 12-28 |
| 810 | PD02346 | PHOTOSYSTEM II PROTEIN PRECURSOR | PD02346F 12.89 4.340e-09 317-354 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | PHOTOSYNTHESIS. | |
| 811 | BL00685 | CBF-A/NF-YB subunit proteins. | BL00685B 14.41 6.779e-14 54-95 BL00685A 11.22 4.798e-13 5-54 |
| 812 | PR00080 | ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE | PR00080A 9.32 9.419e-10 93-105 |
| 813 | BL00357 | Histone H2B proteins. | BL00357 7.74 1.988e-17 22-65 |
| 815 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 7.923e-15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e-14 18-31 PD00066 13.92 7.000e-13 130-143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e-13 102-115 PD00066 13.92 4.429e-12 186-199 PD00066 13.92 1.783e-11 74-87 |
| 816 | BL01195 | Peptidyl-tRNA hydrolase proteins. | BL01195C 20.12 3.348e-20 100-139 |
| 820 | BL00520 | Interleukin-10 family proteins. | BL00520A 6.21 6.471e-09 1-14 |
| 822 | BL00972 | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972A 11.93 8.113e-09 224-242 |
| 825 | PR00876 | NEMATODE METALLOTHIONEIN SIGNATURE | PR00876B 7.66 2.268e-10 101-115 |
| 829 | PD02855 | FLAVOPROTEIN PROTEIN DNA/PANTOTHEN. | PD02855A 18.37 4.732e-28 88-124 PD02855B 8.36 6.478e-09 132-142 |
| 830 | PR00405 | HIV REV INTERACTING PROTEIN SIGNATURE | PR00405B 11.83 7.000e-21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-13 25-45 |
| 831 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 1.000e-09 47-61 PR00019B 11.36 1.720e-09 136-150 PR00019B 11.36 3.880e-09 44-58 |
| 832 | PR00011 | TYPE III EGF-LIKE SIGNATURE | PR00011B 13.08 3.438e-16 164-183 PR00011D 14.03 6.850e-16 164-183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e-12 231-260 PR00011D 14.03 9.852e-11 212-231 |
| 834 | PD00306 | PROTEIN GLYCOPROTEIN PRECURSOR RE. | PD00306A 10.26 7.000e-12 232-246 |
| 835 | PD00306 | PROTEIN GLYCOPROTEIN PRECURSOR RE. | PD00306A 10.26 4.000e-10 290-304 |
| 836 | PD00306 | PROTEIN GLYCOPROTEIN PRECURSOR RE. | PD00306A 10.26 7.000e-12 216-230 |
| 837 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 3.898e-09 78-111 |
| 839 | PD02784 | PROTEIN NUCLEAR RIBONUCLEOPROTEIN. | PD02784B 26.46 8.302e-09 73-116 |
| 840 | PR00700 | PROTEIN TYROSINE PHOSPHATASE SIGNATURE | PR00700B 16.80 5.091e-22 369-390 PR00700D 12.47 5.765e-21 491-510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 11 538-549 PR00700E 17.57 3.100e-10 522-538 |
| 841 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109E 12.27 5.404e-13 134-153 |
| 844 | PD02785 | PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP. | PD02785E 14.43 1.000e-40 58-112 PD02785A 15.23 1.915e-28 8-57 |
| 845 | BL00826 | MARCKS family proteins. | BL00826C 7.63 6.738e-09 203-230 |
| 846 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 4.429e-10 15-24 |
| 849 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 1.000e-08 340-349 |
| 850 | PR00308 | TYPE I ANTIFREEZE PROTEIN SIGNATURE | PR00308A 5.90 6.506e-09 12-27 |
| 851 | PD02411 | PROTEIN TRANSCRIPTION REGULATION NUCLEAR. | PD02411 21.89 7.000e-16 246-280 |
| 852 | BL00420 | Speract receptor repeat proteins domain proteins. | BL00420B 22.67 1.000e-40 723-778 BL00420B 22.67 1.321e-38 933-988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 587-642 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 808-819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1018-1029 BL00420C 11.90 7.955e-10 567-578 |
| 853 | BL00420 | Speract receptor repeat proteins domain proteins. | BL00420B 22.67 1.000e-40 756-811 BL00420B 22.67 1.321e-38 966-1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 620-675 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 841-852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1051-1062 BL00420C 11.90 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 7.955e-10 567-578 |
| 857 | PR00388 | 3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE | PR00388A 10.45 2.778e-09 64-83 |
| 859 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147 |
| 861 | PR00988 | URIDINE KINASE SIGNATURE | PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-10 60-72 |
| 863 | BL00215 | Mitochondrial energy transfer proteins. | BL00215B 10.44 8.071e-12 41-54 |
| 864 | PR00775 | 90 KD HEAT SHOCK PROTEIN SIGNATURE | PR00775E 8.06 1.000e-24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e-17 153-171 PR00775G 10.64 6.850e-15 267-286 PR00775F 12.76 6.769e-14 249-267 |
| 866 | DM01688 | 2 POLY-IG RECEPTOR. | DM01688G 16.45 9.460e-09 89-121 |
| 867 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 5.596e-29 14-53 |
| 868 | BL01287 | RNA 3'-terminal phosphate cyclase proteins. | BL01287A 17.95 2.688e-26 16-48 |
| 869 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 6.464e-10 304-337 |
| 872 | BL00046 | Histone H2A proteins. | BL00046 12.95 1.000e-40 30-85 |
| 874 | BL00188 | Biotin-requiring enzymes attachment site proteins. | BL00188 30.29 9.036e-32 665-711 |
| 876 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 7.686e-09 298-315 |
| 877 | PD02102 | SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. | PD02102A 16.74 4.176e-10 97-141 |
| 879 | BL01189 | Ribosomal protein S12e proteins. | BL01189A 14.27 1.000e-40 35-71 BL01189B 13.49 1.000e-40 71-125 |
| 882 | BL00284 | Serpins proteins. | BL00284C 28.56 6.400e-25 62-104 BL00284B 17.99 6.182e-12 35-56 |
| 889 | BL00216 | Sugar transport proteins. | BL00216B 27.64 4.375e-21 35-85 |
| 896 | PR00391 | PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE | PR00391E 12.50 7.785e-15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-13 191-207 PR00391A 7.83 5.390e-11 16-36 |
| 897 | PR00327 | ICE NUCLEATION PROTEIN | PR00327C 6.37 5.247e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | SIGNATURE | 09 313-328 |
| 898 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 7.800e-26 386-432 BL00039A 18.44 6.674e-16 113-152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-11 236-260 |
| 901 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 8.200e-16 254-267 PD00066 13.92 8.200e-16 282-295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e-16 366-379 PD00066 13.92 8.200e-16 394-407 PD00066 13.92 8.200e-14 338-351 |
| 902 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 9.321e-11 6-50 |
| 903 | PR00806 | VINCULIN SIGNATURE | PR00806B 4.28 9.160e-09 97-111 |
| 904 | PR00381 | KINESIN LIGHT CHAIN SIGNATURE | PR00381E 8.75 6.586e-25 335-356 PR00381B 18.17 2.667e-24 204-224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e-24 226-245 PR00381D 13.94 1.084e-22 291-309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e-13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e-11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e-09 333-351 PR00381C 12.48 7.120e-09 310-329 |
| 906 | PR00345 | STATHMIN FAMILY SIGNATURE | PR00345C 4.54 8.557e-09 525-549 |
| 907 | PR00345 | STATHMIN FAMILY SIGNATURE | PR00345C 4.54 8.557e-09 513-537 |
| 908 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 9.308e-11 144-155 |
| 910 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 2.800e-30 48-87 |
| 912 | BL01104 | Ribosomal protein L13e proteins. | BL01104C 15.14 6.000e-09 364-392 |
| 922 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 3.842e-09 500-511 |
| 923 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 2.500e-09 323-338 PR00320C 13.01 5.500e-09 187-202 |
| 924 | PD02181 | PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT. | PD02181D 12.85 8.609e-09 36-64 |
| 926 | BL00019 | Actinin-type actin-binding domain proteins. | BL00019C 14.66 7.453e-25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e-11 205-235 BL00019A 12.56 2.373e-10 34-45 |
| 928 | BL00678 | Trp-Asp (WD) repeat | BL00678 9.67 9.308e-11 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | proteins proteins. | 273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217 |
| 929 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 1.857e-10 137-146 |
| 930 | BL01085 | Ribulose-phosphate 3-epimerase family proteins. | BL01085D 16.55 4.600e-24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 172-202 BL01085C 21.81 2.038e-14 66-97 |
| 931 | BL01085 | Ribulose-phosphate 3-epimerase family proteins. | BL01085D 16.55 4.600e-24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 190-220 BL01085C 21.81 2.038e-14 66-97 |
| 933 | PD00301 | PROTEIN REPEAT MUSCLE CALCIUM-BI. | PD00301A 10.24 6.400e-09 160-171 |
| 936 | PF00168 | C2 domain proteins. | PF00168C 27.49 4.000e-12 336-362 |
| 937 | BL00415 | Synapsins proteins. | BL00415N 4.29 9.519e-10 5-49 |
| 940 | PR00862 | PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE | PR00862D 16.17 4.086e-09 63-84 |
| 945 | BL01230 | RNA methyltransferase trmA family proteins. | BL01230B 11.62 2.373e-09 407-420 |
| 948 | BL00479 | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 7.429e-18 52-68 BL00479A 19.86 2.200e-13 26-49 |
| 949 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 1.474e-09 100-111 |
| 954 | PD01311 | PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE. | PD01311A 30.23 5.909e-10 66-111 |
| 955 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 3.250e-12 47-60 |
| 956 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 3.250e-12 47-60 |
| 957 | BL00379 | CDP-alcohol phosphatidyltransferases proteins. | BL00379 24.64 1.610e-15 111-148 |
| 959 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 1.884e-10 31-75 |
| 960 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 3.438e-14 110-154 |
| 962 | BL00061 | Short-chain dehydrogenases/reductase s family proteins. | BL00061B 25.79 6.586e-13 198-236 |
| 963 | PR00502 | MUTT DOMAIN SIGNATURE | PR00502A 15.06 8.200e-11 210-225 |
| 966 | PR00308 | TYPE I ANTIFREEZE PROTEIN SIGNATURE | PR00308A 5.90 7.035e-09 55-70 |
| 967 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 1.286e-12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-10 73-93 DM01206B 10.69 3.962e-09 108-128 DM01206B 10.69 5.671e-09 38-58 |
| 969 | PF01008 | Initiation factor 2 subunit. | PF01008B 25.59 4.724e-31 417-460 PF01008C 12.25 5.333e-18 506-526 PF01008A 20.14 5.875e-15 369-390 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| 970 | BL01277 | Ribonuclease PH proteins. | BL01277C 10.18 7.648e-10 112-143 BL01277A 17.39 9.806e-10 40-78 |
| 975 | BL01159 | WW/rsp5/WWP domain proteins. | BL01159 13.85 3.605e-12 130-145 BL01159 13.85 4.122e-10 171-186 |
| 977 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791C 20.98 2.235e-09 55-94 |
| 978 | BL01167 | Ribosomal protein L17 proteins. | BL01167B 20.66 8.258e-19 88-127 |
| 979 | BL00478 | LIM domain proteins. | BL00478B 14.79 9.357e-13 33-48 BL00478B 14.79 7.250e-12 98-113 |
| 980 | PR00312 | CALSEQUESTRIN SIGNATURE | PR00312E 8.32 3.423e-36 169-199 PR00312I 15.78 5.286e-35 332-361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e-35 263-291 PR00312J 13.73 5.688e-34 363-392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e-33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e-32 230-258 PR00312A 11.70 6.914e-27 35-59 |
| 981 | PF00992 | Troponin. | PF00992A 16.67 8.816e-09 414-449 |
| 982 | PR00299 | ALPHA CRYSTALLIN SIGNATURE | PR00299F 13.20 2.367e-09 127-149 |
| 983 | BL01150 | Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins. | BL01150B 17.16 1.000e-40 156-202 BL01150A 14.10 8.200e-39 100-138 |
| 986 | BL00795 | Involucrin proteins. | BL00795C 17.06 7.211e-14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e-10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e-09 3-48 |
| 987 | BL00939 | Ribosomal protein L1e proteins. | BL00939F 17.27 5.393e-09 810-840 |
| 988 | PR00452 | SH3 DOMAIN SIGNATURE | PR00452B 11.65 6.538e-11 525-541 |
| 989 | PR00452 | SH3 DOMAIN SIGNATURE | PR00452B 11.65 6.538e-11 497-513 |
| 994 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 2.500e-25 146-189 |
| 997 | BL01304 | ubiH/COQ6 monooxygenase family proteins. | BL01304A 8.05 3.893e-11 65-79 |
| 998 | DM01767 | 5 TRANSMITTER DOMAIN. | DM01767B 10.07 7.868e-09 22-39 |
| 1000 | PR00926 | MITOCHONDRIAL CARRIER PROTEIN SIGNATURE | PR00926C 16.07 1.750e-24 73-94 PR00926D 10.53 3.250e-23 126-145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e- 15 11-25 PR00926F 17.75 5.565e-09 120- 143 |
| 1005 | BL00406 | Actins proteins. | BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46 |
| 1006 | BL00406 | Actins proteins. | BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46 |
| 1007 | PR00304 | TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE | PR00304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431 |
| 1009 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. | PD01066 19.43 2.929e- 32 9-48 |
| 1011 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. | PD01066 19.43 2.929e- 32 68-107 |
| 1012 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 6.143e- 10 64-73 |
| 1016 | PD01168 | SYNTHETASE LIGASE PROTEIN ALANYL. | PD01168H 12.08 1.000e- 11 174-194 |
| 1018 | PD00930 | PROTEIN GTPASE DOMAIN ACTIVATION. | PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183 |
| 1022 | BL00175 | Phosphoglycerate mutase family phosphohistidine proteins. | BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111 |
| 1025 | PR00305 | 14-3-3 PROTEIN ZETA SIGNATURE | PR00305D 16.34 1.439e- 10 158-185 |
| 1026 | BL00353 | HMC1/2 proteins. | BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335 |
| 1028 | BL00183 | Ubiquitin-conjugating enzymes proteins. | BL00183 28.97 1.310e- 33 43-91 |
| 1033 | PF00580 | UvrD/REP helicase. | PF00580A 13.37 4.720e- 09 111-133 |
| 1034 | PR00413 | HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE | PR00413E 15.78 3.429e- 09 154-171 |
| 1037 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. | PD01066 19.43 9.657e- 09 5-44 |
| 1038 | PD01796 | PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU. | PD01796 15.01 4.259e- 11 55-82 |
| 1039 | BL00299 | Ubiquitin domain proteins. | BL00299 28.84 9.036e- 09 17-69 |
| 1040 | PR00970 | ARGININE ADP- RIBOSYLTRANSFERASE | PR00970A 17.73 6.143e- 20 56-78 PR00970D |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | SIGNATURE | 9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e-13 86-105 PR00970C 11.05 1.643e-11 115-130 PR00970E 11.23 9.820e-11 202-218 |
| 1042 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 2.200e-10 243-254 |
| 1043 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 6.786e-13 114-128 PR00048A 10.52 1.000e-09 172-186 |
| 1045 | BL00615 | C-type lectin domain proteins. | BL00615A 16.68 1.720e-11 218-236 BL00615B 12.25 1.857e-10 317-331 |
| 1046 | BL01092 | Adenylate cyclases class-I proteins. | BL01092N 13.54 8.924e-10 3-40 |
| 1047 | BL01216 | ATP-citrate lyase / succinyl-CoA ligases family proteins. | BL01216D 21.75 4.316e-28 314-344 BL01216A 13.91 1.000e-10 97-112 |
| 1049 | DM00031 | IMMUNOGLOBULIN V REGION. | DM00031B 15.41 7.618e-12 102-136 |
| 1050 | BL01073 | Ribosomal protein L24e proteins. | BL01073 24.30 1.000e-40 12-62 |
| 1054 | BL00571 | Amidases proteins. | BL00571 25.69 5.875e-31 160-212 |
| 1055 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 5.235e-11 98-117 BL00030B 7.03 4.316e-09 137-147 |
| 1058 | BL00223 | Annexins repeat proteins domain proteins. | BL00223C 24.79 8.754e-23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-11 118-152 |
| 1060 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 3.455e-35 158-201 |
| 1064 | BL00455 | Putative AMP-binding domain proteins. | BL00455 13.31 6.211e-13 280-296 |
| 1065 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 2.000e-09 115-129 PR00019B 11.36 3.880e-09 87-101 |
| 1066 | PR00326 | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE | PR00326A 8.75 4.600e-16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-14 172-191 PR00326D 19.09 1.257e-13 217-236 |
| 1071 | PD02870 | RECEPTOR INTERLEUKIN-1 PRECURSOR. | PD02870B 18.83 8.518e-11 164-197 |
| 1072 | PF00856 | SET domain proteins. | PF00856A 26.14 5.976e-09 350-387 |
| 1075 | BL01009 | Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. | BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-11 159-175 |
| 1077 | PR00724 | CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE | PR00724A 10.91 1.000e-08 366-379 |
| 1078 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 1.000e-12 170-195 BL00215A 15.82 7.529e-10 79-104 |
| 1079 | BL00678 | Trp-Asp (WD) repeat | BL00678 9.67 4.316e-09 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | proteins proteins. | 298-309 |
| 1081 | BL00326 | Tropomyosins proteins. | BL00326A 14.01 7.398e-10 23-57 |
| 1094 | BL00460 | Glutathione peroxidases selenocysteine proteins. | BL00460A 28.67 3.204e-18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e-12 162-182 BL00460C 14.35 5.500e-09 133-156 |
| 1095 | PD02811 | PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN. | PD02811A 20.67 3.017e-22 67-105 PD02811B 17.07 2.263e-21 118-151 PD02811C 13.25 5.696e-13 154-167 |
| 1096 | PD02811 | PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN. | PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160 |
| 1097 | BL00479 | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 6.143e-09 200-216 |
| 1105 | PF00881 | Nitroreductase family. | PF00881A 27.15 9.229e-13 111-147 |
| 1109 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 3.077e-10 15-37 PR00449E 13.50 1.857e-09 185-208 PR00449D 10.79 8.364e-09 131-145 |
| 1115 | PR00405 | HIV REV INTERACTING PROTEIN SIGNATURE | PR00405B 11.83 5.737e-20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-10 63-85 |
| 1116 | BL00355 | HMG14 and HMG17 proteins. | BL00355 5.97 2.528e-25 20-51 |
| 1117 | BL00355 | HMG14 and HMG17 proteins. | BL00355 5.97 2.528e-25 20-51 |
| 1120 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107B 13.31 4.857e-10 290-306 |
| 1123 | PR00412 | EPOXIDE HYDROLASE SIGNATURE | PR00412F 18.76 9.526e-12 301-324 |
| 1125 | PR00186 | HEMERYTHRIN SIGNATURE | PR00186A 13.62 2.800e-09 87-101 |
| 1129 | BL00170 | Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur. | BL00170C 18.49 3.077e-33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-15 10-37 |
| 1131 | BL00636 | Nt-dnaJ domain proteins. | BL00636A 8.07 5.304e-15 29-46 BL00636B 15.11 1.360e-14 59-80 |
| 1132 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 6.211e-09 29-40 |
| 1133 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 6.211e-09 29-40 |
| 1136 | BL00990 | Clathrin adaptor complexes medium chain proteins. | BL00990C 18.78 4.176e-38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-27 157-187 BL00990D 16.13 5.320e-18 403-422 |
| 1137 | PR00314 | CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE | PR00314B 15.68 8.000e-34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | 32 159-188 PR00314A 14.53 1.281e-22 13-34 |
| 1139 | BL011115 | GTP-binding nuclear protein ran proteins. | BL011115A 10.22 6.364e-13 13-57 |
| 1141 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107A 18.39 4.000e-19 451-482 BL00107B 13.31 3.077e-12 519-535 |
| 1148 | PR00685 | TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE | PR00685A 13.62 4.676e-09 21-42 |
| 1155 | PD01652 | RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB. | PD01652B 8.50 9.396e-10 522-574 PD01652B 8.50 9.463e-10 740-792 |
| 1157 | PD02894 | HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE. | PD02894A 21.96 7.873e-28 81-127 PD02894B 13.93 1.188e-27 178-211 |
| 1159 | BL00623 | GMC oxidoreductases proteins. | BL00623E 15.00 3.531e-20 391-414 BL00623C 10.86 4.240e-20 155-176 |
| 1161 | PD01937 | DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-. | PD01937A 6.68 3.475e-09 330-341 |
| 1162 | PD01937 | DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-. | PD01937A 6.68 3.475e-09 221-232 |
| 1163 | PR00624 | HISTONE H5 SIGNATURE | PR00624D 11.94 7.455e-10 214-239 PR00624D 11.94 1.961e-09 312-337 |
| 1167 | BL00226 | Intermediate filaments proteins. | BL00226B 23.86 7.384e-09 302-350 |
| 1177 | BL01032 | Protein phosphatase 2C proteins. | BL01032G 8.33 1.422e-10 34-48 |
| 1178 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320A 16.74 1.794e-10 205-220 PR00320C 13.01 7.840e-10 205-220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e-09 35-50 PR00320B 12.19 9.100e-09 79-94 |
| 1180 | PR00454 | ETS DOMAIN SIGNATURE | PR00454D 10.89 4.150e-19 765-784 |
| 1181 | BL00291 | Prion protein. | BL00291A 4.49 8.962e-11 152-187 |
| 1184 | BL00720 | Guanine-nucleotide dissociation stimulators CDC25 family sign. | BL00720B 16.57 4.103e-18 1089-1113 |
| 1185 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 4.553e-13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-11 104-129 |
| 1187 | BL00983 | Ly-6 / u-PAR domain proteins. | BL00983C 12.69 2.761e-10 77-93 |
| 1188 | BL00878 | Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment s1. | BL00878B 10.95 6.000e-16 189-204 BL00878C 17.74 8.435e-15 225-245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-09 270-289 |
| 1191 | PD02939 | PROTEIN GLUTATHIONE SYNTHETASE SY. | PD02939B 10.10 2.723e-12 203-220 PD02939C 20.01 1.000e-11 224-252 |
| 1193 | PR00345 | STATHMIN FAMILY SIGNATURE | PR00345B 7.12 2.800e-28 72-101 PR00345B |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 8.54 7.652e-28 149-174 PR00345C 4.54 9.100e-28 101-125 PR00345D 10.97 1.964e-24 125-149 PR00345A 13.46 5.645e-16 43-62 |
| 1194 | PR00345 | STATHMIN FAMILY SIGNATURE | PR00345B 7.12 2.800e-28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e-28 137-161 PR00345D 10.97 1.964e-24 161-185 PR00345A 13.46 5.645e-16 79-98 |
| 1195 | PF00995 | Sec1 family. | PF00995B 17.37 1.120e-13 224-264 |
| 1196 | BL00982 | Bacterial-type phytoene dehydrogenase proteins. | BL00982A 18.41 6.738e-11 15-47 |
| 1197 | BL01298 | Dihydrodipicolinate reductase proteins. | BL01298A 13.90 5.959e-09 51-73 |
| 1203 | BL00061 | Short-chain dehydrogenases/reductase s family proteins. | BL00061B 25.79 1.000e-14 152-190 |
| 1204 | PR00118 | BETA-LACTAMASE CLASS A SIGNATURE | PR00118F 16.42 9.386e-09 213-229 |
| 1206 | BL01183 | ubiE/COQ5 methyltransferase family proteins. | BL01183B 21.31 1.429e-37 184-229 BL01183D 27.71 8.535e-27 264-307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258 |
| 1208 | BL00979 | G-protein coupled receptors family 3 proteins. | BL00979L 20.63 2.485e-09 105-146 |
| 1209 | PF00023 | Ank repeat proteins. | PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55 |
| 1212 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 7.750e-14 227-241 PR00048A 10.52 4.316e-11 199-213 |
| 1213 | PR00450 | RECOVERIN FAMILY SIGNATURE | PR00450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64 |
| 1216 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 5.598e-10 179-230 |
| 1219 | PR00456 | RIBOSOMAL PROTEIN P2 SIGNATURE | PR00456E 3.06 5.348e-11 249-264 |
| 1222 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 7.231e-15 295-308 PD00066 13.92 7.231e-15 406-419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e-12 434-447 PD00066 13.92 3.348e-11 350-363 |
| 1223 | BL50058 | G-protein gamma subunit profile. | BL50058 27.23 1.000e-40 13-61 |
| 1226 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 8.439e-09 279-330 |
| 1227 | BL00437 | Catalase proximal heme-ligand proteins. | BL00437A 18.82 1.000e-40 49-101 BL00437B 16.28 1.000e-40 114-168 BL00437C 21.86 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | 1.000e-40 190-239 BL00437D 25.72 1.000e-40 248-301 BL00437E 23.95 1.000e-40 327-379 |
| 1230 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 8.297e-10 6-60 |
| 1231 | PR00735 | GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE | PR00735A 11.19 6.857e-09 391-405 |
| 1232 | PR00497 | NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE | PR00497A 6.92 5.553e-10 158-176 |
| 1233 | PR00497 | NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE | PR00497A 6.92 5.553e-10 158-176 |
| 1235 | BL00866 | Carbamoyl-phosphate synthase subdomain proteins. | BL00866B 36.29 2.776e-09 75-121 |
| 1237 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 1.818e-21 36-79 |
| 1243 | PR00403 | WW DOMAIN SIGNATURE | PR00403B 12.19 1.184e-11 10-25 |
| 1246 | PD01168 | SYNTHETASE LIGASE PROTEIN ALANYL. | PD01168L 9.47 2.837e-10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e-10 183-198 |
| 1249 | BL00018 | EF-hand calcium-binding domain proteins. | BL00018 7.41 2.800e-10 183-196 |
| 1254 | BL00183 | Ubiquitin-conjugating enzymes proteins. | BL00183 28.97 2.440e-36 96-144 |
| 1255 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 5.670e-11 8-52 |
| 1256 | BL00373 | Phosphoribosylglycinamide formyltransferase proteins. | BL00373C 10.35 3.348e-12 143-156 |
| 1258 | PR00011 | TYPE III EGF-LIKE SIGNATURE | PR00011B 13.08 3.217e-10 174-193 |
| 1259 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 8.286e-10 31-40 |
| 1261 | PR00070 | DIHYDROFOLATE REDUCTASE SIGNATURE | PR00070D 11.63 1.000e-15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e-12 16-27 |
| 1262 | BL00462 | Gamma-glutamyltranspeptidase proteins. | BL00462A 20.89 6.438e-24 140-183 BL00462B 17.88 5.500e-20 230-267 BL00462C 27.41 2.023e-11 292-347 |
| 1263 | BL00038 | Myc-type, 'helix-loop-helix' dimerization domain proteins. | BL00038B 16.97 9.455e-11 62-83 |
| 1264 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 5.670e-11 17-61 |
| 1266 | PR00837 | ALLERGEN V5/TPX-1 FAMILY SIGNATURE | PR00837C 17.21 2.714e-18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e-12 201-215 |
| 1269 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449C 17.27 9.308e-22 40-63 PR00449B 13.50 1.000e-16 137-160 PR00449D 10.79 3.520e-11 102-116 |
| 1270 | BL00276 | Channel forming collicins proteins. | BL00276A 8.87 1.500e-09 17-29 |
| 1275 | PD02327 | GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO. | PD02327C 15.47 9.769e-09 228-243 |
| 1276 | PR00412 | EPOXIDE HYDROLASE | PR00412B 12.59 7.894e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | SIGNATURE | 12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23 3.400e-11 100-119 |
| 1277 | PF00756 | Putative esterase. | PF00756C 14.12 9.538e- 10 127-157 |
| 1279 | BL00134 | Serine proteases, trypsin family, histidine proteins. | BL00134A 11.96 9.325e- 13 128-145 |
| 1280 | BL01220 | Phosphatidylethanolamine -binding protein family proteins. | BL01220C 14.75 9.348e- 15 248-276 |
| 1285 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 2.286e- 10 33-42 |
| 1287 | PF00791 | Domain present in ZO-1 and Unc5-like netrin receptors. | PF00791B 28.49 7.182e- 11 288-343 |
| 1292 | PR00802 | SERUM ALBUMIN FAMILY SIGNATURE | PR00802B 16.51 1.610e- 10 81-105 |
| 1297 | PR00716 | M-PHASE INDUCER PHOSPHATASE SIGNATURE | PR00716C 17.65 5.696e- 09 23-44 |
| 1298 | BL00478 | LIM domain proteins. | BL00478B 14.79 6.478e- 14 268-283 |
| 1301 | BL00127 | Pancreatic ribonuclease family proteins. | BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68 |
| 1302 | PR00637 | TYPE 3 BOMBESIN RECEPTOR SIGNATURE | PR00637E 11.27 4.250e- 09 290-306 |
| 1307 | BL00215 | Mitochondrial energy transfer proteins. | BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82 2.658e-13 107-132 |
| 1308 | PR00898 | VASOPRESSIN V2 RECEPTOR SIGNATURE | PR00898H 11.34 4.682e- 09 552-572 |
| 1309 | PD00301 | PROTEIN REPEAT MUSCLE CALCIUM-BI. | PD00301B 5.49 2.731e- 09 390-401 |
| 1310 | BL00983 | Ly-6 / u-PAR domain proteins. | BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22 |
| 1313 | BL00194 | Thioredoxin family proteins. | BL00194 12.16 1.900e- 11 15-28 |
| 1314 | BL00594 | Aromatic amino acids permeases proteins. | BL00594A 16.75 8.969e- 10 53-97 |
| 1316 | BL00134 | Serine proteases, trypsin family, histidine proteins. | BL00134A 11.96 9.325e- 13 128-145 |
| 1320 | BL00783 | Ribosomal protein L13 proteins. | BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86 |
| 1327 | PF00514 | Armadillo/beta-catenin- like repeat proteins. | PF00514A 31.30 7.268e- 11 82-120 |
| 1329 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178 |
| 1331 | PR00497 | NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE | PR00497A 6.92 7.239e- 09 25-43 |
| 1332 | PR00161 | NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE | PR00161C 9.51 4.930e- 09 317-337 |
| 1333 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. | PD01066 19.43 6.769e- 33 10-49 |
| 1336 | PR00700 | PROTEIN TYROSINE PHOSPHATASE SIGNATURE | PR00700D 12.47 2.200e- 09 262-281 |
| 1337 | PR00700 | PROTEIN TYROSINE | PR00700D 12.47 2.200e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | PHOSPHATASE SIGNATURE | 09 211-230 |
| 1340 | PR00860 | VERTEBRATE METALLOTHIONEIN SIGNATURE | PR00860A 5.46 5.034e-13 5-18 |
| 1341 | BL00893 | mutT domain proteins. | BL00893 18.99 6.750e-16 46-71 |
| 1343 | BL01282 | BIR repeat proteins. | BL01282B 30.49 5.974e-21 383-422 |
| 1344 | DM00099 | 4 kw ASSR REDUCTASE TERMINAL DIHYDROPTERIDINE. | DM00099B 14.73 8.313e-09 417-427 |
| 1345 | BL00923 | Aspartate and glutamate racemases proteins. | BL00923B 11.41 5.935e-10 135-146 |
| 1348 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 7.231e-13 44-57 |
| 1350 | PR00193 | MYOSIN HEAVY CHAIN SIGNATURE | PR00193D 14.36 3.571e-32 416-445 PR00193C 12.60 6.318e-31 179-207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e-22 470-499 PR00193A 15.41 1.783e-20 77-97 |
| 1352 | PR00447 | NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN SIGNATURE | PR00447E 9.73 1.554e-15 299-319 PR00447D 13.54 3.408e-15 200-224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-10 353-373 |
| 1353 | BL00303 | S-100/ICaBP type calcium binding protein. | BL00303A 21.77 6.667e-26 45-82 BL00303B 26.15 1.000e-24 93-130 |
| 1355 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 5.950e-29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-18 225-249 BL00039B 19.19 3.182e-14 141-167 |
| 1357 | PF00615 | Regulator of G protein signalling domain proteins. | PF00615B 16.25 2.216e-12 84-101 PF00615C 10.06 8.412e-12 162-176 |
| 1360 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 9.234e-29 10-49 |
| 1361 | PR00925 | NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE | PR00925A 5.47 5.091e-18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-12 53-64 PR00925D 6.56 1.857e-10 76-87 |
| 1362 | BL01272 | Glucokinase regulatory protein family proteins. | BL01272B 19.61 6.870e-30 136-171 BL01272C 11.68 3.314e-25 249-274 BL01272A 6.49 1.231e-18 99-117 |
| 1363 | BL01272 | Glucokinase regulatory protein family proteins. | BL01272B 19.61 6.870e-30 113-148 BL01272C 11.68 3.314e-25 226-251 BL01272A 6.49 1.231e-18 76-94 |
| 1364 | DM00179 | w KINASE ALPHA ADHESION T-CELL. | DM00179 13.97 5.304e-09 167-177 |
| 1368 | PR00169 | POTASSIUM CHANNEL SIGNATURE | PR00169A 16.77 1.592e-09 76-96 |
| 1370 | PR00988 | URIDINE KINASE SIGNATURE | PR00988A 6.39 1.794e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 10 1-19 |
| 1371 | BL00242 | Integrins alpha chain proteins. | BL00242B 8.13 8.615e-09 469-479 |
| 1372 | PR00625 | DNAJ PROTEIN FAMILY SIGNATURE | PR00625B 13.48 7.353e-19 46-67 PR00625A 12.84 1.391e-16 14-34 |
| 1373 | BL00434 | HSF-type DNA-binding domain proteins. | BL00434C 23.85 3.778e-09 90-130 |
| 1374 | PR00962 | LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE | PR00962C 8.00 6.337e-09 505-526 |
| 1375 | PD02475 | MUCIN EPITHELIAL TUMOR-ASSOCIATE. | PD02475A 23.18 8.552e-10 1111-1150 |
| 1376 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 9.571e-32 24-63 |
| 1380 | BL00194 | Thioredoxin family proteins. | BL00194 12.16 8.333e-12 48-61 |
| 1381 | DM01970 | 0 kw ZK632.12 YDR313C ENDOSOMAL III. | DM01970B 8.60 1.458e-15 1123-1136 |
| 1383 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 7.600e-10 243-254 |
| 1384 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 7.600e-10 271-282 |
| 1385 | BL00303 | S-100/ICaBP type calcium binding protein. | BL00303B 26.15 6.203e-10 95-132 |
| 1386 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 5.042e-09 1574-1628 |
| 1387 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 1.000e-11 52-61 |
| 1389 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 3.600e-30 10-49 |
| 1390 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 3.512e-31 32-71 |
| 1392 | PR00308 | TYPE I ANTIFREEZE PROTEIN SIGNATURE | PR00308C 3.83 9.723e-10 127-137 |
| 1393 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 9.625e-25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-16 208-226 PR00380C 13.18 6.538e-16 243-262 |
| 1394 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 3.400e-14 462-475 PD00066 13.92 8.800e-14 348-361 PD00066 13.92 9.571e-12 405-418 PD00066 13.92 6.087e-11 490-503 PD00066 13.92 8.043e-11 320-333 |
| 1398 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 6.786e-32 10-49 |
| 1400 | DM01206 | CORONAVIRUS NUCLEOCAPSID PROTEIN. | DM01206B 10.69 7.038e-09 270-290 |
| 1406 | PD00930 | PROTEIN GTPASE DOMAIN ACTIVATION. | PD00930A 25.62 7.324e-15 363-389 |
| 1407 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 7.500e-10 457-476 |
| 1408 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 9.550e-11 179-193 PR00019A 11.19 8.826e-10 228-242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 09 176-190 |
| 1409 | PR00510 | NEBULIN SIGNATURE | PR00510A 9.09 4.150e-12 182-202 PR00510B 12.96 8.767e-12 210-230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e-09 251-267 |
| 1410 | PD00078 | REPEAT PROTEIN ANK NUCLEAR ANKYR. | PD00078B 13.14 5.696e-09 31-44 |
| 1412 | BL00358 | Ribosomal protein L5 proteins. | BL00358B 22.76 1.000e-40 57-103 BL00358C 13.75 6.087e-14 122-136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e-11 33-44 |
| 1414 | BL00282 | Kazal serine protease inhibitors family proteins. | BL00282 16.88 7.338e-10 511-534 |
| 1415 | BL00023 | Type II fibronectin collagen-binding domain proteins. | BL00023 24.31 4.300e-29 40-77 |
| 1417 | PR00681 | RIBOSOMAL PROTEIN S1 SIGNATURE | PR00681G 12.54 2.149e-09 38-60 |
| 1418 | DM00973 | 3 kw RESISTANCE BENOMYL YLLO28W CYCLOHEXIMIDE. | DM00973A 21.17 1.462e-09 171-208 |
| 1419 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319B 11.47 1.571e-09 428-443 |
| 1420 | PD01941 | TRANSMEMBRANE COTRANSPORTER SYMP. | PD01941A 14.81 1.000e-40 142-196 PD01941B 15.02 7.049e-30 400-447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e-19 488-543 PD01941D 27.18 9.614e-18 641-690 PD01941F 28.52 5.382e-15 1038-1093 |
| 1422 | PR00205 | CADHERIN SIGNATURE | PR00205B 11.39 8.043e-12 199-217 |
| 1423 | PR00209 | ALPHA/BETA GLIADIN FAMILY SIGNATURE | PR00209B 4.88 6.318e-11 1009-1028 |
| 1424 | BL50002 | Src homology 3 (SH3) domain proteins profile. | BL50002A 14.19 8.200e-14 367-386 BL50002A 14.19 9.250e-12 298-317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-09 244-258 |
| 1425 | PF00628 | PHD-finger. | PF00628 15.84 3.045e-12 330-345 |
| 1426 | PF00628 | PHD-finger. | PF00628 15.84 3.045e-12 377-392 |
| 1427 | PR00405 | HIV REV INTERACTING PROTEIN SIGNATURE | PR00405B 11.83 5.114e-16 281-299 PR00405A 17.71 4.306e-14 262-282 |
| 1428 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 5.219e-34 147-193 |
| 1429 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320C 13.01 8.920e-10 577-592 |
| 1430 | PR00378 | INOSITOL PHOSPHATASE SIGNATURE | PR00378D 16.86 7.563e-12 295-314 PR00378B 13.80 8.650e-10 166-186 |
| 1431 | PR00928 | GRAVES DISEASE CARRIER | PR00928B 13.53 3.769e- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | PROTEIN SIGNATURE | 10 103-124 |
| 1433 | BL01113 | Clq domain proteins. | BL01113B 18.26 7.049e-15 14-50 BL01113C 13.18 7.000e-12 82-102 |
| 1434 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319B 11.47 7.983e-10 135-150 |
| 1436 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030A 14.39 1.000e-12 84-103 |
| 1438 | BL00290 | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 2.500e-09 250-268 BL00290A 20.89 4.000e-09 188-211 |
| 1440 | PR00806 | VINCULIN SIGNATURE | PR00806B 4.28 4.960e-09 38-52 |
| 1441 | PR00806 | VINCULIN SIGNATURE | PR00806B 4.28 4.960e-09 88-102 |
| 1444 | BL00422 | Granins proteins. | BL00422D 19.48 1.000e-08 114-138 |
| 1445 | PD01841 | PHOSPHORYLASE KINASE ALPHA MUSCL. | PD01841A 21.71 1.000e-40 73-123 PD01841B 14.35 1.000e-40 144-185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e-40 296-345 PD01841G 24.26 1.000e-40 349-403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e-40 895-932 PD01841L 18.42 1.000e-40 1083-1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e-35 1041-1071 PD01841H 21.30 3.189e-31 435-472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-20 1175-1194 |
| 1446 | PF00816 | H-NS histone family. | PF00816B 13.84 8.875e-09 190-220 |
| 1447 | PR00048 | C2H2-TYPE ZINC FINGER SIGNATURE | PR00048A 10.52 2.080e-09 402-416 |
| 1448 | DM00315 | 072 RIBONUCLEASE INHIBITOR. | DM00315D 18.40 7.393e-09 23-67 |
| 1451 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030B 7.03 2.800e-10 94-104 |
| 1454 | DM01688 | 2 POLY-IG RECEPTOR. | DM01688D 13.44 7.146e-09 382-405 |
| 1455 | PF00777 | Sialyltransferase family. | PF00777C 18.60 2.929e-22 4-59 |
| 1457 | BL00927 | Trehalase proteins. | BL00927C 10.83 8.085e-09 42-53 |
| 1460 | BL00545 | Aldose 1-epimerase proteins. | BL00545C 11.28 7.353e-17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-09 140-153 |
| 1466 | PR00097 | ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE | PR00097C 9.42 9.069e-09 233-245 |
| 1472 | BL01129 | Hypothetical yabO/yceC/sfhB family proteins. | BL01129E 13.25 5.250e-22 170-195 BL01129C 25.56 9.526e-18 63-106 |
| 1473 | BL00790 | Receptor tyrosine kinase class V proteins. | BL00790I 20.01 2.821e-09 2114-2145 |
| 1475 | PF00686 | Starch binding domain proteins. | PF00686A 13.45 9.100e-09 267-277 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| 1477 | PF00566 | Probable rabGAP domain proteins. | PF00566A 12.64 7.333e-10 466-476 |
| 1478 | BL00030 | Eukaryotic RNA-binding region RNP-1 proteins. | BL00030B 7.03 9.400e-10 43-53 |
| 1479 | DM00406 | GLIADIN. | DM00406 7.73 8.541e-10 292-305 |
| 1480 | BL00290 | Immunoglobulins and major histocompatibility complex proteins. | BL00290B 13.17 2.385e-15 69-87 BL00290A 20.89 5.091e-11 12-35 |
| 1481 | PR00150 | PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE | PR00150F 10.45 9.039e-09 21-51 |
| 1482 | PF00780 | Domain found in NIK1-like kinases, mouse citron and yeast ROM. | PF00780I 14.69 4.825e-09 107-137 |
| 1483 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 1.153e-09 108-162 |
| 1485 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 5.909e-25 17-56 |
| 1486 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107B 13.31 1.529e-09 34-50 |
| 1488 | BL00039 | DEAD-box subfamily ATP-dependent helicases proteins. | BL00039D 21.67 9.586e-10 116-162 |
| 1490 | BL00166 | Enoyl-CoA hydratase/isomerase proteins. | BL00166D 22.87 2.607e-24 190-226 BL00166C 18.93 5.500e-14 140-167 BL00166B 16.92 9.357e-11 93-115 |
| 1491 | BL00452 | Guanylate cyclases proteins. | BL00452D 28.59 3.700e-31 63-106 BL00452E 11.92 3.045e-13 115-131 |
| 1492 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 3.667e-09 532-546 |
| 1497 | BL00107 | Protein kinases ATP-binding region proteins. | BL00107B 13.31 1.000e-11 384-400 BL00107A 18.39 5.345e-11 322-353 |
| 1500 | PF00876 | Ogre family. | PF00876E 7.99 1.947e-10 107-117 |
| 1502 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 4.789e-24 112-155 |
| 1503 | BL00027 | 'Homeobox' domain proteins. | BL00027 26.43 4.789e-24 112-155 |
| 1505 | BL01177 | Anaphylatoxin domain proteins. | BL01177E 20.64 5.800e-24 448-475 BL01177C 17.39 5.333e-19 402-421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e-15 427-445 |
| 1506 | BL00972 | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 5.500e-14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e-10 341-363 |
| 1512 | BL00523 | Sulfatases proteins. | BL00523E 19.27 4.536e-22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e-09 159-170 BL00523G 9.46 5.333e-09 256-266 |
| 1516 | BL00914 | Syntaxin / epimorphin family proteins. | BL00914 24.91 7.045e-14 168-218 |
| 1518 | BL00600 | Aminotransferases class-III pyridoxal-phosphate attachment si. | BL00600A 17.98 6.143e-19 98-122 BL00600E 16.43 1.771e-17 302- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|--|
| | | | 331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e- 15 160-186 BL00600C 16.18 6.040e-12 190- 206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e- 10 281-295 |
| 1523 | PD00930 | PROTEIN GTPASE DOMAIN ACTIVATION. | PD00930B 33.72 9.600e- 18 41-82 |
| 1528 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e- 09 106-121 |
| 1538 | DM01970 | 0 kw ZK632.12 YDR313C ENDOSOMAL III. | DM01970B 8.60 4.508e- 15 171-184 |
| 1539 | PF00781 | Diacylglycerol kinase catalytic domain proteins (presumed). | PF00781D 11.11 7.593e- 10 103-127 |
| 1540 | PR00965 | OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE | PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406 |
| 1541 | BL01013 | Oxysterol-binding protein family proteins. | BL01013D 26.81 9.719e- 17 163-207 |
| 1543 | PD02699 | PROTEIN DNA-BINDING BINDING DNA. | PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509 |
| 1544 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82 |
| 1547 | BL00951 | ER lumen protein retaining receptor proteins. | BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 BL00951B 14.23 6.250e- 33 38-69 |
| 1548 | BL00536 | Ubiquitin-activating enzyme proteins. | BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279 |
| 1549 | PR00139 | ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE | PR00139C 11.72 9.679e- 09 550-569 |
| 1553 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 5.119e- 09 58-73 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| 1556 | BL00061 | Short-chain dehydrogenases/reductase s family proteins. | BL00061B 25.79 6.276e-13 67-105 |
| 1557 | BL01228 | Hypothetical cof family proteins. | BL01228D 17.44 8.105e-12 107-132 |
| 1558 | BL01228 | Hypothetical cof family proteins. | BL01228D 17.44 8.105e-12 107-132 |
| 1559 | BL01228 | Hypothetical cof family proteins. | BL01228D 17.44 8.105e-12 107-132 |
| 1562 | BL00522 | DNA polymerase family X proteins. | BL00522C 11.90 6.600e-18 412-436 BL00522B 27.30 1.738e-16 364-410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551-575 |
| 1563 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 1.947e-11 46-59 |
| 1564 | BL00299 | Ubiquitin domain proteins. | BL00299 28.84 2.823e-10 324-376 |
| 1566 | BL01013 | Oxysterol-binding protein family proteins. | BL01013D 26.81 8.594e-17 184-228 BL01013C 9.97 4.906e-12 14-24 |
| 1567 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306 |
| 1570 | BL00479 | Phorbol esters / diacylglycerol binding domain proteins. | BL00479B 12.57 5.235e-17 297-313 BL00479A 19.86 6.625e-15 271-294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e-12 173-189 |
| 1576 | PR00665 | OXYTOCIN RECEPTOR SIGNATURE | PR00665G 12.36 4.673e-24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e-22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-15 11-25 |
| 1577 | DM00099 | 4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE. | DM00099B 14.73 9.308e-10 127-137 |
| 1579 | BL00524 | Somatomedin B domain proteins. | BL00524A 9.65 6.776e-14 52-73 |
| 1580 | PD02894 | HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE. | PD02894B 13.93 6.959e-16 182-215 PD02894A 21.96 2.125e-10 57-103 |
| 1581 | BL00411 | Kinesin motor domain proteins. | BL00411C 15.04 5.292e-12 32-54 BL00411H 15.66 4.441e-11 245-276 |
| 1582 | PR00604 | CLASS IA AND IB CYTOCHROME C SIGNATURE | PR00604A 11.13 2.440e-09 79-87 |
| 1584 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 1.000e-10 225-238 |
| 1585 | DM01551 | kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER. | DM01551C 14.62 9.455e-11 125-145 |
| 1586 | DM01354 | kw TRANSCRIPTASE REVERSE II ORF2. | DM01354S 11.61 7.750e-09 474-495 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| 1587 | PR00072 | MALIC ENZYME SIGNATURE | PR00072B 13.77 7.955e-33 180-210 PR00072A 12.75 6.040e-25 120-145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-22 276-295 PR00072E 10.54 1.360e-19 301-318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e-15 332-349 |
| 1589 | BL00191 | Cytochrome b5 family, heme-binding domain proteins. | BL00191H 15.64 1.537e-22 61-113 BL00191K 17.38 9.027e-12 398-442 |
| 1590 | DM01970 | 0 kw ZK632.12 YDR313C ENDOSOMAL III. | DM01970B 8.60 7.716e-13 211-224 DM01970B 8.60 2.157e-12 94-107 |
| 1591 | DM00517 | 5 kw NUCLEAR 60.7 NUP1 CHROMOSOME. | DM00517B 10.96 6.625e-16 1175-1193 DM00517A 8.21 1.000e-11 1015-1026 |
| 1592 | BL00037 | Myb DNA-binding domain proteins repeat proteins proteins. | BL00037B 15.92 3.250e-27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e-10 146-164 |
| 1595 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 1.514e-09 110-127 |
| 1598 | PF00628 | PHD-finger. | PF00628 15.84 3.250e-11 1667-1682 |
| 1599 | PR00014 | FIBRONECTIN TYPE III REPEAT SIGNATURE | PR00014D 12.04 5.500e-09 980-995 |
| 1600 | BL00518 | Zinc finger, C3HC4 type (RING finger), proteins. | BL00518 12.23 6.571e-10 30-39 |
| 1602 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 5.402e-10 136-187 |
| 1605 | PF00651 | BTB (also known as BR-C/Ttk) domain proteins. | PF00651 15.00 3.571e-10 44-57 |
| 1607 | BL00252 | Interferon alpha, beta and delta family proteins. | BL00252A 18.49 6.657e-23 20-57 BL00252B 19.78 9.125e-16 58-109 |
| 1610 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 1.000e-08 61-94 |
| 1611 | BL00904 | Protein prenyltransferases alpha subunit repeat proteins proteins. | BL00904C 8.98 7.353e-10 91-125 BL00904D 1.47 6.018e-09 127-168 |
| 1612 | PF00168 | C2 domain proteins. | PF00168C 27.49 3.250e-09 365-391 |
| 1613 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 6.051e-09 932-983 BL00412D 16.54 7.153e-09 933-984 |
| 1614 | BL00559 | Eukaryotic molybdopterin oxidoreductases proteins. | BL00559I 13.63 3.531e-25 54-83 BL00559K 13.17 2.957e-18 197-224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e-16 266-284 |
| 1615 | PD01427 | TRANSFERASE METHYLTRANSFERASE BI. | PD01427B 22.45 3.025e-22 500-541 PD01427A 19.94 8.773e-18 439- |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|---|
| | | | 472 |
| 1616 | BL00115 | Eukaryotic RNA polymerase II heptapeptide repeat proteins. | BL00115Z 3.12 7.485e-09 152-201 BL00115Z 3.12 9.603e-09 145-194 |
| 1617 | BL00303 | S-100/ICaBP type calcium binding protein. | BL00303B 26.15 7.750e-32 51-88 BL00303A 21.77 1.947e-31 4-41 |
| 1618 | BL01254 | Fetuin family proteins. | BL01254F 10.02 8.754e-09 137-147 |
| 1619 | PD01888 | PEPTIDE REDUCTASE PROTEIN METHI. | PD01888B 25.10 1.000e-40 47-97 PD01888C 21.56 7.000e-30 125-155 PD01888A 12.84 8.800e-15 7-23 |
| 1621 | PR00239 | MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE | PR00239E 1.58 3.455e-09 692-704 PR00239E 1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-09 702-714 PR00239E 1.58 5.193e-09 703-715 |
| 1622 | PR00860 | VERTEBRATE METALLOTHIONEIN SIGNATURE | PR00860B 7.04 1.900e-18 27-41 PR00860C 9.61 1.474e-14 41-51 PR00860A 5.46 1.720e-14 5-18 |
| 1624 | PR00784 | MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE | PR00784D 15.86 8.027e-11 77-95 |
| 1626 | BL00325 | Actin-depolymerizing proteins. | BL00325B 21.66 1.000e-40 93-139 BL00325A 24.83 6.786e-23 61-93 |
| 1631 | BL00064 | L-lactate dehydrogenase proteins. | BL00064B 23.57 1.000e-40 82-130 BL00064C 17.28 1.000e-40 137-182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.882e-36 286-331 BL00064A 21.16 1.000e-33 22-60 BL00064D 14.19 6.500e-31 182-212 |
| 1632 | PR00063 | RIBOSOMAL PROTEIN L27 SIGNATURE | PR00063B 15.24 9.700e-11 59-84 PR00063A 11.71 1.614e-09 34-59 |
| 1634 | PR00239 | MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE | PR00239D 0.00 1.105e-11 36-49 PR00239C 3.51 2.538e-09 37-45 |
| 1636 | BL01210 | Caveolins proteins. | BL01210B 13.92 9.531e-10 133-183 |
| 1637 | BL00982 | Bacterial-type phytoene dehydrogenase proteins. | BL00982A 18.41 5.388e-11 11-43 |
| 1639 | BL01183 | ubiE/COQ5 methyltransferase family proteins. | BL01183B 21.31 8.144e-12 132-177 |
| 1640 | PR00015 | GRAM-POSITIVE COCCUS SURFACE PROTEIN ANCHOR SIGNATURE | PR00015B 9.84 8.468e-10 128-149 |
| 1641 | PR00320 | G-PROTEIN BETA WD-40 REPEAT SIGNATURE | PR00320B 12.19 5.935e-11 364-379 PR00320A 16.74 7.828e-11 364-379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-10 364-379 PR00320B 12.19 5.114e-10 279-294 PR00320A 16.74 1.659e-09 279-294 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| | | | PR00320A 16.74 2.098e-09 229-244 |
| 1642 | PF00023 | Ank repeat proteins. | PF00023A 16.03 6.464e-09 114-130 |
| 1643 | PR00169 | POTASSIUM CHANNEL SIGNATURE | PR00169A 16.77 1.806e-11 74-94 |
| 1644 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539 |
| 1645 | BL01108 | Ribosomal protein L24 proteins. | BL01108A 20.33 7.366e-17 56-89 |
| 1646 | PR00380 | KINESIN HEAVY CHAIN SIGNATURE | PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310 |
| 1647 | DM01242 | 3 THREONINE--TRNA LIGASE. | DM01242C 17.15 9.791e-37 340-381 DM01242E 23.00 5.071e-31 463-505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e-18 265-314 DM01242F 10.61 7.618e-14 526-540 |
| 1649 | PD00126 | PROTEIN REPEAT DOMAIN TPR NUCLEA. | PD00126A 22.53 5.500e-10 13-34 |
| 1651 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 6.720e-11 431-485 |
| 1652 | BL00933 | FGGY family of carbohydrate kinases proteins. | BL00933A 17.50 4.673e-12 11-35 BL00933E 13.80 9.217e-09 456-472 |
| 1653 | BL00795 | Involucrin proteins. | BL00795C 17.06 2.988e-10 70-115 |
| 1654 | BL00982 | Bacterial-type phytoene dehydrogenase proteins. | BL00982A 18.41 7.750e-17 302-334 |
| 1655 | BL00982 | Bacterial-type phytoene dehydrogenase proteins. | BL00982A 18.41 7.750e-17 282-314 |
| 1656 | BL00741 | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 1.391e-16 607-630 |
| 1657 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 7.938e-11 114-136 |
| 1658 | PR00910 | LUTEOVIRUS ORF6 PROTEIN SIGNATURE | PR00910A 2.51 8.889e-10 442-455 |
| 1659 | BL00972 | Ubiquitin carboxyl-terminal hydrolases family 2 proteins. | BL00972D 22.55 4.140e-12 376-401 BL00972E 20.72 5.629e-09 446-468 |
| 1660 | BL00406 | Actins proteins. | BL00406D 12.58 8.767e-15 188-243 |
| 1661 | PR00105 | CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE | PR00105A 10.36 4.900e-13 1140-1157 PR00105B 12.32 2.800e-12 1259-1274 PR00105C 10.86 1.000e-10 1305-1319 |
| 1662 | BL00280 | Pancreatic trypsin inhibitor (Kunitz) family proteins. | BL00280 24.61 3.172e-33 3119-3163 |
| 1663 | PR00319 | BETA G-PROTEIN (TRANSDUCIN) SIGNATURE | PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e-19 51-68 PR00319B 11.47 8.200e-19 70-85 |

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|------------|---------------|---|--|
| 1664 | BL00018 | EF-hand calcium-binding domain proteins. | BL00018 7.41 5.050e-10 489-502 |
| 1667 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 8.500e-38 7-46 |
| 1669 | BL01153 | NOL1/NOP2/sun family proteins. | BL01153D 19.69 1.188e-17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e-10 13-37 |
| 1671 | PR00678 | PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE | PR00678H 9.13 3.100e-10 1146-1169 |
| 1672 | BL00598 | Chromo domain proteins. | BL00598 14.45 8.500e-20 27-49 |
| 1673 | PR00326 | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE | PR00326A 8.75 8.329e-09 686-707 |
| 1674 | PR00049 | WILM'S TUMOUR PROTEIN SIGNATURE | PR00049D 0.00 7.580e-11 343-358 PR00049D 0.00 1.286e-10 342-357 |
| 1676 | PR00747 | GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE | PR00747H 12.76 8.636e-19 427-448 PR00747G 14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328 |
| 1677 | PR00747 | GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE | PR00747H 12.76 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210 |
| 1680 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331 |
| 1681 | BL00678 | Trp-Asp (WD) repeat proteins proteins. | BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254 |
| 1683 | PR00326 | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE | PR00326A 8.75 1.346e-13 389-410 |
| 1685 | PR00646 | RDC1 ORPHAN RECEPTOR SIGNATURE | PR00646H 6.32 4.188e-09 755-771 |
| 1690 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 6.644e-09 75-129 |
| 1691 | PR00456 | RIBOSOMAL PROTEIN P2 SIGNATURE | PR00456E 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435 |
| 1692 | PR00456 | RIBOSOMAL PROTEIN P2 SIGNATURE | PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504 |
| 1693 | BL00674 | AAA-protein family proteins. | BL00674C 22.60 8.043e-24 274-317 BL00674B |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|---|---|
| | | | 4.46 4.000e-23 241-263 BL00674D 23.41 8.560e-18 338-385 BL00674E 15.24 1.720e-15 414-434 |
| 1697 | PR00409 | PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE | PR00409F 12.70 4.388e-10 427-447 |
| 1698 | PR00466 | CYTOCHROME B-245 HEAVY CHAIN SIGNATURE | PR00466C 10.17 3.443e-13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e-09 498-517 |
| 1699 | BL00028 | Zinc finger, C2H2 type, domain proteins. | BL00028 16.07 9.217e-12 283-300 BL00028 16.07 3.769e-11 255-272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e-11 227-244 BL00028 16.07 1.600e-10 199-216 |
| 1700 | BL01019 | ADP-ribosylation factors family proteins. | BL01019A 13.20 3.348e-15 62-102 BL01019B 19.49 4.000e-15 107-162 |
| 1703 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 2.484e-12 200-239 |
| 1707 | PR00109 | TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE | PR00109B 12.27 4.558e-14 134-153 |
| 1710 | PR00019 | LEUCINE-RICH REPEAT SIGNATURE | PR00019A 11.19 2.565e-10 116-130 PR00019B 11.36 4.600e-09 113-127 PR00019B 11.36 7.120e-09 204-218 |
| 1711 | BL01159 | WW/resp5/WWP domain proteins. | BL01159 13.85 6.523e-11 232-247 BL01159 13.85 5.408e-10 613-628 |
| 1712 | PF00023 | Ank repeat proteins. | PF00023A 16.03 7.000e-10 187-203 |
| 1713 | PF00642 | Zinc finger C-x8-C-x5-C-x3-H type (and similar). | PF00642 11.59 9.550e-11 230-241 |
| 1714 | PF00642 | Zinc finger C-x8-C-x5-C-x3-H type (and similar). | PF00642 11.59 9.550e-11 230-241 |
| 1715 | BL01115 | GTP-binding nuclear protein ran proteins. | BL01115A 10.22 7.129e-09 7-51 |
| 1718 | BL00353 | HMG1/2 proteins. | BL00353C 14.83 6.018e-10 136-183 BL00353B 11.47 8.866e-09 86-136 |
| 1719 | BL00412 | Neuromodulin (GAP-43) proteins. | BL00412D 16.54 5.408e-09 432-483 |
| 1721 | BL00038 | Myc-type, 'helix-loop-helix' dimerization domain proteins. | BL00038B 16.97 8.448e-12 79-100 BL00038A 13.61 4.000e-11 52-68 |
| 1723 | PD00567 | PROTEIN RNA-BINDING RNA REPEAT HYD. | PD00567C 9.17 8.500e-09 418-428 |
| 1724 | BL01279 | Protein-L-isoaspartate (D-aspartate) O-methyltransferase signa. | BL01279A 24.27 5.663e-12 233-281 |
| 1728 | BL00018 | EF-hand calcium-binding domain proteins. | BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170 |
| 1730 | BL00594 | Aromatic amino acids permeases proteins. | BL00594A 16.75 1.089e-09 17-61 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| 1731 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 9.676e-10 296-350 |
| 1732 | BL01160 | Kinesin light chain repeat proteins. | BL01160B 19.54 9.676e-10 316-370 |
| 1733 | PF00850 | Histone deacetylase family. | PF00850F 15.70 4.349e-22 246-279 PF00850D 14.76 6.850e-20 177-201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-14 281-323 |
| 1734 | BL00354 | HMG-I and HMG-Y DNA-binding domain proteins (Ahook). | BL00354C 6.61 5.932e-09 292-307 |
| 1735 | DM00179 | w KINASE ALPHA ADHESION T-CELL. | DM00179 13.97 5.263e-10 492-502 |
| 1743 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167 |
| 1744 | PR00449 | TRANSFORMING PROTEIN P21 RAS SIGNATURE | PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167 |
| 1745 | BL00720 | Guanine-nucleotide dissociation stimulators CDC25 family sign. | BL00720B 16.57 8.297e-15 136-160 |
| 1746 | PR00081 | GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE | PR00081B 10.38 6.727e-11 45-57 PR00081E 17.54 3.935e-10 150-168 |
| 1747 | BL00439 | Acyltransferases ChoActase / COT / CPT family proteins. | BL00439H 18.24 8.435e-14 65-91 BL00439G 13.40 2.895e-12 3-14 |
| 1749 | PR00819 | CBXX/CFQX SUPERFAMILY SIGNATURE | PR00819B 10.83 7.158e-11 4-20 |
| 1751 | PD00066 | PROTEIN ZINC-FINGER METAL-BINDI. | PD00066 13.92 3.400e-14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e-13 61-74 PD00066 13.92 6.571e-12 117-130 |
| 1753 | BL01013 | Oxysterol-binding protein family proteins. | BL01013D 26.81 6.516e-18 33-77 |
| 1754 | BL00790 | Receptor tyrosine kinase class V proteins. | BL00790I 20.01 2.393e-09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e-09 287-318 |
| 1756 | PD01066 | PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. | PD01066 19.43 9.750e-35 10-49 |
| 1758 | DM00406 | GLIADIN. | DM00406 7.73 7.600e-09 653-666 |
| 1762 | PD02929 | ADHESION GLYCOPROTEIN PRECURSOR I. | PD02929A 28.27 4.529e-09 224-278 |
| 1765 | PR00326 | GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE | PR00326A 8.75 5.950e-11 146-167 |
| 1775 | PF00023 | Ank repeat proteins. | PF00023A 16.03 3.077e-14 523-539 |
| 1776 | BL00942 | glpT family of transporters proteins. | BL00942F 15.07 4.343e-10 371-389 BL00942B 20.36 8.040e-09 94-137 |
| 1777 | DM00215 | PROLINE-RICH PROTEIN 3. | DM00215 19.43 2.373e-09 279-312 |

| SEQ ID NO: | ACCESSION NO. | DESCRIPTION | RESULTS* |
|------------|---------------|--|--|
| 1778 | BL00084 | Copper type II, ascorbate-dependent monooxygenases proteins. | BL00084D 25.11 3.700e-20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e-11 107-158 |
| 1779 | BL01013 | Oxysterol-binding protein family proteins. | BL01013D 26.81 3.758e-18 611-655 BL01013A 25.14 2.881e-15 344-380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e-12 409-420 |
| 1783 | BL00741 | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 8.138e-13 492-515 |
| 1784 | BL00741 | Guanine-nucleotide dissociation stimulators CDC24 family sign. | BL00741B 14.27 8.138e-13 492-515 |

* results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TRADOC5:1416223.1(%CRJ011.DOC)

TABLE 4

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 2 | ig | Immunoglobulin domain | 2.1e-32 | 109.5 |
| 3 | pkinase | Eukaryotic protein kinase domain | 1.3e-29 | 110.7 |
| 4 | zf-C2H2 | Zinc finger, C2H2 type | 1.6e-21 | 84.9 |
| 5 | fn3 | Fibronectin type III domain | 0 | 1097.1 |
| 6 | fn3 | Fibronectin type III domain | 0 | 1035.0 |
| 7 | fn3 | Fibronectin type III domain | 0 | 1090.4 |
| 8 | fn3 | Fibronectin type III domain | 0 | 1097.1 |
| 9 | TBC | TBC domain | 4e-40 | 146.7 |
| 10 | p450 | Cytochrome P450 | 9.5e-17 | 62.0 |
| 12 | ank | Ank repeat | 6e-20 | 79.7 |
| 14 | ig | Immunoglobulin domain | 1.7e-05 | 22.7 |
| 15 | zf-MYND | MYND finger | 1.3e-06 | 35.4 |
| 16 | zf-MYND | MYND finger | 1.3e-06 | 35.4 |
| 17 | zf-C2H2 | Zinc finger, C2H2 type | 1.7e-99 | 343.9 |
| 18 | CAP_GLY | CAP-Gly domain | 1.2e-25 | 98.7 |
| 20 | IMPDH_C | IMP dehydrogenase / GMP reductase C terminus | 1.6e-119 | 410.5 |
| 21 | IMPDH_C | IMP dehydrogenase / GMP reductase C terminus | 4.3e-102 | 352.6 |
| 22 | pkinase | Eukaryotic protein kinase domain | 2.4e-79 | 277.0 |
| 23 | pkinase | Eukaryotic protein kinase domain | 8.4e-74 | 258.6 |
| 25 | RNA_pol_A | RNA polymerase alpha subunit | 0 | 1077.7 |
| 26 | Clq | Clq domain | 1.9e-10 | 44.4 |
| 27 | Ribosomal_L23 | Ribosomal protein L23 | 7.8e-32 | 111.2 |
| 28 | Ribosomal_L23 | Ribosomal protein L23 | 1e-29 | 104.2 |
| 30 | zf-A20 | A20-like zinc finger | 1.5e-10 | 48.5 |
| 31 | zf-A20 | A20-like zinc finger | 1.5e-10 | 48.5 |
| 32 | FMN_dh | FMN-dependent dehydrogenase | 5.4e-179 | 608.1 |
| 34 | PID | Phosphotyrosine interaction domain (PTB/PID) | 3.8e-59 | 209.9 |
| 35 | ig | Immunoglobulin domain | 1.4e-13 | 48.8 |
| 36 | ig | Immunoglobulin domain | 1.4e-13 | 48.8 |
| 40 | kinesin | Kinesin motor domain | 6.7e-76 | 265.6 |
| 44 | Ets | Ets-domain | 1.4e-56 | 182.1 |
| 45 | Ets | Ets-domain | 1.4e-56 | 182.1 |
| 46 | LRR | Leucine Rich Repeat | 1.7e-13 | 58.3 |
| 48 | zf-C2H2 | Zinc finger, C2H2 type | 2.3e-162 | 552.8 |
| 49 | ITAM | Immunoreceptor tyrosine-based activation mot | 1.4e-05 | 31.9 |
| 50 | UCH-2 | Ubiquitin carboxyl-terminal hydrolase family | 1.1e-26 | 102.0 |
| 51 | UCH-2 | Ubiquitin carboxyl-terminal hydrolase family | 1.1e-26 | 102.0 |
| 52 | ras | Ras family | 8.5e-45 | 162.3 |
| 53 | PRK | Phosphoribulokinase | 2.1e-65 | 230.7 |
| 54 | myb_DNA-binding | Myb-like DNA-binding domain | 0.096 | 15.2 |
| 55 | voltage_CLC | Voltage gated chloride channels | 3.3e-186 | 631.9 |
| 56 | sugar_tr | Sugar (and other) transporter | 0.00015 | -64.3 |
| 57 | TBC | TBC domain | 2.2e-37 | 137.6 |
| 58 | ank | Ank repeat | 5.9e-25 | 96.3 |
| 59 | ank | Ank repeat | 5.9e-25 | 96.3 |
| 67 | PMP22_Claudin | PMP-22/EMP/MP20/Claudin family | 7.9e-49 | 175.6 |
| 68 | C2 | C2 domain | 7.9e-54 | 192.2 |
| 69 | C2 | C2 domain | 2.3e-54 | 194.0 |
| 70 | Kelch | Kelch motif | 9.4e-99 | 341.5 |
| 72 | ig | Immunoglobulin domain | 8.2e-28 | 94.7 |
| 73 | pkinase | Eukaryotic protein kinase | 8e-69 | 242.1 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| | | domain | | |
| 74 | pkinase | Eukaryotic protein kinase domain | 2.8e-38 | 140.6 |
| 76 | zf-C4 Topoisom | Topoisomerase DNA binding C4 zinc fing | 5.4e-54 | 192.8 |
| 83 | Peptidase_S9 | Prolyl oligopeptidase family | 4.3e-10 | 36.8 |
| 84 | fn3 | Fibronectin type III domain | 4.1e-51 | 183.2 |
| 86 | SH2 | Src homology domain 2 | 3.1e-22 | 67.7 |
| 88 | ig | Immunoglobulin domain | 0.0091 | 14.0 |
| 89 | WD40 | WD domain, G-beta repeat | 2.1e-21 | 84.6 |
| 92 | laminin G | Laminin G domain | 6.1e-27 | 98.5 |
| 93 | AMP-binding | AMP-binding enzyme | 2.4e-13 | -37.2 |
| 95 | pkinase | Eukaryotic protein kinase domain | 1.4e-59 | 211.4 |
| 96 | pkinase | Eukaryotic protein kinase domain | 2.6e-51 | 183.9 |
| 97 | adh_short | short chain dehydrogenase | 2e-61 | 217.5 |
| 98 | kinesin | Kinesin motor domain | 2.2e-86 | 300.4 |
| 101 | IRS | PTB domain (IRS-1 type) | 5.4e-36 | 133.0 |
| 102 | AAA | ATPases associated with various cellular act | 6.8e-05 | -5.2 |
| 104 | pkinase | Eukaryotic protein kinase domain | 2.7e-73 | 256.9 |
| 106 | ras | Ras family | 8.3e-24 | 92.5 |
| 107 | FYVE | FYVE zinc finger | 5.4e-27 | 100.7 |
| 108 | Cyt_reductase | FAD/NAD-binding Cytochrome reductase | 7.7e-61 | 215.5 |
| 109 | zf-C2H2 | Zinc finger, C2H2 type | 2.3e-122 | 420.0 |
| 113 | pkinase | Eukaryotic protein kinase domain | 4e-88 | 306.2 |
| 116 | PH | PH domain | 3.1e-11 | 45.2 |
| 117 | lipocalin | Lipocalin / cytosolic fatty-acid binding pr | 2.4e-14 | 53.5 |
| 118 | pkinase | Eukaryotic protein kinase domain | 4.5e-20 | 76.3 |
| 120 | WD40 | WD domain, G-beta repeat | 2.4e-14 | 61.1 |
| 121 | WD40 | WD domain, G-beta repeat | 2.4e-14 | 61.1 |
| 123 | IF5_eIF4_eIF2 | eIF4-gamma/eIF5/eIF2-epsilon | 1e-32 | 122.2 |
| 124 | ig | Immunoglobulin domain | 6.5e-08 | 30.6 |
| 127 | mito_carr | Mitochondrial carrier proteins | 3e-16 | 58.6 |
| 128 | PP2C | Protein phosphatase 2C | 2.2e-71 | 250.6 |
| 129 | ATP1G1_PLM_MAT8 | ATP1G1/PLM/MAT8 family | 3.1e-20 | 80.6 |
| 130 | pfkB | pfkB family carbohydrate kinase | 4.5e-42 | 137.1 |
| 133 | ACBP | Acyl CoA binding protein | 4.6e-22 | 86.7 |
| 134 | rrm | RNA recognition motif. | 1.2e-31 | 118.5 |
| 135 | IQ | IQ calmodulin-binding motif | 2.6e-08 | 41.0 |
| 136 | ATP1G1_PLM_MAT8 | ATP1G1/PLM/MAT8 family | 9.3e-22 | 85.7 |
| 139 | WH2 | Wiskott Aldrich syndrome homology region 2 | 0.0067 | 23.1 |
| 140 | zf-C2H2 | Zinc finger, C2H2 type | 1.7e-82 | 287.5 |
| 141 | Peptidase_S26 | Signal peptidase I | 5.7e-10 | 35.7 |
| 143 | arf | ADP-ribosylation factor family | 1.2e-39 | 145.2 |
| 146 | KRAB | KRAB box | 7.3e-30 | 112.6 |
| 148 | DUF6 | Integral membrane protein DUF6 | 0.096 | 8.0 |
| 149 | PDEase | 3'5'-cyclic nucleotide phosphodiesterase | 3.8e-80 | 231.1 |
| 151 | S4 | S4 domain | 1.1e-08 | 42.3 |
| 153 | tRNA-synt_id | tRNA synthetases class I (R) | 3.8e-103 | 356.1 |
| 154 | Cyt_reductase | FAD/NAD-binding Cytochrome reductase | 7.8e-60 | 212.2 |
| 155 | ras | Ras family | 3.6e-28 | 107.0 |
| 157 | actin | Actin | 3.8e-26 | 87.1 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-------------------|--|----------|------------|
| 158 | Jacalin | Jacalin-like lectin domain | 0.09 | -24.9 |
| 160 | Zn_carbopept | Zinc carboxypeptidase | 5e-138 | 471.9 |
| 165 | pkinaase | Eukaryotic protein kinase domain | 5.1e-67 | 236.1 |
| 167 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 5.3e-07 | 27.0 |
| 168 | Ribosomal_S15 | Ribosomal protein S15 | 1.1e-06 | 29.0 |
| 169 | DEAD | DEAD/DEAH box helicase | 1e-48 | 157.0 |
| 171 | DUF59 | Domain of unknown function DUF59 | 0.07 | -17.4 |
| 172 | pkinaase | Eukaryotic protein kinase domain | 3.7e-15 | 58.6 |
| 173 | globin | Globin | 4.6e-18 | 67.4 |
| 174 | WW | WW domain | 7.3e-06 | 32.9 |
| 175 | ras | Ras family | 1e-31 | 118.8 |
| 178 | ATP1G1_PLM_MAT8 | ATP1G1/PLM/MAT8 family | 2.5e-17 | 71.0 |
| 179 | zf-C2H2 | Zinc finger, C2H2 type | 1.5e-99 | 344.2 |
| 180 | Clq | Clq domain | 8.8e-72 | 251.9 |
| 190 | Y_phosphatase | Protein-tyrosine phosphatase | 4.9e-287 | 967.0 |
| 191 | efhand | EF hand | 7.5e-16 | 66.1 |
| 193 | pkinaase | Eukaryotic protein kinase domain | 6.5e-82 | 285.6 |
| 194 | bromodomain | Bromodomain | 5.8e-31 | 111.4 |
| 195 | PALP | Pyridoxal-phosphate dependent enzyme | 2.5e-64 | 227.1 |
| 197 | DnaJ | DnaJ domain | 1.6e-38 | 141.4 |
| 199 | RrnaAD | Ribosomal RNA adenine dimethylases | 0.00018 | 16.9 |
| 200 | acid_phosphatase | Histidine acid phosphatase | 2.5e-10 | 37.2 |
| 201 | WH2 | Wiskott Aldrich syndrome homology region 2 | 0.00048 | 26.9 |
| 204 | vATP-synt_AC39 | ATP synthase (C/AC39) subunit | 1.3e-159 | 543.7 |
| 205 | vATP-synt_AC39 | ATP synthase (C/AC39) subunit | 1.6e-139 | 476.9 |
| 206 | ldl_recept_a | Low-density lipoprotein receptor domain | 2.4e-25 | 97.6 |
| 209 | ank | Ank repeat | 1.4e-19 | 78.4 |
| 210 | Rhomboid | Rhomboid family | 0.0035 | 1.2 |
| 211 | Clq | Clq domain | 1.6e-70 | 247.7 |
| 212 | UQ_con | Ubiquitin-conjugating enzyme | 7.4e-74 | 258.8 |
| 213 | UQ_con | Ubiquitin-conjugating enzyme | 1e-53 | 191.9 |
| 215 | DEAD | DEAD/DEAH box helicase | 1.8e-43 | 140.4 |
| 216 | PMP22_Claudin | PMP-22/EMP/MP20/Claudin family | 4.5e-21 | 83.4 |
| 218 | Glycosyl_transf_2 | Glycosyl transferases | 4e-21 | 83.6 |
| 219 | lg | Immunoglobulin domain | 0.092 | 10.7 |
| 222 | WD40 | WD domain, G-beta repeat | 7.4e-23 | 89.4 |
| 224 | TPR | TPR Domain | 1.2e-08 | 42.1 |
| 225 | DnaJ_CXXCXGXG | DnaJ central domain (4 repeats) | 1.5e-38 | 141.5 |
| 226 | DnaJ_CXXCXGXG | DnaJ central domain (4 repeats) | 1.5e-38 | 141.5 |
| 229 | HSP70 | Hsp70 protein | 2.4e-54 | 194.0 |
| 230 | GSHPx | Glutathione peroxidases | 3.4e-47 | 170.2 |
| 231 | tsp_1 | Thrombospondin type 1 domain | 0.0075 | 17.1 |
| 233 | cyclin | Cyclin | 4.6e-144 | 492.0 |
| 234 | ras | Ras family | 4.8e-50 | 179.7 |
| 235 | LRR | Leucine Rich Repeat | 1.2e-30 | 115.3 |
| 236 | LRR | Leucine Rich Repeat | 6.7e-29 | 109.4 |
| 237 | PDZ | PDZ domain (Also known as DHR or GLGF). | 1.7e-09 | 45.0 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 244 | dCMP_cyt_deam | Cytidine and deoxycytidylate deaminase | 2.5e-05 | 31.1 |
| 245 | ig | Immunoglobulin domain | 6.7e-08 | 30.5 |
| 248 | wnt | wnt family of developmental signaling protei | 9.1e-270 | 742.6 |
| 250 | mito_carr | Mitochondrial carrier proteins | 1.3e-55 | 193.6 |
| 254 | adenylatekinase | Adenylate kinase | 1.8e-14 | 55.7 |
| 255 | Cation_efflux | Cation efflux family | 2.8e-33 | 124.0 |
| 256 | SH3 | SH3 domain | 3.9e-14 | 60.4 |
| 257 | Aa_trans | Transmembrane amino acid transporter protein | 2.6e-52 | 187.2 |
| 258 | adenylatekinase | Adenylate kinase | 2.1e-110 | 380.2 |
| 259 | HIT | HIT family | 8.2e-07 | 25.3 |
| 260 | Bacterial_PQQ | PQQ enzyme repeat | 1.6e-15 | 65.0 |
| 262 | proteasome | Proteasome A-type and B-type | 6.5e-64 | 225.7 |
| 267 | pkinase | Eukaryotic protein kinase domain | 6.3e-27 | 101.0 |
| 270 | filament | Intermediate filament proteins | 3.2e-150 | 512.5 |
| 271 | Choline_kinase | Choline/ethanolamine kinase | 2e-67 | 237.4 |
| 277 | Ribosomal_S7 | Ribosomal protein S7p/S5e | 3.3e-20 | 80.6 |
| 279 | pkinase | Eukaryotic protein kinase domain | 3.3e-77 | 269.9 |
| 280 | WD40 | WD domain, G-beta repeat | 7.8e-73 | 255.4 |
| 281 | WD40 | WD domain, G-beta repeat | 7.8e-73 | 255.4 |
| 284 | zf-DHHC | DHHC zinc finger domain | 4.6e-24 | 93.4 |
| 287 | Exonuclease | Exonuclease | 1.4e-67 | 238.0 |
| 291 | SAM | SAM domain (Sterile alpha motif) | 0.034 | 11.2 |
| 292 | SAM | SAM domain (Sterile alpha motif) | 0.034 | 11.2 |
| 294 | zf-C2H2 | Zinc finger, C2H2 type | 1.4e-29 | 111.7 |
| 295 | zf-C2H2 | Zinc finger, C2H2 type | 2.2e-125 | 430.0 |
| 296 | mito_carr | Mitochondrial carrier proteins | 4.1e-59 | 205.5 |
| 297 | HMG_box | HMG (high mobility group) box | 6.7e-29 | 109.4 |
| 302 | Glycos_transf_4 | Glycosyl transferase | 5e-87 | 302.5 |
| 304 | tRNA-synt_2 | tRNA synthetases class II (D, K and N) | 1.1e-84 | 294.8 |
| 305 | KRAB | KRAB box | 2e-44 | 161.0 |
| 306 | rrm | RNA recognition motif. | 2.7e-44 | 160.6 |
| 308 | 7tm_1 | 7 transmembrane receptor (rhodopsin family) | 5.2e-39 | 126.1 |
| 309 | DNA_polymeraseX | DNA polymerase X family | 2.4e-64 | 227.2 |
| 311 | F-box | F-box domain. | 9.5e-08 | 39.2 |
| 312 | ig | Immunoglobulin domain | 6.8e-19 | 65.9 |
| 313 | Ets | Ets-domain | 8.1e-60 | 192.3 |
| 315 | Kelch | Kelch motif | 1.3e-106 | 367.6 |
| 317 | arf | ADP-ribosylation factor family | 3.2e-35 | 130.4 |
| 318 | sugar_tr | Sugar (and other) transporter | 0.0003 | -73.1 |
| 320 | pkinase | Eukaryotic protein kinase domain | 8.1e-83 | 288.6 |
| 322 | pkinase | Eukaryotic protein kinase domain | 4.9e-81 | 282.6 |
| 324 | Xlink | Extracellular link domain | 4.5e-143 | 331.5 |
| 326 | ARID | ARID DNA binding domain | 5.1e-37 | 136.4 |
| 327 | HMG_box | HMG (high mobility group) box | 6.7e-29 | 109.4 |
| 328 | cadherin | Cadherin domain | 8.1e-81 | 281.9 |
| 331 | chromo | 'chromo' (CHRromatin Organization Modifier) | 4e-18 | 66.7 |
| 333 | Peptidase_M2_2 | Glycoprotease family | 1.2e-136 | 467.4 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 335 | vwa | von Willebrand factor type A domain | 2.3e-07 | 37.9 |
| 339 | ras | Ras family | 7.8e-07 | -59.1 |
| 340 | zf-C2H2 | Zinc finger, C2H2 type | 8.2e-64 | 225.4 |
| 342 | zf-C2H2 | Zinc finger, C2H2 type | 2.4e-85 | 297.0 |
| 343 | ig | Immunoglobulin domain | 0.0005 | 18.0 |
| 346 | pkinase | Eukaryotic protein kinase domain | 6.5e-65 | 229.1 |
| 347 | pkinase | Eukaryotic protein kinase domain | 6.5e-65 | 229.1 |
| 351 | EGF | EGF-like domain | 8.5e-20 | 79.2 |
| 352 | ank | Ank repeat | 2.5e-101 | 350.0 |
| 354 | TBC | TBC domain | 5.1e-15 | 63.3 |
| 355 | PHD | PHD finger | 3.2e-07 | 37.4 |
| 358 | DUF6 | Integral membrane protein DUF6 | 0.033 | 15.8 |
| 359 | zf-C2H2 | Zinc finger, C2H2 type | 7.4e-20 | 79.4 |
| 361 | ank | Ank repeat | 6.6e-34 | 126.1 |
| 362 | ArfGap | Putative GTP-ase activating protein for Arf | 4.7e-53 | 189.7 |
| 363 | efhand | EF hand | 5.4e-10 | 46.6 |
| 367 | LRR | Leucine Rich Repeat | 8.8e-44 | 158.9 |
| 368 | laminin_G | Laminin G domain | 1.5e-33 | 121.7 |
| 369 | PP2C | Protein phosphatase 2C | 5.3e-20 | 73.9 |
| 372 | LIM | LIM domain containing proteins | 9.9e-15 | 57.1 |
| 373 | KRAB | KRAB box | 4.8e-23 | 90.0 |
| 376 | ion_trans | Ion transport protein | 2.9e-09 | -4.2 |
| 377 | Beach | Beige/BEACH domain | 4.9e-208 | 704.5 |
| 380 | pkinase | Eukaryotic protein kinase domain | 1.6e-94 | 327.5 |
| 381 | AMP-binding | AMP-binding enzyme | 1.4e-07 | -140.3 |
| 382 | HECT | HECT-domain (ubiquitin-transferase). | 1.3e-07 | -13.5 |
| 384 | ank | Ank repeat | 2.5e-101 | 350.0 |
| 386 | ig | Immunoglobulin domain | 9.5e-06 | 23.6 |
| 388 | zf-C2H2 | Zinc finger, C2H2 type | 1.7e-42 | 154.6 |
| 389 | ig | Immunoglobulin domain | 2.8e-15 | 54.3 |
| 390 | mito_carr | Mitochondrial carrier proteins | 3.5e-67 | 233.2 |
| 392 | TPR | TPR Domain | 6.1e-17 | 69.7 |
| 393 | SH3 | SH3 domain | 3.5e-09 | 43.9 |
| 394 | AAA | ATPases associated with various cellular act | 4.1e-21 | 83.6 |
| 396 | spectrin | Spectrin repeat | 2.1e-67 | 237.3 |
| 397 | zf-C2H2 | Zinc finger, C2H2 type | 0.0066 | 23.1 |
| 399 | fn3 | Fibronectin type III domain | 4.1e-102 | 352.6 |
| 400 | WD40 | WD domain, G-beta repeat | 0.00049 | 26.8 |
| 401 | E1_dehydrog | Dehydrogenase E1 component | 3e-119 | 409.6 |
| 402 | fn3 | Fibronectin type III domain | 0 | 1719.6 |
| 404 | LRR | Leucine Rich Repeat | 2.1e-10 | 48.0 |
| 405 | cadherin | Cadherin domain | 8.1e-81 | 281.9 |
| 406 | zf-CXXC | CXXC zinc finger | 5e-15 | 63.4 |
| 410 | RhoGEF | RhoGEF domain | 1.1e-23 | 92.1 |
| 411 | F-box | F-box domain. | 4.2e-06 | 33.7 |
| 412 | SNF2_N | SNF2 and others N-terminal domain | 5.8e-16 | 61.6 |
| 415 | CPSase_L_cha in | Carbamoyl-phosphate synthase (CPSase) | 1.5e-172 | 586.6 |
| 418 | LRR | Leucine Rich Repeat | 3.8e-24 | 93.6 |
| 419 | DENN | DENN (AEX-3) domain | 2e-58 | 207.5 |
| 420 | RasGEF | RasGEF domain | 8.1e-43 | 155.7 |
| 421 | ank | Ank repeat | 1.4e-153 | 523.7 |
| 424 | G-patch | G-patch domain | 1e-19 | 78.9 |
| 425 | pkinase | Eukaryotic protein kinase domain | 2.2e-31 | 117.1 |
| 426 | Plexin_repea t | Plexin repeat | 0.0023 | 24.6 |
| 427 | Plexin_repea | Plexin repeat | 0.0023 | 24.6 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-------------------------|--|----------|------------|
| | t | | | |
| 429 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 8.6e-11 | 39.2 |
| 431 | DEAD | DEAD/DEAH box helicase | 1e-66 | 214.0 |
| 432 | SH3 | SH3 domain | 3.4e-16 | 67.2 |
| 433 | GTP_CDC | Cell division protein | 2.1e-114 | 393.5 |
| 436 | Collagen | Collagen triple helix repeat (20 copies) | 4.6e-194 | 658.1 |
| 438 | Ricin_B_lectin | Similarity to lectin domain of ricin b | 0.0085 | 10.5 |
| 441 | Alpha_adaptin_C | Alpha adaptin carboxyl-terminal domain | 1.2e-256 | 866.0 |
| 442 | Alpha_adaptin_C | Alpha adaptin carboxyl-terminal domain | 1.8e-235 | 795.7 |
| 443 | PDZ | PDZ domain (Also known as DHR or GLGF). | 1.9e-65 | 230.9 |
| 445 | LON | ATP-dependent protease La (LON) domain | 0.00012 | -17.1 |
| 446 | ig | Immunoglobulin domain | 0.00011 | 20.1 |
| 451 | sushi | Sushi domain (SCR repeat) | 1.4e-18 | 75.2 |
| 452 | fn3 | Fibronectin type III domain | 1.5e-06 | 35.2 |
| 454 | pyridoxal_dependent | Pyridoxal-dependent decarboxylase conse | 8.3e-14 | 50.3 |
| 456 | kinesin | Kinesin motor domain | 4.9e-217 | 734.4 |
| 457 | neur_chan | Neurotransmitter-gated ion-channel | 1e-175 | 597.1 |
| 458 | Josephin | Josephin | 0.0002 | 18.7 |
| 468 | bZIP | bZIP transcription factor | 1.7e-07 | 31.8 |
| 470 | NTP_transferase | Nucleotidyl transferase | 6.3e-06 | -26.3 |
| 471 | WD40 | WD domain, G-beta repeat | 2e-28 | 107.9 |
| 473 | LIM | LIM domain containing proteins | 0.00021 | 20.7 |
| 477 | zf-RanBP | Zn-finger in Ran binding protein and others. | 0.028 | 21.0 |
| 479 | WD40 | WD domain, G-beta repeat | 6.5e-18 | 73.0 |
| 480 | KRAB | KRAB box | 1e-31 | 118.8 |
| 481 | ArfGap | Putative GTP-ase activating protein for Arf | 8.4e-66 | 232.0 |
| 485 | SH2 | Src homology domain 2 | 0.011 | 11.4 |
| 486 | Clg | Clg domain | 4.3e-74 | 259.6 |
| 487 | derm | Double-stranded RNA binding motif | 1.1e-47 | 171.9 |
| 489 | zf-C2H2 | Zinc finger, C2H2 type | 4.8e-153 | 521.9 |
| 490 | Alpha_adaptin_C | Alpha adaptin carboxyl-terminal domain | 3.4e-222 | 751.6 |
| 492 | SKI | Shikimate kinase | 1.2e-10 | 48.8 |
| 497 | ENV_polyprotein | ENV polyprotein (coat polyprotein) | 2.6e-22 | 77.6 |
| 498 | abhydrolase_2 | Phospholipase/Carboxylesterase | 0.041 | -48.1 |
| 500 | rrm | RNA recognition motif. | 5.4e-34 | 126.4 |
| 501 | WW | WW domain | 4.6e-18 | 73.4 |
| 502 | ig | Immunoglobulin domain | 1.1e-10 | 39.5 |
| 504 | abhydrolase | alpha/beta hydrolase fold | 0.045 | -3.6 |
| 505 | vwa | von Willebrand factor type A domain | 7.1e-62 | 219.0 |
| 508 | Na_K_ATPase_C | Na+/K+ ATPase C-terminus | 2.3e-145 | 496.3 |
| 509 | Exonuclease | Exonuclease | 1.3e-56 | 201.5 |
| 510 | Glycosyl_transferase_f1 | Glycosyl transferases group 1 | 2.9e-06 | 27.0 |
| 511 | Glycosyl_transferase_f1 | Glycosyl transferases group 1 | 2.9e-06 | 27.0 |
| 512 | Glycosyl_transferase_f1 | Glycosyl transferases group 1 | 1.9e-09 | 38.5 |
| 514 | pro_isomerase | Cyclophilin type peptidyl-prolyl cis-tr | 1.8e-63 | 221.4 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|------------------|--|----------|------------|
| 515 | EGF | EGF-like domain | 1.9e-18 | 74.7 |
| 516 | Surp | Surp module | 4.3e-38 | 140.0 |
| 523 | ig | Immunoglobulin domain | 3.3e-06 | 25.0 |
| 526 | UBX | UBX domain | 1.1e-34 | 128.6 |
| 528 | adh_zinc | Zinc-binding dehydrogenases | 2.7e-34 | 127.4 |
| 530 | SAM | SAM domain (Sterile alpha motif) | 0.046 | 10.0 |
| 531 | adh_short | short chain dehydrogenase | 0.0025 | -34.1 |
| 532 | mito_carr | Mitochondrial carrier proteins | 2.5e-81 | 281.7 |
| 533 | mito_carr | Mitochondrial carrier proteins | 2e-61 | 213.5 |
| 534 | thiolase | Thiolase | 3.5e-183 | 622.0 |
| 535 | FMO-like | Flavin-binding monooxygenase-like | 0 | 1153.7 |
| 536 | SCAN | SCAN domain | 4e-55 | 196.6 |
| 537 | tRNA-synt_1 | tRNA synthetases class I (I, L, M and V) | 3.1e-136 | 466.0 |
| 538 | tRNA-synt_1 | tRNA synthetases class I (I, L, M and V) | 3.1e-136 | 466.0 |
| 539 | tRNA-synt_1 | tRNA synthetases class I (I, L, M and V) | 1.9e-117 | 403.6 |
| 540 | tRNA-synt_1 | tRNA synthetases class I (I, L, M and V) | 3.1e-136 | 466.0 |
| 541 | vATP-synt_E | ATP synthase (E/31 kDa) subunit | 5.9e-85 | 295.7 |
| 543 | zf-C2H2 | Zinc finger, C2H2 type | 5.5e-69 | 242.6 |
| 544 | DUF101 | Protein of unknown function DUF101 | 8.5e-38 | 139.0 |
| 545 | TGFb_propept ide | TGF-beta propeptide | 1.1e-67 | 238.2 |
| 547 | WD40 | WD domain, G-beta repeat | 2.6e-32 | 120.8 |
| 548 | RHD | Rel homology domain (RHD). | 1.6e-238 | 686.2 |
| 549 | MMR_HSR1 | GTPase of unknown function | 5.4e-67 | 236.0 |
| 551 | HECT | HECT-domain (ubiquitin-transferase). | 4.3e-127 | 435.6 |
| 554 | MHC_II_alpha | Class II histocompatibility antigen, alp | 3.5e-74 | 259.8 |
| 555 | zf-UBR1 | Putative zinc finger in N-recogin | 3.3e-16 | 67.3 |
| 556 | Kelch | Kelch motif | 5.5e-29 | 109.7 |
| 561 | AMP-binding | AMP-binding enzyme | 2.8e-06 | -163.7 |
| 562 | PABP | Poly-adenylate binding protein, unique domai | 4.9e-38 | 139.8 |
| 564 | Gag_p30 | Gag P30 core shell protein | 1.2e-67 | 238.2 |
| 566 | PWWP | PWWP domain | 8.1e-16 | 66.0 |
| 567 | SCAN | SCAN domain | 7.3e-68 | 238.9 |
| 569 | pkinase | Eukaryotic protein kinase domain | 1.5e-84 | 294.3 |
| 570 | pkinase | Eukaryotic protein kinase domain | 1.5e-84 | 294.3 |
| 571 | CN_hydrolase | Carbon-nitrogen hydrolase | 0.00081 | -79.7 |
| 572 | myosin_head | Myosin head (motor domain) | 0 | 1495.2 |
| 573 | myosin_head | Myosin head (motor domain) | 0 | 1490.4 |
| 575 | Surp | Surp module | 1.7e-23 | 91.5 |
| 576 | Surp | Surp module | 1.7e-23 | 91.5 |
| 577 | DNA_pol_B | DNA polymerase family B | 0 | 1138.6 |
| 578 | PDZ | PDZ domain (Also known as DHR or GLGF). | 8.3e-09 | 42.7 |
| 579 | LRR | Leucine Rich Repeat | 4.9e-21 | 83.3 |
| 580 | neur_chan | Neurotransmitter-gated ion-channel | 5.9e-177 | 601.3 |
| 583 | sushi | Sushi domain (SCR repeat) | 0 | 1673.0 |
| 584 | DEAD | DRAD/DEAH box helicase | 7.3e-36 | 116.3 |
| 586 | KH-domain | KH domain | 2.9e-13 | 57.5 |
| 587 | G-patch | G-patch domain | 2.3e-14 | 61.2 |
| 589 | LIM | LIM domain containing proteins | 2.3e-36 | 133.4 |
| 590 | bromodomain | Bromodomain | 6.6e-32 | 114.7 |
| 591 | bromodomain | Bromodomain | 6.6e-32 | 114.7 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|------------------|--|----------|------------|
| 592 | hormone_rec | Ligand-binding domain of nuclear hormone | 3.5e-22 | 87.1 |
| 593 | PHD | PHD-finger | 3.8e-12 | 53.8 |
| 594 | cadherin | Cadherin domain | 4.2e-99 | 342.7 |
| 596 | pkinase | Eukaryotic protein kinase domain | 5e-92 | 319.2 |
| 597 | WD40 | WD domain, G-beta repeat | 0.00054 | 26.7 |
| 600 | FG-GAP | FG-GAP repeat | 4.3e-75 | 262.9 |
| 602 | G_Adapt_CT | Gamma-adaptin, C-terminus | 1.1e-53 | 191.8 |
| 603 | pkinase | Eukaryotic protein kinase domain | 2.3e-86 | 300.4 |
| 605 | Collagen | Collagen triple helix repeat (20 copies) | 8e-42 | 152.4 |
| 606 | mito_carr | Mitochondrial carrier proteins | 6.3e-67 | 232.3 |
| 608 | PWWP | PWWP domain | 2.6e-28 | 107.5 |
| 609 | PWWP | PWWP domain | 2.6e-28 | 107.5 |
| 613 | CAP_GLY | CAP-Gly domain | 0.0046 | 20.1 |
| 615 | RFX_DNA_bind ing | RFX DNA-binding domain | 5.2e-54 | 192.9 |
| 616 | kinesin | Kinesin motor domain | 1.1e-81 | 284.8 |
| 617 | kinesin | Kinesin motor domain | 8.4e-80 | 278.5 |
| 618 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 0.0098 | 13.1 |
| 620 | MATH | MATH domain | 7.8e-05 | 22.2 |
| 621 | Y_phosphatas e | Protein-tyrosine phosphatase | 1.4e-32 | 121.6 |
| 622 | pkinase | Eukaryotic protein kinase domain | 4.4e-40 | 146.6 |
| 623 | BNR | BNR repeat | 2.1e-11 | 51.3 |
| 624 | molybdopteri n | Prokaryotic molybdopterin oxidoreductas | 1.4e-12 | 42.2 |
| 625 | TPR | TPR Domain | 1.1e-17 | 72.2 |
| 627 | cNMP_binding | Cyclic nucleotide-binding domain | 3.7e-58 | 206.6 |
| 630 | adh_short | short chain dehydrogenase | 5e-17 | 70.0 |
| 631 | zf-C2H2 | Zinc finger, C2H2 type | 2.1e-88 | 307.1 |
| 632 | rrm | RNA recognition motif. | 4e-05 | 30.5 |
| 635 | pkinase | Eukaryotic protein kinase domain | 1.6e-104 | 360.7 |
| 636 | Fork_head | Fork head domain | 5.9e-27 | 103.0 |
| 637 | pkinase | Eukaryotic protein kinase domain | 3.8e-70 | 246.5 |
| 642 | TPR | TPR Domain | 4.8e-08 | 40.1 |
| 643 | efhand | EF hand | 1.9e-27 | 104.6 |
| 647 | SNF2_N | SNF2 and others N-terminal domain | 1.2e-101 | 351.1 |
| 648 | PseudoU_synt h_2 | RNA pseudouridylate synthase | 1.9e-55 | 197.6 |
| 650 | zf-C2H2 | Zinc finger, C2H2 type | 0.0087 | 22.7 |
| 651 | ank | Ank repeat | 1.3e-17 | 71.9 |
| 652 | I_LWEQ | I/LWEQ domain | 9.5e-101 | 341.0 |
| 653 | neur_chan | Neurotransmitter-gated ion-channel | 4.1e-171 | 581.8 |
| 654 | tsp_1 | Thrombospondin type 1 domain | 4.1e-47 | 169.9 |
| 659 | FH2 | Formin Homology 2 Domain | 1e-107 | 371.2 |
| 661 | pou | Pou domain - N-terminal to homeobox domain | 5.3e-45 | 162.9 |
| 662 | C2 | C2 domain | 6.7e-19 | 76.2 |
| 663 | C2 | C2 domain | 6.7e-19 | 76.2 |
| 664 | C2 | C2 domain | 6.7e-19 | 76.2 |
| 667 | GST | Glutathione S-transferases. | 9.3e-34 | 114.4 |
| 668 | LRR | Leucine Rich Repeat | 9.3e-31 | 115.6 |
| 670 | spectrin | Spectrin repeat | 4e-57 | 203.2 |
| 671 | I_LWEQ | I/LWEQ domain | 9.5e-101 | 341.0 |
| 672 | ABC_tran | ABC transporter | 5.3e-60 | 212.8 |
| 674 | WD40 | WD domain, G-beta repeat | 4.8e-24 | 93.3 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 675 | WD40 | WD domain, G-beta repeat | 4.8e-24 | 93.3 |
| 676 | LRR | Leucine Rich Repeat | 0.0015 | 25.2 |
| 679 | zf-CCCH | Zinc finger C-x8-C-x5-C-x3-H type | 2.6e-29 | 107.7 |
| 680 | zf-C2H2 | Zinc finger, C2H2 type | 5.2e-05 | 30.1 |
| 681 | CH | Calponin homology (CH) domain | 2.4e-17 | 71.1 |
| 682 | DSPc | Dual specificity phosphatase, catalytic doma | 4.3e-43 | 156.6 |
| 683 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 0.051 | 10.8 |
| 687 | Synapsin | Synapsin | 0 | 1890.8 |
| 689 | PR55 | Protein phosphatase 2A regulatory subunit PR | 0 | 1038.8 |
| 691 | homeobox | Homeobox domain | 8.5e-30 | 112.4 |
| 696 | Peptidase_M24 | metallopeptidase family M24 | 2.6e-59 | 210.5 |
| 697 | RhoGEF | RhoGEF domain | 9.5e-35 | 128.9 |
| 698 | PHD | PHD-finger | 0.008 | 9.3 |
| 701 | zf-C2H2 | Zinc finger, C2H2 type | 5.5e-123 | 422.0 |
| 702 | Sulfatase | Sulfatase | 3e-231 | 781.6 |
| 703 | zf-C2H2 | Zinc finger, C2H2 type | 5.7e-20 | 79.8 |
| 707 | Acyl_transf | Acyl transferase domain | 1.1e-22 | 88.8 |
| 708 | WD40 | WD domain, G-beta repeat | 4.8e-19 | 76.7 |
| 710 | Ran_BP1 | RanBP1 domain. | 8.4e-06 | -7.3 |
| 713 | DEAD | DEAD/DEAH box helicase | 9.9e-42 | 134.9 |
| 714 | PH | PH domain | 1.6e-09 | 39.0 |
| 715 | DSPc | Dual specificity phosphatase, catalytic doma | 1.5e-37 | 138.2 |
| 717 | Sialyltransf | Sialyltransferase family | 7.5e-31 | 115.9 |
| 718 | ig | Immunoglobulin domain | 1e-29 | 100.8 |
| 719 | integrin_B | Integrins, beta chain | 0 | 1125.4 |
| 720 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 1.1e-08 | 32.4 |
| 722 | Peptidase_C2 | Calpain family cysteine protease | 3e-145 | 495.9 |
| 723 | ig | Immunoglobulin domain | 2.2e-05 | 22.4 |
| 724 | F-box | F-box domain. | 0.007 | 23.0 |
| 725 | Nop | Putative snRNA binding domain | 8.1e-58 | 205.5 |
| 726 | Nop | Putative snRNA binding domain | 8.1e-58 | 205.5 |
| 727 | WD40 | WD domain, G-beta repeat | 7.5e-26 | 99.3 |
| 730 | dsrm | Double-stranded RNA binding motif | 0.027 | 12.1 |
| 731 | dynammin | Dynammin family | 4.2e-16 | 66.9 |
| 733 | zf-CCCH | Zinc finger C-x8-C-x5-C-x3-H type | 2.8e-10 | 41.7 |
| 735 | CDP-OH_P_transf | CDP-alcohol phosphatidyltransferase | 4.2e-26 | 100.1 |
| 738 | DEAD | DEAD/DEAH box helicase | 8.6e-57 | 182.5 |
| 739 | TSC22 | TSC-22/dip/bun family | 6.5e-32 | 119.5 |
| 742 | ras | Ras family | 2.2e-100 | 346.9 |
| 743 | PMI_typeI | Phosphomannose isomerase type I | 1.2e-243 | 822.9 |
| 747 | trypsin | Trypsin | 6.4e-88 | 279.4 |
| 748 | kazal | Kazal-type serine protease inhibitor domain | 2.2e-52 | 187.4 |
| 749 | efhand | EF hand | 6.3e-06 | 33.1 |
| 751 | PHD | PHD-finger | 4.9e-16 | 66.7 |
| 752 | zf-C2H2 | Zinc finger, C2H2 type | 3.2e-21 | 83.9 |
| 753 | Hydrolase | haloacid dehalogenase-like hydrolase | 6.1e-11 | 49.8 |
| 754 | Ribosomal_L39 | Ribosomal L39 protein | 0.00018 | 26.7 |
| 755 | PH | PH domain | 3.6e-14 | 55.7 |
| 758 | SCAN | SCAN domain | 1.4e-53 | 191.5 |
| 759 | PA | PA domain | 0.0065 | 23.1 |
| 760 | arf | ADP-ribosylation factor family | 2.2e-19 | 77.8 |
| 761 | CIDE-N | CIDE-N domain | 2.2e-40 | 147.6 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|---|----------|------------|
| 762 | histone | Core histone H2A/H2B/H3/H4 | 9.9e-53 | 188.6 |
| 763 | zf-MYND | MYND finger | 4.1e-14 | 60.3 |
| 764 | pou | Pou domain - N-terminal to homeobox domain | 1e-52 | 188.6 |
| 767 | vwc | von Willebrand factor type C domain | 2.9e-34 | 127.3 |
| 769 | efhand | EF hand | 4.8e-11 | 50.1 |
| 770 | zf-C4 | Zinc finger, C4 type (two domains) | 2.4e-53 | 181.6 |
| 772 | ras | Ras family | 7e-90 | 312.0 |
| 773 | Sulfatase | Sulfatase | 1e-142 | 487.5 |
| 775 | zf-C2H2 | Zinc finger, C2H2 type | 1.1e-12 | 55.5 |
| 776 | zf-C2H2 | Zinc finger, C2H2 type | 1.1e-12 | 55.5 |
| 777 | zf-C2H2 | Zinc finger, C2H2 type | 1.1e-12 | 55.5 |
| 778 | rrm | RNA recognition motif. | 2.1e-32 | 121.1 |
| 779 | G6PD | Glucose-6-phosphate dehydrogenase | 1.5e-76 | 236.6 |
| 780 | spectrin | Spectrin repeat | 3.7e-29 | 110.3 |
| 781 | mito_carr | Mitochondrial carrier proteins | 4.6e-57 | 198.5 |
| 782 | SCAN | SCAN domain | 1.3e-24 | 95.2 |
| 783 | PDZ | PDZ domain (Also known as DHR or GLGF). | 4.1e-07 | 37.1 |
| 785 | DEAD | DEAD/DEAH box helicase | 6e-06 | 21.7 |
| 786 | ras | Ras family | 5.3e-39 | 143.0 |
| 787 | RNase_HII | Ribonuclease HII | 2.5e-67 | 237.1 |
| 790 | PI3_PI4_kinase | Phosphatidylinositol 3- and 4-kinases | 5.4e-108 | 372.2 |
| 795 | cadherin | Cadherin domain | 2.5e-40 | 147.4 |
| 796 | ARID | ARID DNA binding domain | 1.6e-20 | 81.6 |
| 797 | trypsin | Trypsin | 9.9e-20 | 64.8 |
| 799 | CH | Calponin homology (CH) domain | 3.7e-15 | 63.8 |
| 801 | Gal-bind_lectin | Vertebrate galactoside-binding lectin | 4.1e-25 | 88.7 |
| 803 | WD40 | WD domain, G-beta repeat | 0.00082 | 26.1 |
| 806 | TBC | TBC domain | 1.8e-26 | 101.4 |
| 807 | TBC | TBC domain | 1.8e-26 | 101.4 |
| 808 | CN_hydrolase | Carbon-nitrogen hydrolase | 8.8e-80 | 278.5 |
| 811 | CBFD_NFYB_HMF | Histone-like transcription factor | 6e-14 | 59.8 |
| 812 | adh_short | short chain dehydrogenase | 8.1e-20 | 79.3 |
| 814 | IMP4 | Domain of unknown function | 3.3e-71 | 250.0 |
| 815 | zf-C2H2 | Zinc finger, C2H2 type | 8.2e-66 | 232.1 |
| 816 | Pept_tRNA_hydro | Peptidyl-tRNA hydrolase | 1.6e-37 | 138.0 |
| 817 | ARID | ARID DNA binding domain | 2.5e-18 | 74.3 |
| 826 | IF5_eIF4_eIF2 | eIF4-gamma/eIF5/eIF2-epsilon | 1.6e-32 | 121.5 |
| 830 | ArfGap | Putative GTP-ase activating protein for Arf | 1.5e-53 | 191.3 |
| 831 | LRR | Leucine Rich Repeat | 2.1e-26 | 101.1 |
| 832 | laminin_EGF | Laminin EGF-like (Domains III and V) | 2e-57 | 204.2 |
| 839 | rrm | RNA recognition motif. | 1.3e-22 | 88.5 |
| 840 | Y_phosphatase | Protein-tyrosine phosphatase | 2.6e-119 | 409.8 |
| 841 | pkinase | Eukaryotic protein kinase domain | 3.4e-100 | 346.3 |
| 844 | Ribosomal_L22e | Ribosomal L22e protein family | 1e-64 | 228.4 |
| 846 | IBR | IBR domain | 9e-15 | 62.5 |
| 849 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 7.4e-07 | 26.5 |
| 850 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 0.00016 | 18.9 |
| 851 | SET | SET domain | 5e-30 | 113.2 |
| 852 | SRCR | Scavenger receptor cysteine- | 0 | 1025.4 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| | | rich domain | | |
| 853 | SRCR | Scavenger receptor cysteine-rich domain | 0 | 1025.4 |
| 857 | lactamase_B | Metallo-beta-lactamase superfamily | 0.012 | -6.0 |
| 858 | COX6A | Cytochrome c oxidase subunit Via | 3.4e-58 | 206.7 |
| 859 | rrm | RNA recognition motif. | 5.4e-45 | 162.9 |
| 861 | PRK | Phosphoribulokinase | 5.1e-62 | 219.4 |
| 863 | mito_carr | Mitochondrial carrier proteins | 2.9e-53 | 185.5 |
| 864 | HSP90 | Hsp90 protein | 4.7e-158 | 538.5 |
| 866 | ig | Immunoglobulin domain | 4e-12 | 44.1 |
| 867 | zf-C2H2 | Zinc finger, C2H2 type | 7e-135 | 461.5 |
| 872 | histone | Core histone H2A/H2B/H3/H4 | 4.9e-41 | 149.8 |
| 874 | CPSase_L_cha in | Carbamoyl-phosphate synthase (CPSase) | 2.1e-218 | 739.0 |
| 879 | Ribosomal_S12e | Ribosomal protein S12e | 2.1e-98 | 340.3 |
| 882 | serpin | Serpins (serine protease inhibitors) | 2.5e-42 | 145.7 |
| 883 | Patatin | Patatin | 1.2e-51 | 182.0 |
| 884 | RA | Ras association (RalGDS/AF-6) domain | 0.044 | 8.0 |
| 887 | DUF92 | Integral membrane protein DUF92 | 2.7e-12 | 54.3 |
| 889 | sugar_tr | Sugar (and other) transporter | 8.2e-63 | 222.1 |
| 893 | DUF28 | Domain of unknown function DUF28 | 1.3e-43 | 158.3 |
| 896 | IP_trans | Phosphatidylinositol transfer protein | 6.5e-98 | 338.7 |
| 898 | DEAD | DEAD/DEAH box helicase | 1.5e-48 | 156.5 |
| 899 | KE2 | KE2 family protein | 7e-61 | 215.7 |
| 900 | KE2 | KE2 family protein | 4.3e-51 | 183.2 |
| 901 | zf-C2H2 | Zinc finger, C2H2 type | 2.7e-57 | 203.8 |
| 902 | ras | Ras family | 2.3e-75 | 263.8 |
| 904 | TPR | TPR Domain | 3.2e-22 | 87.2 |
| 906 | GBP | Guanylate-binding protein | 8.9e-253 | 853.1 |
| 907 | GBP | Guanylate-binding protein | 1.1e-239 | 809.6 |
| 908 | WD40 | WD domain, G-beta repeat | 2.6e-26 | 100.8 |
| 909 | PH | PH domain | 1.3e-09 | 39.4 |
| 910 | zf-C2H2 | Zinc finger, C2H2 type | 2.5e-39 | 144.1 |
| 913 | Epimerase | NAD dependent epimerase/dehydratase family | 5e-07 | -88.5 |
| 921 | TBC | TBC domain | 1.5e-09 | 30.7 |
| 922 | WD40 | WD domain, G-beta repeat | 1.6e-25 | 98.2 |
| 923 | WD40 | WD domain, G-beta repeat | 8.2e-07 | 36.1 |
| 924 | Hydrolase | haloacid dehalogenase-like hydrolase | 2.9e-05 | 29.1 |
| 925 | UQ_con | Ubiquitin-conjugating enzyme | 0.00033 | -27.6 |
| 926 | CH | Calponin homology (CH) domain | 3.3e-53 | 190.2 |
| 928 | WD40 | WD domain, G-beta repeat | 5.9e-48 | 172.7 |
| 929 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 3.1e-10 | 37.4 |
| 930 | Ribul_P_3_ep im | Ribulose-phosphate 3 epimerase family | 7.2e-105 | 361.8 |
| 931 | Ribul_P_3_ep im | Ribulose-phosphate 3 epimerase family | 1.2e-96 | 334.4 |
| 936 | C2 | C2 domain | 2.2e-62 | 220.7 |
| 937 | NAP_family | Nucleosome assembly protein (NAP) | 1.1e-22 | 84.6 |
| 940 | abhydrolase | alpha/beta hydrolase fold | 0.011 | 3.1 |
| 944 | Tropomyosin | Tropomyosins | 3.2e-07 | 25.1 |
| 948 | pkinase | Eukaryotic protein kinase domain | 3.4e-75 | 263.2 |
| 949 | WD40 | WD domain, G-beta repeat | 1.8e-27 | 104.7 |
| 950 | Acyltransferase | Acyltransferase | 1.6e-07 | 38.4 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|---|----------|------------|
| 951 | SAM | SAM domain (Sterile alpha motif) | 0.014 | 14.5 |
| 954 | GFO_IDH_MocA | Oxidoreductase family | 1.3e-11 | 52.0 |
| 955 | BTB | BTB/POZ domain | 7e-22 | 86.1 |
| 956 | BTB | BTB/POZ domain | 7e-22 | 86.1 |
| 957 | CDP-OH_P_transf | CDP-alcohol phosphatidyltransferase | 0.053 | -22.2 |
| 959 | ras | Ras family | 2.4e-97 | 336.8 |
| 960 | ras | Ras family | 8.4e-43 | 155.6 |
| 961 | Acetyltransf | Acetyltransferase (GNAT) family | 1.2e-08 | 42.2 |
| 962 | adh_short | short chain dehydrogenase | 2.4e-31 | 117.6 |
| 963 | mutT | Bacterial mutT protein | 5.6e-06 | 26.2 |
| 969 | IF-2B | Initiation factor 2 subunit family | 8.4e-193 | 653.9 |
| 970 | RNase_PH | 3' exoribonuclease family | 9e-24 | 92.4 |
| 975 | WW | WW domain | 5.7e-25 | 96.4 |
| 977 | PDZ | PDZ domain (Also known as DHR or GLGF). | 3.6e-21 | 83.7 |
| 978 | Ribosomal_L17 | Ribosomal protein L17 | 2.4e-20 | 81.0 |
| 979 | LIM | LIM domain containing proteins | 5.8e-42 | 152.8 |
| 980 | Calsequestrin | Calsequestrin | 1.7e-297 | 1001.7 |
| 982 | HSP20 | Hsp20/alpha crystallin family | 1.2e-10 | 43.2 |
| 983 | oxidored_q6 | NADH ubiquinone oxidoreductase, 20 Kd sub | 4.8e-63 | 222.9 |
| 988 | TBC | TBC domain | 2.2e-50 | 180.8 |
| 989 | TBC | TBC domain | 2.2e-50 | 180.8 |
| 993 | tRNA_int_endo | tRNA intron endonuclease | 0.0017 | -34.2 |
| 994 | homeobox | Homeobox domain | 4e-18 | 73.6 |
| 997 | pyr_redox | Pyridine nucleotide-disulphide oxidoreductase | 0.012 | 11.6 |
| 1000 | mito_carr | Mitochondrial carrier proteins | 9.7e-123 | 421.2 |
| 1001 | RA | Ras association (RalGDS/AF-6) domain | 1.2e-15 | 65.4 |
| 1004 | DUF81 | Domain of unknown function DUF81 | 0.099 | 10.2 |
| 1005 | actin | Actin | 1.3e-174 | 574.3 |
| 1006 | actin | Actin | 3.1e-130 | 428.6 |
| 1007 | cpn60_TCP1 | TCP-1/cpn60 chaperonin family | 3.7e-195 | 661.8 |
| 1008 | TPR | TPR Domain | 8.1e-44 | 159.0 |
| 1009 | zf-C2H2 | Zinc finger, C2H2 type | 3.6e-61 | 216.6 |
| 1011 | zf-C2H2 | Zinc finger, C2H2 type | 3.6e-61 | 216.6 |
| 1012 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 4.7e-15 | 53.1 |
| 1016 | tRNA-synt_2c | tRNA synthetases class II (A) | 2.3e-15 | 55.2 |
| 1018 | RhoGAP | RhoGAP domain | 1.6e-78 | 274.3 |
| 1022 | PGAM | Phosphoglycerate mutase family | 3.8e-18 | 69.7 |
| 1026 | HMG_box | HMG (high mobility group) box | 8.4e-20 | 79.2 |
| 1027 | TBC | TBC domain | 7.3e-45 | 162.5 |
| 1028 | UQ_con | Ubiquitin-conjugating enzyme | 1.4e-49 | 178.1 |
| 1032 | PDZ | PDZ domain (Also known as DHR or GLGF). | 0.028 | 16.3 |
| 1034 | Hydrolase | haloacid dehalogenase-like hydrolase | 2e-21 | 84.6 |
| 1037 | KRAB | KRAB box | 4.8e-06 | 32.4 |
| 1038 | Cation_efflux | Cation efflux family | 7.1e-42 | 152.5 |
| 1040 | ART | NAD:arginine ADP-ribosyltransferase | 4.7e-47 | 169.1 |
| 1042 | WD40 | WD domain, G-beta repeat | 1.9e-18 | 74.7 |
| 1043 | zf-C2H2 | Zinc finger, C2H2 type | 3.7e-24 | 93.7 |
| 1045 | lectin_c | Lectin C-type domain | 1.9e-28 | 108.0 |
| 1046 | Glucosamine_iso | Glucosamine-6-phosphate isomerase | 0.00013 | -25.1 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-----------------|--|----------|------------|
| 1047 | ligase-CoA | CoA-ligases | 4.5e-80 | 279.4 |
| 1049 | ig | Immunoglobulin domain | 1.7e-09 | 35.6 |
| 1050 | Ribosomal_L24e | Ribosomal protein L24e | 2e-33 | 124.5 |
| 1054 | Amidase | Amidase | 4.3e-152 | 518.7 |
| 1055 | rrm | RNA recognition motif. | 3.8e-26 | 100.3 |
| 1058 | annexin | Annexin | 6.9e-44 | 159.2 |
| 1059 | PMP22_Claudin | PMP-22/EMP/MP20/Claudin family | 0.023 | -23.6 |
| 1060 | homeobox | Homeobox domain | 3.2e-31 | 117.2 |
| 1062 | Acyltransferase | Acyltransferase | 0.00065 | 10.5 |
| 1064 | AMP-binding | AMP-binding enzyme | 6.6e-100 | 345.3 |
| 1065 | LRR | Leucine Rich Repeat | 3.3e-14 | 60.6 |
| 1066 | GTP1_OBG | GTP1/OBG family | 4.8e-41 | 141.8 |
| 1071 | ig | Immunoglobulin domain | 8.4e-48 | 159.1 |
| 1072 | PHD | PHD-finger | 6.8e-07 | 36.3 |
| 1074 | DENN | DENN (AEX-3) domain | 8.3e-33 | 121.5 |
| 1075 | SCP | SCP-like extracellular protein | 4.7e-41 | 149.8 |
| 1077 | OLF | Olfactomedin-like domain | 2.2e-66 | 234.0 |
| 1078 | mito_carr | Mitochondrial carrier proteins | 1e-42 | 149.3 |
| 1079 | WD40 | WD domain, G-beta repeat | 6.2e-45 | 162.7 |
| 1087 | START | START domain | 1.5e-48 | 174.7 |
| 1093 | DSFp | Dual specificity phosphatase, catalytic doma | 3.3e-63 | 223.4 |
| 1094 | GSHPx | Glutathione peroxidases | 9.6e-41 | 148.8 |
| 1095 | DUF25 | Domain of unknown function DUF25 | 2e-75 | 264.0 |
| 1096 | DUF25 | Domain of unknown function DUF25 | 6e-75 | 262.4 |
| 1105 | Nitroreductase | Nitroreductase family | 1.3e-13 | 58.6 |
| 1106 | PTE | Phosphotriesterase family | 1.3e-179 | 610.1 |
| 1107 | DAGKc | Diacylglycerol kinase catalytic domain | 0.00049 | 19.6 |
| 1109 | ras | Ras family | 1.3e-15 | 40.7 |
| 1115 | ArfGap | Putative GTP-ase activating protein for Arf | 9.7e-47 | 168.7 |
| 1116 | HMG14_17 | HMG14 and HMG17 | 4.4e-21 | 83.5 |
| 1117 | HMG14_17 | HMG14 and HMG17 | 9.9e-12 | 52.4 |
| 1119 | FAA_hydrolase | Fumarylacetoacetate (FAA) hydrolase fam | 2e-83 | 290.6 |
| 1120 | pkinase | Eukaryotic protein kinase domain | 1.4e-94 | 327.6 |
| 1123 | abhydrolase | alpha/beta hydrolase fold | 9.2e-23 | 89.0 |
| 1129 | pro_isomerase | Cyclophilin type peptidyl-prolyl cis-tr | 2.2e-56 | 197.1 |
| 1131 | DnaJ | DnaJ domain | 1.6e-30 | 114.9 |
| 1132 | WD40 | WD domain, G-beta repeat | 1.3e-19 | 78.6 |
| 1133 | WD40 | WD domain, G-beta repeat | 1.8e-15 | 64.9 |
| 1134 | PH | PH domain | 0.0015 | 17.8 |
| 1136 | Adap_comp_sub | Adaptor complexes medium subunit family | 1.2e-256 | 866.0 |
| 1137 | Adap_comp_sub | Adaptor complexes medium subunit family | 2.5e-209 | 708.8 |
| 1139 | ras | Ras family | 1.5e-86 | 301.0 |
| 1141 | pkinase | Eukaryotic protein kinase domain | 9.4e-74 | 258.4 |
| 1152 | Acyltransferase | Acyltransferase | 1.2e-05 | 29.9 |
| 1153 | IRS | PTB domain (IRS-1 type) | 5.4e-55 | 196.1 |
| 1155 | ig | Immunoglobulin domain | 1.3e-31 | 106.9 |
| 1157 | Asparaginase_2 | Asparaginase | 6.4e-72 | 252.3 |
| 1159 | GMC_oxred | GMC oxidoreductases | 4.7e-142 | 485.3 |
| 1160 | zf-AN1 | AN1-like Zinc finger | 0.00021 | 27.9 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|---------------------|---|----------|------------|
| 1163 | linker_histo ne | linker histone H1 and H5 family | 3.8e-14 | 60.4 |
| 1164 | DED | Death effector domain | 3.9e-05 | 30.5 |
| 1165 | IRS | PTB domain (IRS-1 type) | 2.6e-43 | 157.3 |
| 1166 | IRS | PTB domain (IRS-1 type) | 2.6e-43 | 157.3 |
| 1168 | SAM | SAM domain (Sterile alpha motif) | 0.04 | 10.5 |
| 1170 | abhydrolase | alpha/beta hydrolase fold | 0.098 | -7.5 |
| 1174 | SAP | SAP domain | 3.9e-10 | 47.1 |
| 1177 | PP2C | Protein phosphatase 2C | 5.3e-31 | 112.5 |
| 1178 | WD40 | WD domain, G-beta repeat | 4.7e-35 | 129.9 |
| 1180 | Ets | Ets-domain | 1.8e-09 | 33.3 |
| 1181 | Collagen | Collagen triple helix repeat (20 copies) | 0.00016 | 24.7 |
| 1182 | TCL1_MTCP1 | TCL1/MTCP1 family | 9.5e-56 | 198.6 |
| 1184 | RasGEF | RasGEF domain | 1.7e-88 | 307.4 |
| 1185 | mito_carr | Mitochondrial carrier proteins | 1.5e-62 | 217.3 |
| 1187 | UPAR_LY6 | u-PAR/Ly-6 domain | 0.0042 | 15.6 |
| 1188 | Orn_DAP_Arg_ deC | Pyridoxal-dependent decarboxylase | 6.2e-128 | 430.6 |
| 1193 | Stathmin | Stathmin family | 1.8e-90 | 314.0 |
| 1194 | Stathmin | Stathmin family | 1.8e-90 | 314.0 |
| 1195 | Sec1 | Sec1 family | 3.2e-183 | 622.1 |
| 1196 | pyr_redox | Pyridine nucleotide-disulphide oxidoreductase | 3.1e-32 | 111.8 |
| 1197 | Glyco_transf _8 | Glycosyl transferase family 8 | 1.2e-09 | 45.5 |
| 1202 | K_tetra | K+ channel tetramerisation domain | 0.022 | -16.8 |
| 1203 | adh_short | short chain dehydrogenase | 8.3e-45 | 162.3 |
| 1206 | UbiE_methylt ran | ubiE/COQ5 methyltransferase family | 1.3e-121 | 417.4 |
| 1208 | 7tm_3 | 7 transmembrane receptor | 7.2e-09 | 29.0 |
| 1209 | ank | Ank repeat | 3.9e-15 | 63.7 |
| 1210 | vATP- synt_AC39 | ATP synthase (C/AC39) subunit | 2.5e-128 | 439.7 |
| 1212 | zf-C2H2 | Zinc finger, C2H2 type | 5.5e-17 | 69.9 |
| 1213 | efhand | EF hand | 3.2e-07 | 37.4 |
| 1219 | rrm | RNA recognition motif | 2.1e-40 | 147.7 |
| 1220 | DUF6 | Integral membrane protein DUF6 | 0.015 | 21.5 |
| 1222 | SCAN | SCAN domain | 1.5e-71 | 251.1 |
| 1223 | G-gamma | GGL domain | 3.6e-36 | 129.5 |
| 1227 | catalase | Catalase | 0 | 1158.9 |
| 1232 | PX | PX domain | 2.2e-15 | 64.5 |
| 1233 | PX | PX domain | 2.2e-15 | 64.5 |
| 1236 | FCH | Fes/CIP4 homology domain | 3.3e-09 | 44.0 |
| 1241 | Peptidase_M2 0 | Peptidase family M20/M25/M40 | 2e-63 | 224.1 |
| 1243 | WW | WW domain | 0.044 | 17.9 |
| 1247 | UPF0006 | Metalloenzyme of unknown function UPF0006 | 6.3e-61 | 215.8 |
| 1248 | Glycos_trans f_2 | Glycosyl transferases | 4.5e-10 | 46.9 |
| 1249 | efhand | EF hand | 4e-11 | 50.4 |
| 1254 | UQ_con | Ubiquitin-conjugating enzyme | 2.1e-73 | 257.3 |
| 1255 | ras | Ras family | 2.2e-62 | 220.7 |
| 1256 | formyl_trans f | Formyl transferase | 4.9e-30 | 108.3 |
| 1259 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 5.3e-13 | 46.4 |
| 1261 | Dihfolate_re d | Dihydrofolate reductase | 2.1e-69 | 241.7 |
| 1262 | G_glu_transp ept | Gamma-glutamyltranspeptidase | 1.8e-110 | 380.4 |
| 1263 | PAS | PAS domain | 1.3e-08 | 36.9 |
| 1265 | LRR | Leucine Rich Repeat | 4.2e-22 | 86.9 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|---------------|---|----------|------------|
| 1266 | SCP | SCP-like extracellular protein | 6e-29 | 108.0 |
| 1267 | K_tetra | K ⁺ channel tetramerisation domain | 2.8e-27 | 104.0 |
| 1269 | ras | Ras family | 1.3e-85 | 297.9 |
| 1275 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 4.2e-10 | 37.0 |
| 1276 | abhydrolase | alpha/beta hydrolase fold | 5.4e-23 | 89.8 |
| 1277 | abhydrolase | alpha/beta hydrolase fold | 5.6e-21 | 83.1 |
| 1279 | trypsin | Trypsin | 4.4e-41 | 132.0 |
| 1280 | PBP | Phosphatidylethanolamine-binding protein | 1.3e-13 | 58.7 |
| 1285 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 5.6e-14 | 49.6 |
| 1287 | ank | Ank repeat | 1.7e-52 | 187.8 |
| 1294 | fn3 | Fibronectin type III domain | 0.026 | 20.9 |
| 1295 | GBP | Guanylate-binding protein | 0.00026 | -70.0 |
| 1296 | PMP22_Claudin | PMP-22/EMP/MP20/Claudin family | 6.9e-41 | 149.3 |
| 1297 | Rhodanese | Rhodanese-like domain | 3.2e-14 | 60.7 |
| 1298 | LIM | LIM domain containing proteins | 5.8e-21 | 79.1 |
| 1301 | rnaseA | Pancreatic ribonucleases | 4.9e-43 | 145.2 |
| 1307 | mito_carr | Mitochondrial carrier proteins | 2.1e-53 | 186.0 |
| 1308 | WD40 | WD domain, G-beta repeat | 1.6e-17 | 71.6 |
| 1310 | UPAR_LY6 | u-PAR/Ly-6 domain | 7.1e-20 | 75.5 |
| 1313 | thioredo | Thioredoxin | 3.6e-05 | 21.6 |
| 1314 | Aa_trans | Transmembrane amino acid transporter protein | 1.5e-67 | 237.9 |
| 1316 | trypsin | Trypsin | 4.4e-41 | 132.0 |
| 1320 | Ribosomal_L13 | Ribosomal protein L13 | 3.9e-62 | 219.8 |
| 1327 | Armadillo_se | Armadillo/beta-catenin-like repeats | 0.0054 | 23.4 |
| 1328 | KRAB | KRAB box | 0.052 | -5.6 |
| 1329 | rrm | RNA recognition motif. | 2.1e-40 | 147.7 |
| 1330 | Bcl-2 | Apoptosis regulator proteins, Bcl-2 family | 0.014 | -1.6 |
| 1331 | PX | PX domain | 2.1e-10 | 48.0 |
| 1333 | KRAB | KRAB box | 1.8e-36 | 134.6 |
| 1334 | UPP_syntheta | Putative undecaprenyl diphosphate synt | 2.3e-89 | 310.3 |
| 1335 | UPP_syntheta | Putative undecaprenyl diphosphate synt | 1.8e-59 | 211.0 |
| 1336 | DSPc | Dual specificity phosphatase, catalytic doma | 1.2e-31 | 118.6 |
| 1337 | DSPc | Dual specificity phosphatase, catalytic doma | 2.3e-12 | 54.5 |
| 1338 | TPR | TPR Domain | 0.00021 | 28.1 |
| 1340 | metalthio | Metallothionein | 0.013 | 20.3 |
| 1341 | mutT | Bacterial mutT protein | 5.8e-09 | 36.5 |
| 1343 | Band_41 | FERM domain (Band 4.1 family) | 1.3e-38 | 122.5 |
| 1344 | Kelch | Kelch motif | 1.4e-44 | 161.5 |
| 1345 | Antifreeze | Antifreeze protein | 1.2e-10 | 48.8 |
| 1347 | 3Beta_HSD | 3-beta hydroxysteroid dehydrogenase/isomera | 0.086 | -177.2 |
| 1348 | BTB | BTB/POZ domain | 5.3e-28 | 106.5 |
| 1349 | DUF6 | Integral membrane protein DUF6 | 0.033 | 15.8 |
| 1350 | myosin_head | Myosin head (motor domain) | 0 | 1088.7 |
| 1352 | Nramp | Natural resistance-associated macrophage pro | 1.2e-202 | 686.6 |
| 1353 | S_100 | S-100/ICaBP type calcium binding domain | 5.3e-23 | 89.9 |
| 1355 | DEAD | DRAD/DEAH box helicase | 3.6e-65 | 209.0 |
| 1356 | C2 | C2 domain | 2.4e-15 | 64.4 |
| 1357 | RBD | Raf-like Ras-binding domain | 4.2e-57 | 203.1 |
| 1360 | zf-C2H2 | Zinc finger, C2H2 type | 7.4e-141 | 481.4 |
| 1361 | HMG14_17 | HMG14 and HMG17 | 7.9e-40 | 145.7 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|--------------------|---|----------|------------|
| 1362 | SIS | SIS domain | 3.8e-30 | 113.6 |
| 1363 | SIS | SIS domain | 1.3e-28 | 108.5 |
| 1364 | ig | Immunoglobulin domain | 0.00026 | 19.0 |
| 1368 | K_tetra | K ⁺ channel tetramerisation domain | 1.1e-16 | 68.9 |
| 1371 | Collagen | Collagen triple helix repeat (20 copies) | 2.2e-113 | 390.1 |
| 1372 | DnaJ | DnaJ domain | 6.6e-36 | 132.7 |
| 1376 | KRAB | KRAB box | 2.1e-38 | 141.0 |
| 1378 | ELM2 | ELM2 domain | 2e-23 | 91.3 |
| 1380 | thioredo | Thioredoxin | 1.2e-23 | 82.8 |
| 1381 | ank | Ank repeat | 2.3e-83 | 290.4 |
| 1382 | BTB | BTB/POZ domain | 3e-11 | 50.8 |
| 1383 | WD40 | WD domain, G-beta repeat | 1.6e-19 | 78.3 |
| 1384 | WD40 | WD domain, G-beta repeat | 6.3e-24 | 92.9 |
| 1387 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 1.1e-09 | 35.6 |
| 1389 | zf-C2H2 | Zinc finger, C2H2 type | 5.5e-50 | 179.5 |
| 1390 | zf-C2H2 | Zinc finger, C2H2 type | 2.5e-85 | 296.9 |
| 1393 | kinesin | Kinesin motor domain | 7.8e-188 | 637.4 |
| 1394 | zf-C2H2 | Zinc finger, C2H2 type | 1.2e-49 | 178.4 |
| 1398 | KRAB | KRAB box | 5.1e-22 | 86.6 |
| 1402 | bZIP | bZIP transcription factor | 0.035 | 13.1 |
| 1405 | sugar_tr | Sugar (and other) transporter | 0.003 | -101.5 |
| 1406 | RhoGAP | RhoGAP domain | 8.9e-47 | 168.8 |
| 1407 | rrm | RNA recognition motif. | 1e-35 | 132.1 |
| 1408 | LRR | Leucine Rich Repeat | 2.1e-13 | 58.0 |
| 1409 | Nebulin_repe at | Nebulin repeat | 6e-54 | 192.6 |
| 1410 | ank | Ank repeat | 1.6e-17 | 71.6 |
| 1412 | Ribosomal_L5 _C | ribosomal L5P family C-terminus | 8.2e-58 | 205.5 |
| 1415 | trypsin | Trypsin | 4.7e-85 | 270.4 |
| 1416 | aminotran_1 | Aminotransferases class-I | 4.4e-05 | -91.2 |
| 1417 | S1 | S1 RNA binding domain | 1.6e-07 | 33.1 |
| 1419 | WD40 | WD domain, G-beta repeat | 2.2e-09 | 44.6 |
| 1422 | cadherin | Cadherin domain | 8.3e-42 | 152.3 |
| 1424 | SH3 | SH3 domain | 2.5e-80 | 280.3 |
| 1425 | PHD | PHD-finger | 3.2e-17 | 70.6 |
| 1426 | PHD | PHD-finger | 3.2e-17 | 70.6 |
| 1427 | ArfGap | Putative GTP-ase activating protein for Arf | 1e-37 | 138.8 |
| 1428 | helicase_C | Helicases conserved C-terminal domain | 1e-26 | 102.2 |
| 1429 | WD40 | WD domain, G-beta repeat | 3.9e-07 | 37.2 |
| 1430 | inositol_P | Inositol monophosphatase family | 2.5e-10 | 40.2 |
| 1431 | mito_carr | Mitochondrial carrier proteins | 4.3e-83 | 287.7 |
| 1433 | Clq | Clq domain | 2.9e-16 | 66.2 |
| 1434 | WD40 | WD domain, G-beta repeat | 1.6e-13 | 58.3 |
| 1435 | Inos-1- P_synth | Myo-inositol-1-phosphate synthase | 7e-228 | 770.4 |
| 1436 | rrm | RNA recognition motif. | 1.4e-34 | 128.3 |
| 1438 | ig | Immunoglobulin domain | 1.3e-12 | 45.6 |
| 1440 | G_Adapt_CT | Gamma-adaptin, C-terminus | 3.4e-67 | 236.7 |
| 1441 | G_Adapt_CT | Gamma-adaptin, C-terminus | 3.4e-67 | 236.7 |
| 1443 | Kelch | Kelch motif | 0.00013 | 28.7 |
| 1446 | ARID | ARID DNA binding domain | 1.8e-21 | 84.7 |
| 1447 | zf-C2H2 | Zinc finger, C2H2 type | 9.4e-28 | 105.6 |
| 1448 | AMP-binding | AMP-binding enzyme | 2.6e-07 | -145.1 |
| 1451 | rrm | RNA recognition motif. | 6.5e-21 | 82.9 |
| 1454 | ig | Immunoglobulin domain | 5.6e-44 | 146.7 |
| 1455 | Sialyltransf | Sialyltransferase family | 5.4e-21 | 83.2 |
| 1460 | Aldose_epim | Aldose 1-epimerase | 1.9e-35 | 131.2 |
| 1461 | C2 | C2 domain | 4e-18 | 73.6 |
| 1470 | TIG | IPT/TIG domain | 3.1e-19 | 77.3 |
| 1472 | PseudoU_synt | RNA pseudouridylation synthase | 4.3e-16 | 66.9 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|-------------------|--|----------|------------|
| | h_2 | | | |
| 1474 | DENN | DENN (AEX-3) domain | 1.3e-44 | 161.6 |
| 1475 | Cation_efflux | Cation efflux family | 4.6e-49 | 176.4 |
| 1477 | TBC | TBC domain | 8e-47 | 169.0 |
| 1478 | rrm | RNA recognition motif. | 2e-21 | 84.6 |
| 1480 | ig | Immunoglobulin domain | 5.5e-06 | 24.3 |
| 1484 | Telo_bind_alpha | Telomere-binding protein alpha subunit | 0.028 | -225.9 |
| 1485 | zf-C2H2 | Zinc finger, C2H2 type | 1.8e-68 | 240.9 |
| 1486 | pkinase | Eukaryotic protein kinase domain | 9.5e-13 | 49.9 |
| 1488 | helicase_C | Helicases conserved C-terminal domain | 1.4e-15 | 65.2 |
| 1489 | DUF89 | Protein of unknown function DUF89 | 0.079 | -132.4 |
| 1490 | ECH | Enoyl-CoA hydratase/isomerase family | 5.2e-41 | 149.7 |
| 1491 | guanylate_cyclase | Adenylate and Guanylate cyclase catalyt | 5.9e-46 | 166.1 |
| 1492 | LRR | Leucine Rich Repeat | 3.4e-19 | 77.2 |
| 1495 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) | 7.1e-10 | 36.3 |
| 1497 | pkinase | Eukaryotic protein kinase domain | 1e-22 | 85.8 |
| 1500 | SH3 | SH3 domain | 9.3e-05 | 27.2 |
| 1502 | homeobox | Homeobox domain | 0.084 | 13.8 |
| 1503 | homeobox | Homeobox domain | 0.084 | 13.8 |
| 1505 | EGF | EGF-like domain | 2.7e-23 | 90.8 |
| 1506 | UCH-2 | Ubiquitin carboxyl-terminal hydrolase family | 2.7e-21 | 84.2 |
| 1508 | Peptidase_M20 | Peptidase family M20/M25/M40 | 2.8e-28 | 101.6 |
| 1511 | PX | PX domain | 1.9e-11 | 51.5 |
| 1512 | Sulfatase | Sulfatase | 2.8e-35 | 130.7 |
| 1516 | Syntaxin | Syntaxin | 0.011 | -62.3 |
| 1518 | aminotran_3 | Aminotransferases class-III pyridoxal-pho | 9.7e-106 | 305.6 |
| 1520 | ig | Immunoglobulin domain | 0.075 | 11.0 |
| 1521 | RA | Ras association (RalGDS/AF-6) domain | 0.013 | 13.3 |
| 1523 | RhoGAP | RhoGAP domain | 2.5e-05 | 18.7 |
| 1528 | WD40 | WD domain, G-beta repeat | 5.4e-24 | 93.1 |
| 1535 | impB/mucB/samB | impB/mucB/samB family | 7.8e-95 | 328.5 |
| 1538 | FYVE | FYVE zinc finger | 3.2e-27 | 101.5 |
| 1539 | DAGKc | Diacylglycerol kinase catalytic domain | 6e-07 | 36.5 |
| 1540 | Ocular_alb | Ocular albinism type 1 protein | 0 | 1184.7 |
| 1653 | SAP | SAP domain | 6e-06 | 33.2 |
| 1654 | Amino_oxidase | Flavin containing amine oxidase | 3.2e-43 | 157.0 |
| 1655 | Amino_oxidase | Flavin containing amine oxidase | 3.2e-43 | 157.0 |
| 1656 | RhoGEF | RhoGEF domain | 1.4e-24 | 95.1 |
| 1657 | MMR_HSR1 | GTPase of unknown function | 0.0011 | -45.5 |
| 1659 | UCH-2 | Ubiquitin carboxyl-terminal hydrolase family | 2.5e-11 | 51.1 |
| 1660 | actin | Actin | 6.6e-21 | 69.9 |
| 1661 | BAH | BAH domain | 1.7e-82 | 287.5 |
| 1662 | vwa | von Willebrand factor type A domain | 0 | 1909.4 |
| 1663 | WD40 | WD domain, G-beta repeat | 1.4e-67 | 237.9 |
| 1667 | zf-C2H2 | Zinc finger, C2H2 type | 1.3e-93 | 324.4 |
| 1669 | Nol1_Nop2_sun | NOL1/NOP2/sun family | 1.3e-23 | 84.3 |
| 1671 | SH2 | Src homology domain 2 | 5.4e-15 | 46.9 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|------------|----------------|--|----------|------------|
| 1672 | chromo | 'chromo' (CHRromatin Organization Modifier) | 2.1e-18 | 67.7 |
| 1674 | zf-CCCH | Zinc finger C-x8-C-x5-C-x3-H type | 0.0025 | 17.6 |
| 1676 | Glyco_hydro_47 | Glycosyl hydrolase family 47 | 1.8e-187 | 636.2 |
| 1677 | Glyco_hydro_47 | Glycosyl hydrolase family 47 | 4.5e-74 | 259.5 |
| 1680 | WD40 | WD domain, G-beta repeat | 1.1e-27 | 105.5 |
| 1681 | WD40 | WD domain, G-beta repeat | 1.1e-27 | 105.5 |
| 1683 | MMR_HSR1 | GTPase of unknown function | 1.8e-78 | 274.1 |
| 1691 | rrm | RNA recognition motif. | 1.8e-37 | 137.9 |
| 1692 | rrm | RNA recognition motif. | 1.8e-37 | 137.9 |
| 1693 | AAA | ATPases associated with various cellular act | 1.3e-81 | 284.5 |
| 1697 | Ferric_reduc t | Ferric reductase like transmembrane com | 8.4e-82 | 285.2 |
| 1698 | Ferric_reduc t | Ferric reductase like transmembrane com | 3.5e-53 | 190.1 |
| 1699 | zf-C2H2 | Zinc finger, C2H2 type | 4.4e-34 | 126.6 |
| 1700 | arf | ADP-ribosylation factor family | 9e-19 | 75.8 |
| 1702 | GTP_EFTU | Elongation factor Tu family | 0.014 | 11.4 |
| 1703 | SCAN | SCAN domain | 1.8e-54 | 194.4 |
| 1707 | pkinase | Eukaryotic protein kinase domain | 1.2e-88 | 307.9 |
| 1709 | WD40 | WD domain, G-beta repeat | 0.0035 | 24.0 |
| 1710 | LRR | Leucine Rich Repeat | 1.2e-30 | 115.3 |
| 1711 | WW | WW domain | 7.6e-12 | 52.8 |
| 1712 | ank | Ank repeat | 4.2e-34 | 126.7 |
| 1713 | zf-CCCH | Zinc finger C-x8-C-x5-C-x3-H type | 2.6e-09 | 38.3 |
| 1714 | zf-CCCH | Zinc finger C-x8-C-x5-C-x3-H type | 2.6e-09 | 38.3 |
| 1715 | ras | Ras family | 4.4e-41 | 149.9 |
| 1718 | HMG_box | HMG (high mobility group) box | 8.3e-21 | 82.6 |
| 1719 | TBC | TBC domain | 1.1e-45 | 165.2 |
| 1721 | HLH | Helix-loop-helix DNA-binding domain | 9.2e-10 | 45.9 |
| 1723 | dsrm | Double-stranded RNA binding motif | 2.9e-05 | 30.9 |
| 1724 | RrnaAD | Ribosomal RNA adenine dimethylases | 0.045 | 9.2 |
| 1725 | CIDE-N | CIDE-N domain | 5.9e-40 | 146.2 |
| 1726 | HAT | HAT (Half-A-TPR) repeats | 2.9e-44 | 160.5 |
| 1728 | efhand | EF hand | 5.1e-20 | 79.9 |
| 1733 | Hist_deacetyl | Histone deacetylase family | 1.7e-104 | 360.6 |
| 1735 | LRR | Leucine Rich Repeat | 4.6e-34 | 126.6 |
| 1739 | PI-PLC-X | Phosphatidylinositol-specific phospholipase | 0.0023 | 16.1 |
| 1743 | ras | Ras family | 3.7e-10 | -21.3 |
| 1744 | ras | Ras family | 3.7e-10 | -21.3 |
| 1745 | RasGEF | RasGEF domain | 3.2e-49 | 176.9 |
| 1746 | adh_short | short chain dehydrogenase | 7.1e-08 | 34.6 |
| 1751 | zf-C2H2 | Zinc finger, C2H2 type | 9e-39 | 142.2 |
| 1754 | fn3 | Fibronectin type III domain | 5.5e-101 | 348.9 |
| 1756 | zf-C2H2 | Zinc finger, C2H2 type | 6.3e-93 | 322.1 |
| 1758 | rrm | RNA recognition motif. | 0.017 | 21.2 |
| 1760 | Nop | Putative snRNA binding domain | 6.1e-95 | 328.8 |
| 1761 | Nop | Putative snRNA binding domain | 6.1e-95 | 328.8 |
| 1765 | MMR_HSR1 | GTPase of unknown function | 6.4e-41 | 149.4 |
| 1769 | CN_hydrolase | Carbon-nitrogen hydrolase | 3e-06 | -43.9 |
| 1775 | ank | Ank repeat | 4.1e-07 | 37.1 |
| 1779 | Oxysterol_BP | Oxysterol-binding protein | 4.7e-56 | 199.6 |
| 1783 | RhoGEF | RhoGEF domain | 1.6e-23 | 91.6 |
| 1784 | RhoGEF | RhoGEF domain | 1.6e-23 | 91.6 |

| SEQ ID NO: | PFAM NAME | DESCRIPTION | p-value | PFAM SCORE |
|---------------|-----------|------------------------|---------|---------------|
| 1785 | rrm | RNA recognition motif. | 6.4e-14 | 59.7 |

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TABLE 5

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 1 | 1-21 | 0.991 | 0.955 |
| 2 | 1-31 | 0.995 | 0.944 |
| 3 | 1-33 | 0.949 | 0.736 |
| 4 | 1-19 | 0.970 | 0.951 |
| 5 | 1-26 | 0.971 | 0.863 |
| 6 | 1-26 | 0.971 | 0.863 |
| 7 | 1-26 | 0.971 | 0.863 |
| 8 | 1-26 | 0.971 | 0.863 |
| 9 | 1-46 | 0.982 | 0.901 |
| 10 | 1-21 | 0.991 | 0.955 |
| 11 | 1-23 | 0.989 | 0.899 |
| 12 | 1-25 | 0.955 | 0.803 |
| 13 | 1-18 | 0.932 | 0.625 |
| 14 | 1-18 | 0.938 | 0.876 |
| 15 | 1-25 | 0.941 | 0.811 |
| 16 | 1-17 | 0.972 | 0.939 |
| 17 | 1-27 | 0.964 | 0.777 |
| 18 | 1-16 | 0.914 | 0.657 |
| 19 | 1-19 | 0.953 | 0.840 |
| 20 | 1-20 | 0.935 | 0.701 |
| 21 | 1-22 | 0.974 | 0.850 |
| 22 | 1-33 | 0.961 | 0.895 |
| 23 | 1-19 | 0.991 | 0.959 |
| 24 | 1-31 | 0.995 | 0.944 |
| 25 | 1-22 | 0.976 | 0.935 |
| 26 | 1-27 | 0.996 | 0.928 |
| 27 | 1-24 | 0.953 | 0.739 |
| 28 | 1-21 | 0.906 | 0.688 |
| 29 | 1-31 | 0.986 | 0.841 |
| 30 | 1-28 | 0.980 | 0.893 |
| 31 | 1-19 | 0.993 | 0.976 |
| 32 | 1-22 | 0.998 | 0.909 |
| 35 | 1-33 | 0.949 | 0.736 |
| 36 | 1-33 | 0.949 | 0.736 |
| 46 | 1-19 | 0.970 | 0.951 |
| 67 | 1-25 | 0.968 | 0.848 |
| 71 | 1-18 | 0.949 | 0.845 |
| 72 | 1-30 | 0.991 | 0.919 |
| 75 | 1-29 | 0.958 | 0.854 |
| 88 | 1-20 | 0.986 | 0.945 |
| 94 | 1-33 | 0.994 | 0.943 |
| 97 | 1-46 | 0.964 | 0.595 |
| 103 | 1-49 | 0.983 | 0.570 |
| 108 | 1-26 | 0.978 | 0.885 |
| 111 | 1-23 | 0.989 | 0.899 |
| 126 | 1-25 | 0.955 | 0.803 |
| 129 | 1-19 | 0.963 | 0.918 |
| 138 | 1-29 | 0.971 | 0.844 |
| 143 | 1-18 | 0.914 | 0.628 |
| 148 | 1-20 | 0.969 | 0.904 |
| 156 | 1-25 | 0.941 | 0.811 |
| 158 | 1-22 | 0.979 | 0.927 |
| 160 | 1-17 | 0.972 | 0.939 |
| 161 | 1-48 | 0.903 | 0.571 |
| 162 | 1-25 | 0.937 | 0.729 |
| 168 | 1-16 | 0.939 | 0.826 |
| 171 | 1-27 | 0.964 | 0.777 |
| 178 | 1-21 | 0.945 | 0.825 |
| 180 | 1-27 | 0.981 | 0.941 |
| 187 | 1-28 | 0.982 | 0.936 |
| 190 | 1-19 | 0.953 | 0.840 |
| 196 | 1-22 | 0.975 | 0.916 |
| 197 | 1-22 | 0.963 | 0.936 |

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 199 | 1-20 | 0.935 | 0.701 |
| 200 | 1-23 | 0.977 | 0.773 |
| 206 | 1-30 | 0.984 | 0.890 |
| 207 | 1-19 | 0.990 | 0.924 |
| 208 | 1-22 | 0.974 | 0.850 |
| 210 | 1-40 | 0.940 | 0.670 |
| 211 | 1-28 | 0.971 | 0.849 |
| 216 | 1-24 | 0.986 | 0.956 |
| 218 | 1-33 | 0.961 | 0.895 |
| 219 | 1-19 | 0.970 | 0.871 |
| 221 | 1-19 | 0.904 | 0.553 |
| 222 | 1-21 | 0.917 | 0.555 |
| 230 | 1-19 | 0.991 | 0.959 |
| 231 | 1-26 | 0.953 | 0.800 |
| 232 | 1-25 | 0.988 | 0.826 |
| 239 | 1-23 | 0.969 | 0.828 |
| 240 | 1-17 | 0.982 | 0.955 |
| 241 | 1-17 | 0.982 | 0.955 |
| 245 | 1-30 | 0.970 | 0.722 |
| 248 | 1-22 | 0.976 | 0.935 |
| 249 | 1-23 | 0.968 | 0.940 |
| 252 | 1-18 | 0.971 | 0.923 |
| 261 | 1-24 | 0.883 | 0.587 |
| 265 | 1-18 | 0.939 | 0.868 |
| 272 | 1-24 | 0.953 | 0.739 |
| 283 | 1-21 | 0.906 | 0.688 |
| 284 | 1-29 | 0.997 | 0.854 |
| 290 | 1-31 | 0.986 | 0.841 |
| 302 | 1-28 | 0.980 | 0.893 |
| 304 | 1-16 | 0.907 | 0.635 |
| 312 | 1-19 | 0.993 | 0.976 |
| 313 | 1-17 | 0.930 | 0.753 |
| 323 | 1-22 | 0.998 | 0.909 |
| 324 | 1-17 | 0.982 | 0.954 |
| 328 | 1-19 | 0.971 | 0.865 |
| 329 | 1-22 | 0.963 | 0.924 |
| 330 | 1-33 | 0.978 | 0.841 |
| 331 | 1-24 | 0.920 | 0.712 |
| 332 | 1-24 | 0.975 | 0.881 |
| 333 | 1-19 | 0.984 | 0.941 |
| 334 | 1-20 | 0.899 | 0.567 |
| 335 | 1-27 | 0.942 | 0.813 |
| 336 | 1-20 | 0.952 | 0.850 |
| 337 | 1-38 | 0.942 | 0.653 |
| 338 | 1-27 | 0.973 | 0.772 |
| 339 | 1-36 | 0.979 | 0.804 |
| 340 | 1-27 | 0.888 | 0.597 |
| 343 | 1-19 | 0.971 | 0.865 |
| 344 | 1-22 | 0.994 | 0.928 |
| 345 | 1-17 | 0.966 | 0.687 |
| 346 | 1-19 | 0.936 | 0.822 |
| 347 | 1-22 | 0.963 | 0.924 |
| 349 | 1-24 | 0.982 | 0.966 |
| 351 | 1-21 | 0.918 | 0.815 |
| 352 | 1-31 | 0.988 | 0.912 |
| 354 | 1-31 | 0.974 | 0.839 |
| 355 | 1-29 | 0.932 | 0.632 |
| 356 | 1-15 | 0.994 | 0.969 |
| 357 | 1-33 | 0.935 | 0.726 |
| 360 | 1-27 | 0.938 | 0.827 |
| 361 | 1-25 | 0.954 | 0.674 |
| 362 | 1-22 | 0.929 | 0.788 |
| 363 | 1-21 | 0.881 | 0.715 |
| 364 | 1-33 | 0.978 | 0.841 |
| 365 | 1-33 | 0.978 | 0.841 |

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 366 | 1-21 | 0.916 | 0.820 |
| 367 | 1-19 | 0.936 | 0.822 |
| 368 | 1-29 | 0.972 | 0.874 |
| 370 | 1-24 | 0.920 | 0.712 |
| 371 | 1-24 | 0.961 | 0.773 |
| 372 | 1-27 | 0.919 | 0.768 |
| 373 | 1-19 | 0.986 | 0.945 |
| 375 | 1-32 | 0.994 | 0.932 |
| 376 | 1-34 | 0.987 | 0.810 |
| 377 | 1-17 | 0.995 | 0.950 |
| 378 | 1-49 | 0.971 | 0.749 |
| 380 | 1-20 | 0.968 | 0.874 |
| 381 | 1-20 | 0.928 | 0.782 |
| 382 | 1-19 | 0.986 | 0.934 |
| 383 | 1-28 | 0.965 | 0.829 |
| 384 | 1-39 | 0.970 | 0.551 |
| 386 | 1-24 | 0.975 | 0.881 |
| 388 | 1-30 | 0.989 | 0.868 |
| 389 | 1-19 | 0.984 | 0.941 |
| 390 | 1-26 | 0.971 | 0.782 |
| 392 | 1-20 | 0.981 | 0.900 |
| 393 | 1-16 | 0.968 | 0.890 |
| 394 | 1-23 | 0.937 | 0.701 |
| 397 | 1-22 | 0.985 | 0.854 |
| 399 | 1-46 | 0.977 | 0.698 |
| 401 | 1-20 | 0.899 | 0.567 |
| 402 | 1-22 | 0.967 | 0.931 |
| 403 | 1-27 | 0.992 | 0.934 |
| 404 | 1-19 | 0.991 | 0.973 |
| 405 | 1-23 | 0.994 | 0.921 |
| 407 | 1-35 | 0.987 | 0.658 |
| 408 | 1-39 | 0.976 | 0.551 |
| 409 | 1-33 | 0.897 | 0.570 |
| 410 | 1-25 | 0.990 | 0.962 |
| 411 | 1-38 | 0.977 | 0.827 |
| 412 | 1-20 | 0.944 | 0.768 |
| 413 | 1-20 | 0.988 | 0.965 |
| 414 | 1-46 | 0.993 | 0.638 |
| 415 | 1-23 | 0.981 | 0.940 |
| 417 | 1-29 | 0.941 | 0.672 |
| 418 | 1-20 | 0.952 | 0.850 |
| 419 | 1-19 | 0.986 | 0.967 |
| 420 | 1-29 | 0.965 | 0.861 |
| 421 | 1-22 | 0.889 | 0.785 |
| 422 | 1-48 | 0.982 | 0.862 |
| 424 | 1-19 | 0.979 | 0.933 |
| 428 | 1-38 | 0.942 | 0.653 |
| 430 | 1-18 | 0.947 | 0.595 |
| 432 | 1-33 | 0.957 | 0.789 |
| 433 | 1-26 | 0.979 | 0.904 |
| 434 | 1-27 | 0.962 | 0.777 |
| 435 | 1-24 | 0.998 | 0.977 |
| 436 | 1-27 | 0.973 | 0.772 |
| 443 | 1-15 | 0.966 | 0.940 |
| 448 | 1-36 | 0.979 | 0.804 |
| 453 | 1-41 | 0.958 | 0.609 |
| 455 | 1-33 | 0.943 | 0.606 |
| 457 | 1-27 | 0.888 | 0.597 |
| 462 | 1-16 | 0.925 | 0.681 |
| 486 | 1-27 | 0.972 | 0.845 |
| 495 | 1-24 | 0.917 | 0.636 |
| 498 | 1-26 | 0.993 | 0.890 |
| 505 | 1-20 | 0.976 | 0.926 |
| 507 | 1-17 | 0.966 | 0.687 |
| 510 | 1-23 | 0.930 | 0.593 |

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 511 | 1-23 | 0.930 | 0.593 |
| 512 | 1-23 | 0.930 | 0.593 |
| 515 | 1-18 | 0.978 | 0.956 |
| 523 | 1-19 | 0.936 | 0.822 |
| 529 | 1-22 | 0.963 | 0.924 |
| 545 | 1-24 | 0.982 | 0.966 |
| 550 | 1-30 | 0.933 | 0.713 |
| 552 | 1-21 | 0.973 | 0.912 |
| 554 | 1-23 | 0.969 | 0.784 |
| 571 | 1-21 | 0.918 | 0.815 |
| 574 | 1-31 | 0.988 | 0.912 |
| 580 | 1-39 | 0.925 | 0.556 |
| 594 | 1-31 | 0.974 | 0.839 |
| 608 | 1-29 | 0.932 | 0.632 |
| 609 | 1-29 | 0.932 | 0.632 |
| 610 | 1-21 | 0.990 | 0.948 |
| 621 | 1-15 | 0.994 | 0.969 |
| 623 | 1-33 | 0.935 | 0.726 |
| 653 | 1-27 | 0.938 | 0.827 |
| 668 | 1-22 | 0.929 | 0.788 |
| 677 | 1-16 | 0.948 | 0.807 |
| 685 | 1-21 | 0.881 | 0.715 |
| 699 | 1-22 | 0.975 | 0.816 |
| 702 | 1-31 | 0.968 | 0.898 |
| 707 | 1-16 | 0.880 | 0.562 |
| 713 | 1-25 | 0.966 | 0.743 |
| 718 | 1-19 | 0.936 | 0.822 |
| 719 | 1-20 | 0.961 | 0.824 |
| 729 | 1-29 | 0.972 | 0.874 |
| 735 | 1-46 | 0.903 | 0.598 |
| 746 | 1-14 | 0.916 | 0.730 |
| 747 | 1-22 | 0.965 | 0.876 |
| 748 | 1-29 | 0.968 | 0.785 |
| 759 | 1-24 | 0.961 | 0.773 |
| 767 | 1-27 | 0.919 | 0.768 |
| 768 | 1-33 | 0.900 | 0.585 |
| 773 | 1-42 | 0.959 | 0.702 |
| 779 | 1-19 | 0.986 | 0.945 |
| 797 | 1-19 | 0.944 | 0.759 |
| 798 | 1-19 | 0.900 | 0.568 |
| 820 | 1-17 | 0.995 | 0.950 |
| 827 | 1-49 | 0.971 | 0.749 |
| 848 | 1-20 | 0.968 | 0.874 |
| 864 | 1-20 | 0.928 | 0.782 |
| 866 | 1-19 | 0.986 | 0.934 |
| 873 | 1-23 | 0.948 | 0.886 |
| 881 | 1-28 | 0.965 | 0.829 |
| 887 | 1-39 | 0.970 | 0.551 |
| 927 | 1-30 | 0.989 | 0.868 |
| 934 | 1-48 | 0.988 | 0.777 |
| 939 | 1-39 | 0.994 | 0.889 |
| 944 | 1-26 | 0.971 | 0.782 |
| 950 | 1-29 | 0.957 | 0.845 |
| 963 | 1-20 | 0.981 | 0.900 |
| 964 | 1-20 | 0.886 | 0.558 |
| 973 | 1-16 | 0.968 | 0.890 |
| 980 | 1-34 | 0.961 | 0.749 |
| 981 | 1-20 | 0.953 | 0.822 |
| 984 | 1-12 | 0.938 | 0.780 |
| 1015 | 1-22 | 0.985 | 0.854 |
| 1040 | 1-46 | 0.977 | 0.698 |
| 1052 | 1-18 | 0.969 | 0.842 |
| 1059 | 1-20 | 0.927 | 0.867 |
| 1065 | 1-33 | 0.983 | 0.918 |
| 1069 | 1-22 | 0.993 | 0.935 |

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 1075 | 1-27 | 0.992 | 0.934 |
| 1080 | 1-19 | 0.931 | 0.829 |
| 1092 | 1-19 | 0.991 | 0.973 |
| 1094 | 1-46 | 0.992 | 0.653 |
| 1095 | 1-30 | 0.974 | 0.929 |
| 1105 | 1-23 | 0.994 | 0.921 |
| 1123 | 1-35 | 0.987 | 0.658 |
| 1138 | 1-32 | 0.954 | 0.613 |
| 1140 | 1-38 | 0.989 | 0.789 |
| 1142 | 1-33 | 0.897 | 0.570 |
| 1152 | 1-25 | 0.990 | 0.962 |
| 1170 | 1-38 | 0.977 | 0.827 |
| 1176 | 1-20 | 0.944 | 0.768 |
| 1187 | 1-20 | 0.988 | 0.965 |
| 1189 | 1-35 | 0.967 | 0.839 |
| 1192 | 1-46 | 0.993 | 0.638 |
| 1193 | 1-16 | 0.925 | 0.710 |
| 1197 | 1-29 | 0.985 | 0.853 |
| 1208 | 1-23 | 0.981 | 0.940 |
| 1225 | 1-29 | 0.941 | 0.672 |
| 1245 | 1-19 | 0.986 | 0.967 |
| 1258 | 1-29 | 0.965 | 0.861 |
| 1265 | 1-22 | 0.889 | 0.785 |
| 1266 | 1-20 | 0.944 | 0.809 |
| 1276 | 1-48 | 0.982 | 0.862 |
| 1292 | 1-19 | 0.979 | 0.933 |
| 1296 | 1-21 | 0.984 | 0.944 |
| 1297 | 1-19 | 0.984 | 0.953 |
| 1332 | 1-38 | 0.942 | 0.653 |
| 1358 | 1-18 | 0.947 | 0.595 |
| 1371 | 1-33 | 0.957 | 0.789 |
| 1380 | 1-26 | 0.979 | 0.904 |
| 1397 | 1-27 | 0.962 | 0.777 |
| 1399 | 1-23 | 0.997 | 0.960 |
| 1404 | 1-24 | 0.998 | 0.977 |
| 1410 | 1-15 | 0.946 | 0.845 |
| 1414 | 1-24 | 0.913 | 0.588 |
| 1415 | 1-19 | 0.982 | 0.929 |
| 1416 | 1-12 | 0.931 | 0.891 |
| 1418 | 1-30 | 0.933 | 0.563 |
| 1420 | 1-20 | 0.881 | 0.561 |
| 1421 | 1-19 | 0.990 | 0.968 |
| 1423 | 1-17 | 0.968 | 0.863 |
| 1424 | 1-21 | 0.885 | 0.591 |
| 1425 | 1-24 | 0.913 | 0.588 |
| 1426 | 1-24 | 0.913 | 0.588 |
| 1428 | 1-25 | 0.967 | 0.899 |
| 1430 | 1-34 | 0.977 | 0.819 |
| 1431 | 1-28 | 0.979 | 0.923 |
| 1432 | 1-36 | 0.957 | 0.613 |
| 1433 | 1-32 | 0.921 | 0.753 |
| 1434 | 1-39 | 0.983 | 0.621 |
| 1435 | 1-25 | 0.910 | 0.631 |
| 1436 | 1-42 | 0.988 | 0.868 |
| 1437 | 1-22 | 0.998 | 0.980 |
| 1442 | 1-20 | 0.918 | 0.753 |
| 1448 | 1-12 | 0.931 | 0.891 |
| 1462 | 1-18 | 0.968 | 0.888 |
| 1490 | 1-20 | 0.881 | 0.561 |
| 1518 | 1-17 | 0.968 | 0.863 |
| 1525 | 1-21 | 0.885 | 0.591 |
| 1547 | 1-28 | 0.974 | 0.891 |
| 1561 | 1-25 | 0.967 | 0.899 |
| 1580 | 1-17 | 0.923 | 0.824 |
| 1593 | 1-28 | 0.979 | 0.923 |

| SEQ ID NO: | POSITION OF SIGNAL IN AMINO ACID SEQUENCE | MaxS (MAXIMUM SCORE) | MeanS (MEAN SCORE) |
|------------|---|-------------------------|-----------------------|
| 1596 | 1-16 | 0.929 | 0.709 |
| 1601 | 1-36 | 0.957 | 0.613 |
| 1606 | 1-22 | 0.979 | 0.831 |
| 1607 | 1-20 | 0.974 | 0.770 |
| 1608 | 1-32 | 0.921 | 0.753 |
| 1614 | 1-33 | 0.969 | 0.829 |
| 1616 | 1-20 | 0.959 | 0.869 |
| 1625 | 1-39 | 0.983 | 0.621 |
| 1632 | 1-25 | 0.910 | 0.631 |
| 1636 | 1-33 | 0.897 | 0.591 |
| 1639 | 1-42 | 0.988 | 0.868 |
| 1645 | 1-20 | 0.927 | 0.568 |
| 1647 | 1-17 | 0.923 | 0.742 |
| 1648 | 1-22 | 0.998 | 0.980 |

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|---|--|
| 1 | 1787 | 3573 | 5359 | 784CIP2_1 | 1103 |
| 2 | 1788 | 3574 | 5360 | 784CIP2_2 | 2673 |
| 3 | 1789 | 3575 | 5361 | 784CIP2_3 | 4117 |
| 4 | 1790 | 3576 | 5362 | 784CIP2_4 | 5556 |
| 5 | 1791 | 3577 | 5363 | 784CIP2_5 | 5562 |
| 6 | 1792 | 3578 | 5364 | 784CIP2_6 | 5562 |
| 7 | 1793 | 3579 | 5365 | 784CIP2_7 | 5562 |
| 8 | 1794 | 3580 | 5366 | 784CIP2_8 | 5562 |
| 9 | 1795 | 3581 | 5367 | 784CIP2_9 | 5563 |
| 10 | 1796 | 3582 | 5368 | 784CIP2_10 | 5564 |
| 11 | 1797 | 3583 | 5369 | 784CIP2_11 | 5565 |
| 12 | 1798 | 3584 | 5370 | 784CIP2_12 | 5689 |
| 13 | 1799 | 3585 | 5371 | 784CIP2_13 | 5729 |
| 14 | 1800 | 3586 | 5372 | 784CIP2_14 | 5745 |
| 15 | 1801 | 3587 | 5373 | 784CIP2_15 | 5777 |
| 16 | 1802 | 3588 | 5374 | 784CIP2_16 | 5777 |
| 17 | 1803 | 3589 | 5375 | 784CIP2_17 | 5789 |
| 18 | 1804 | 3590 | 5376 | 784CIP2_18 | 5792 |
| 19 | 1805 | 3591 | 5377 | 784CIP2_19 | 5804 |
| 20 | 1806 | 3592 | 5378 | 784CIP2_20 | 5805 |
| 21 | 1807 | 3593 | 5379 | 784CIP2_21 | 5805 |
| 22 | 1808 | 3594 | 5380 | 784CIP2_22 | 5844 |
| 23 | 1809 | 3595 | 5381 | 784CIP2_23 | 5844 |
| 24 | 1810 | 3596 | 5382 | 784CIP2_24 | 5850 |
| 25 | 1811 | 3597 | 5383 | 784CIP2_25 | 5867 |
| 26 | 1812 | 3598 | 5384 | 784CIP2_26 | 5973 |
| 27 | 1813 | 3599 | 5385 | 784CIP2_27 | 5995 |
| 28 | 1814 | 3600 | 5386 | 784CIP2_28 | 5995 |
| 29 | 1815 | 3601 | 5387 | 784CIP2_29 | 6005 |
| 30 | 1816 | 3602 | 5388 | 784CIP2_30 | 6007 |
| 31 | 1817 | 3603 | 5389 | 784CIP2_31 | 6007 |
| 32 | 1818 | 3604 | 5390 | 784CIP2_32 | 6009 |
| 33 | 1819 | 3605 | 5391 | 784CIP2_33 | 6012 |
| 34 | 1820 | 3606 | 5392 | 784CIP2_34 | 6015 |
| 35 | 1821 | 3607 | 5393 | 784CIP2_35 | 6016 |
| 36 | 1822 | 3608 | 5394 | 784CIP2_36 | 6016 |
| 37 | 1823 | 3609 | 5395 | 784CIP2_37 | 6018 |
| 38 | 1824 | 3610 | 5396 | 784CIP2_38 | 6018 |
| 39 | 1825 | 3611 | 5397 | 784CIP2_39 | 6018 |
| 40 | 1826 | 3612 | 5398 | 784CIP2_40 | 6023 |
| 41 | 1827 | 3613 | 5399 | 784CIP2_41 | 6070 |
| 42 | 1828 | 3614 | 5400 | 784CIP2_42 | 6081 |
| 43 | 1829 | 3615 | 5401 | 784CIP2_43 | 6089 |
| 44 | 1830 | 3616 | 5402 | 784CIP2_44 | 6118 |
| 45 | 1831 | 3617 | 5403 | 784CIP2_45 | 6118 |
| 46 | 1832 | 3618 | 5404 | 784CIP2_46 | 6130 |
| 47 | 1833 | 3619 | 5405 | 784CIP2_47 | 6177 |
| 48 | 1834 | 3620 | 5406 | 784CIP2_48 | 6189 |
| 49 | 1835 | 3621 | 5407 | 784CIP2_49 | 6191 |
| 50 | 1836 | 3622 | 5408 | 784CIP2_50 | 6204 |
| 51 | 1837 | 3623 | 5409 | 784CIP2_51 | 6204 |
| 52 | 1838 | 3624 | 5410 | 784CIP2_52 | 6284 |
| 53 | 1839 | 3625 | 5411 | 784CIP2_53 | 6367 |
| 54 | 1840 | 3626 | 5412 | 784CIP2_54 | 6436 |
| 55 | 1841 | 3627 | 5413 | 784CIP2_55 | 6442 |
| 56 | 1842 | 3628 | 5414 | 784CIP2_56 | 6445 |
| 57 | 1843 | 3629 | 5415 | 784CIP2_57 | 6457 |
| 58 | 1844 | 3630 | 5416 | 784CIP2_58 | 6458 |
| 59 | 1845 | 3631 | 5417 | 784CIP2_59 | 6458 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|---|--|
| 60 | 1846 | 3632 | 5418 | 784CIP2_60 | 6462 |
| 61 | 1847 | 3633 | 5419 | 784CIP2_61 | 6472 |
| 62 | 1848 | 3634 | 5420 | 784CIP2_62 | 6499 |
| 63 | 1849 | 3635 | 5421 | 784CIP2_63 | 6499 |
| 64 | 1850 | 3636 | 5422 | 784CIP2_64 | 6505 |
| 65 | 1851 | 3637 | 5423 | 784CIP2_65 | 6534 |
| 66 | 1852 | 3638 | 5424 | 784CIP2_66 | 6534 |
| 67 | 1853 | 3639 | 5425 | 784CIP2_67 | 6540 |
| 68 | 1854 | 3640 | 5426 | 784CIP2_68 | 6550 |
| 69 | 1855 | 3641 | 5427 | 784CIP2_69 | 6550 |
| 70 | 1856 | 3642 | 5428 | 784CIP2_70 | 6592 |
| 71 | 1857 | 3643 | 5429 | 784CIP2_71 | 6645 |
| 72 | 1858 | 3644 | 5430 | 784CIP2_72 | 6671 |
| 73 | 1859 | 3645 | 5431 | 784CIP2_73 | 6763 |
| 74 | 1860 | 3646 | 5432 | 784CIP2_74 | 6763 |
| 75 | 1861 | 3647 | 5433 | 784CIP2_75 | 6786 |
| 76 | 1862 | 3648 | 5434 | 784CIP2_76 | 6824 |
| 77 | 1863 | 3649 | 5435 | 784CIP2_77 | 6830 |
| 78 | 1864 | 3650 | 5436 | 784CIP2_78 | 6831 |
| 79 | 1865 | 3651 | 5437 | 784CIP2_79 | 6832 |
| 80 | 1866 | 3652 | 5438 | 784CIP2_80 | 6834 |
| 81 | 1867 | 3653 | 5439 | 784CIP2_81 | 6834 |
| 82 | 1868 | 3654 | 5440 | 784CIP2_82 | 6835 |
| 83 | 1869 | 3655 | 5441 | 784CIP2_83 | 6837 |
| 84 | 1870 | 3656 | 5442 | 784CIP2_84 | 6843 |
| 85 | 1871 | 3657 | 5443 | 784CIP2_85 | 6859 |
| 86 | 1872 | 3658 | 5444 | 784CIP2_86 | 6915 |
| 87 | 1873 | 3659 | 5445 | 784CIP2_87 | 6932 |
| 88 | 1874 | 3660 | 5446 | 784CIP2_88 | 6957 |
| 89 | 1875 | 3661 | 5447 | 784CIP2_89 | 6961 |
| 90 | 1876 | 3662 | 5448 | 784CIP2_90 | 6973 |
| 91 | 1877 | 3663 | 5449 | 784CIP2_91 | 6973 |
| 92 | 1878 | 3664 | 5450 | 784CIP2_93 | 7007 |
| 93 | 1879 | 3665 | 5451 | 784CIP2_94 | 7018 |
| 94 | 1880 | 3666 | 5452 | 784CIP2_95 | 7019 |
| 95 | 1881 | 3667 | 5453 | 784CIP2_96 | 7020 |
| 96 | 1882 | 3668 | 5454 | 784CIP2_97 | 7020 |
| 97 | 1883 | 3669 | 5455 | 784CIP2_98 | 7021 |
| 98 | 1884 | 3670 | 5456 | 784CIP2_99 | 7023 |
| 99 | 1885 | 3671 | 5457 | 784CIP2_100 | 7027 |
| 100 | 1886 | 3672 | 5458 | 784CIP2_101 | 7028 |
| 101 | 1887 | 3673 | 5459 | 784CIP2_102 | 7029 |
| 102 | 1888 | 3674 | 5460 | 784CIP2_103 | 7031 |
| 103 | 1889 | 3675 | 5461 | 784CIP2_104 | 7032 |
| 104 | 1890 | 3676 | 5462 | 784CIP2_105 | 7033 |
| 105 | 1891 | 3677 | 5463 | 784CIP2_106 | 7035 |
| 106 | 1892 | 3678 | 5464 | 784CIP2_107 | 7036 |
| 107 | 1893 | 3679 | 5465 | 784CIP2_108 | 7039 |
| 108 | 1894 | 3680 | 5466 | 784CIP2_109 | 7043 |
| 109 | 1895 | 3681 | 5467 | 784CIP2_110 | 7044 |
| 110 | 1896 | 3682 | 5468 | 784CIP2_111 | 7046 |
| 111 | 1897 | 3683 | 5469 | 784CIP2_112 | 7054 |
| 112 | 1898 | 3684 | 5470 | 784CIP2_113 | 7061 |
| 113 | 1899 | 3685 | 5471 | 784CIP2_114 | 7077 |
| 114 | 1900 | 3686 | 5472 | 784CIP2_115 | 7092 |
| 115 | 1901 | 3687 | 5473 | 784CIP2_116 | 7094 |
| 116 | 1902 | 3688 | 5474 | 784CIP2_117 | 7106 |
| 117 | 1903 | 3689 | 5475 | 784CIP2_118 | 7107 |
| 118 | 1904 | 3690 | 5476 | 784CIP2_119 | 7111 |
| 119 | 1905 | 3691 | 5477 | 784CIP2_120 | 7123 |
| 120 | 1906 | 3692 | 5478 | 784CIP2_121 | 7142 |
| 121 | 1907 | 3693 | 5479 | 784CIP2_122 | 7142 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|---|--|
| 122 | 1908 | 3694 | 5480 | 784CIP2_123 | 7154 |
| 123 | 1909 | 3695 | 5481 | 784CIP2_124 | 7160 |
| 124 | 1910 | 3696 | 5482 | 784CIP2_125 | 7169 |
| 125 | 1911 | 3697 | 5483 | 784CIP2_126 | 7185 |
| 126 | 1912 | 3698 | 5484 | 784CIP2_127 | 7197 |
| 127 | 1913 | 3699 | 5485 | 784CIP2_128 | 7219 |
| 128 | 1914 | 3700 | 5486 | 784CIP2_129 | 7226 |
| 129 | 1915 | 3701 | 5487 | 784CIP2_130 | 7229 |
| 130 | 1916 | 3702 | 5488 | 784CIP2_131 | 7234 |
| 131 | 1917 | 3703 | 5489 | 784CIP2_132 | 7235 |
| 132 | 1918 | 3704 | 5490 | 784CIP2_133 | 7235 |
| 133 | 1919 | 3705 | 5491 | 784CIP2_134 | 7238 |
| 134 | 1920 | 3706 | 5492 | 784CIP2_135 | 7247 |
| 135 | 1921 | 3707 | 5493 | 784CIP2_136 | 7261 |
| 136 | 1922 | 3708 | 5494 | 784CIP2_137 | 7262 |
| 137 | 1923 | 3709 | 5495 | 784CIP2_138 | 7267 |
| 138 | 1924 | 3710 | 5496 | 784CIP2_139 | 7272 |
| 139 | 1925 | 3711 | 5497 | 784CIP2_140 | 7273 |
| 140 | 1926 | 3712 | 5498 | 784CIP2_141 | 7282 |
| 141 | 1927 | 3713 | 5499 | 784CIP2_142 | 7288 |
| 142 | 1928 | 3714 | 5500 | 784CIP2_143 | 7291 |
| 143 | 1929 | 3715 | 5501 | 784CIP2_144 | 7293 |
| 144 | 1930 | 3716 | 5502 | 784CIP2_145 | 7294 |
| 145 | 1931 | 3717 | 5503 | 784CIP2_146 | 7299 |
| 146 | 1932 | 3718 | 5504 | 784CIP2_147 | 7300 |
| 147 | 1933 | 3719 | 5505 | 784CIP2_148 | 7312 |
| 148 | 1934 | 3720 | 5506 | 784CIP2_149 | 7313 |
| 149 | 1935 | 3721 | 5507 | 784CIP2_150 | 7315 |
| 150 | 1936 | 3722 | 5508 | 784CIP2_151 | 7318 |
| 151 | 1937 | 3723 | 5509 | 784CIP2_152 | 7321 |
| 152 | 1938 | 3724 | 5510 | 784CIP2_153 | 7330 |
| 153 | 1939 | 3725 | 5511 | 784CIP2_154 | 7331 |
| 154 | 1940 | 3726 | 5512 | 784CIP2_155 | 7333 |
| 155 | 1941 | 3727 | 5513 | 784CIP2_156 | 7350 |
| 156 | 1942 | 3728 | 5514 | 784CIP2_157 | 7352 |
| 157 | 1943 | 3729 | 5515 | 784CIP2_158 | 7384 |
| 158 | 1944 | 3730 | 5516 | 784CIP2_159 | 7403 |
| 159 | 1945 | 3731 | 5517 | 784CIP2_160 | 7431 |
| 160 | 1946 | 3732 | 5518 | 784CIP2_161 | 7441 |
| 161 | 1947 | 3733 | 5519 | 784CIP2_162 | 7453 |
| 162 | 1948 | 3734 | 5520 | 784CIP2_163 | 7467 |
| 163 | 1949 | 3735 | 5521 | 784CIP2_164 | 7471 |
| 164 | 1950 | 3736 | 5522 | 784CIP2_165 | 7493 |
| 165 | 1951 | 3737 | 5523 | 784CIP2_166 | 7502 |
| 166 | 1952 | 3738 | 5524 | 784CIP2_167 | 7511 |
| 167 | 1953 | 3739 | 5525 | 784CIP2_168 | 7514 |
| 168 | 1954 | 3740 | 5526 | 784CIP2_169 | 7520 |
| 169 | 1955 | 3741 | 5527 | 784CIP2_170 | 7541 |
| 170 | 1956 | 3742 | 5528 | 784CIP2_171 | 7570 |
| 171 | 1957 | 3743 | 5529 | 784CIP2_172 | 7578 |
| 172 | 1958 | 3744 | 5530 | 784CIP2_173 | 7583 |
| 173 | 1959 | 3745 | 5531 | 784CIP2_174 | 7592 |
| 174 | 1960 | 3746 | 5532 | 784CIP2_175 | 7601 |
| 175 | 1961 | 3747 | 5533 | 784CIP2_176 | 7602 |
| 176 | 1962 | 3748 | 5534 | 784CIP2_177 | 7608 |
| 177 | 1963 | 3749 | 5535 | 784CIP2_178 | 7615 |
| 178 | 1964 | 3750 | 5536 | 784CIP2_179 | 7617 |
| 179 | 1965 | 3751 | 5537 | 784CIP2_181 | 7624 |
| 180 | 1966 | 3752 | 5538 | 784CIP2_182 | 7626 |
| 181 | 1967 | 3753 | 5539 | 784CIP2_183 | 7640 |
| 182 | 1968 | 3754 | 5540 | 784CIP2_184 | 7641 |
| 183 | 1969 | 3755 | 5541 | 784CIP2_185 | 7641 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|--|--|
| 184 | 1970 | 3756 | 5542 | 784CIP2_186 | 7641 |
| 185 | 1971 | 3757 | 5543 | 784CIP2_187 | 7642 |
| 186 | 1972 | 3758 | 5544 | 784CIP2_188 | 7649 |
| 187 | 1973 | 3759 | 5545 | 784CIP2_189 | 7656 |
| 188 | 1974 | 3760 | 5546 | 784CIP2_190 | 7657 |
| 189 | 1975 | 3761 | 5547 | 784CIP2_191 | 7657 |
| 190 | 1976 | 3762 | 5548 | 784CIP2_192 | 7662 |
| 191 | 1977 | 3763 | 5549 | 784CIP2_193 | 7668 |
| 192 | 1978 | 3764 | 5550 | 784CIP2_194 | 7673 |
| 193 | 1979 | 3765 | 5551 | 784CIP2_195 | 7690 |
| 194 | 1980 | 3766 | 5552 | 784CIP2_196 | 7700 |
| 195 | 1981 | 3767 | 5553 | 784CIP2_197 | 7709 |
| 196 | 1982 | 3768 | 5554 | 784CIP2_198 | 7736 |
| 197 | 1983 | 3769 | 5555 | 784CIP2_199 | 7737 |
| 198 | 1984 | 3770 | 5556 | 784CIP2_200 | 7744 |
| 199 | 1985 | 3771 | 5557 | 784CIP2_201 | 7771 |
| 200 | 1986 | 3772 | 5558 | 784CIP2_202 | 7786 |
| 201 | 1987 | 3773 | 5559 | 784CIP2_203 | 7791 |
| 202 | 1988 | 3774 | 5560 | 784CIP2_204 | 7797 |
| 203 | 1989 | 3775 | 5561 | 784CIP2_205 | 7806 |
| 204 | 1990 | 3776 | 5562 | 784CIP2_206 | 7812 |
| 205 | 1991 | 3777 | 5563 | 784CIP2_207 | 7812 |
| 206 | 1992 | 3778 | 5564 | 784CIP2_208 | 7818 |
| 207 | 1993 | 3779 | 5565 | 784CIP2_209 | 7822 |
| 208 | 1994 | 3780 | 5566 | 784CIP2_210 | 7827 |
| 209 | 1995 | 3781 | 5567 | 784CIP2_211 | 7830 |
| 210 | 1996 | 3782 | 5568 | 784CIP2_212 | 7835 |
| 211 | 1997 | 3783 | 5569 | 784CIP2_214 | 7840 |
| 212 | 1998 | 3784 | 5570 | 784CIP2_215 | 7858 |
| 213 | 1999 | 3785 | 5571 | 784CIP2_216 | 7858 |
| 214 | 2000 | 3786 | 5572 | 784CIP2_217 | 7861 |
| 215 | 2001 | 3787 | 5573 | 784CIP2_218 | 7866 |
| 216 | 2002 | 3788 | 5574 | 784CIP2_219 | 7868 |
| 217 | 2003 | 3789 | 5575 | 784CIP2_220 | 7896 |
| 218 | 2004 | 3790 | 5576 | 784CIP2_221 | 7898 |
| 219 | 2005 | 3791 | 5577 | 784CIP2_222 | 7900 |
| 220 | 2006 | 3792 | 5578 | 784CIP2_223 | 7906 |
| 221 | 2007 | 3793 | 5579 | 784CIP2_224 | 7908 |
| 222 | 2008 | 3794 | 5580 | 784CIP2_225 | 7909 |
| 223 | 2009 | 3795 | 5581 | 784CIP2_226 | 7917 |
| 224 | 2010 | 3796 | 5582 | 784CIP2_227 | 7932 |
| 225 | 2011 | 3797 | 5583 | 784CIP2_228 | 7940 |
| 226 | 2012 | 3798 | 5584 | 784CIP2_229 | 7940 |
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| 228 | 2014 | 3800 | 5586 | 784CIP2_231 | 7984 |
| 229 | 2015 | 3801 | 5587 | 784CIP2_232 | 8001 |
| 230 | 2016 | 3802 | 5588 | 784CIP2_233 | 8021 |
| 231 | 2017 | 3803 | 5589 | 784CIP2_234 | 8029 |
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| 235 | 2021 | 3807 | 5593 | 784CIP2_238 | 8096 |
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| 237 | 2023 | 3809 | 5595 | 784CIP2_240 | 8113 |
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| 240 | 2026 | 3812 | 5598 | 784CIP2_243 | 8137 |
| 241 | 2027 | 3813 | 5599 | 784CIP2_244 | 8137 |
| 242 | 2028 | 3814 | 5600 | 784CIP2_245 | 8159 |
| 243 | 2029 | 3815 | 5601 | 784CIP2_246 | 8159 |
| 244 | 2030 | 3816 | 5602 | 784CIP2_247 | 8161 |
| 245 | 2031 | 3817 | 5603 | 784CIP2_248 | 8176 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number, corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| 253 | 2039 | 3825 | 5611 | 784CIP2_256 | 8288 |
| 254 | 2040 | 3826 | 5612 | 784CIP2_257 | 8296 |
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| 256 | 2042 | 3828 | 5614 | 784CIP2_259 | 8362 |
| 257 | 2043 | 3829 | 5615 | 784CIP2_260 | 8429 |
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| 260 | 2046 | 3832 | 5618 | 784CIP2_263 | 8472 |
| 261 | 2047 | 3833 | 5619 | 784CIP2_264 | 8502 |
| 262 | 2048 | 3834 | 5620 | 784CIP2_265 | 8504 |
| 263 | 2049 | 3835 | 5621 | 784CIP2_266 | 8507 |
| 264 | 2050 | 3836 | 5622 | 784CIP2_268 | 8509 |
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| 281 | 2067 | 3853 | 5639 | 784CIP2_285 | 8628 |
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| 284 | 2070 | 3856 | 5642 | 784CIP2_288 | 8631 |
| 285 | 2071 | 3857 | 5643 | 784CIP2_289 | 8633 |
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| 292 | 2078 | 3864 | 5650 | 784CIP2_296 | 8667 |
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| 305 | 2091 | 3877 | 5663 | 784CIP2_309 | 9405 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| 319 | 2105 | 3891 | 5677 | 784CIP2_323 | 9923 |
| 320 | 2106 | 3892 | 5678 | 784CIP2_324 | 9938 |
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| 322 | 2108 | 3894 | 5680 | 784CIP2_326 | 10007 |
| 323 | 2109 | 3895 | 5681 | 784CIP2_327 | 10009 |
| 324 | 2110 | 3896 | 5682 | 784CIP2_328 | 10046 |
| 325 | 2111 | 3897 | 5683 | 784CIP2_329 | 10156 |
| 326 | 2112 | 3898 | 5684 | 784CIP2_330 | 10276 |
| 327 | 2113 | 3899 | 5685 | 784CIP2_331 | 10283 |
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| 329 | 2115 | 3901 | 5687 | 784CIP2B_2 | 167 |
| 330 | 2116 | 3902 | 5688 | 784CIP2B_3 | 205 |
| 331 | 2117 | 3903 | 5689 | 784CIP2B_4 | 210 |
| 332 | 2118 | 3904 | 5690 | 784CIP2B_5 | 225 |
| 333 | 2119 | 3905 | 5691 | 784CIP2B_6 | 226 |
| 334 | 2120 | 3906 | 5692 | 784CIP2B_7 | 264 |
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| 342 | 2128 | 3914 | 5700 | 784CIP2B_15 | 358 |
| 343 | 2129 | 3915 | 5701 | 784CIP2B_16 | 368 |
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| 346 | 2132 | 3918 | 5704 | 784CIP2B_19 | 508 |
| 347 | 2133 | 3919 | 5705 | 784CIP2B_20 | 508 |
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| 367 | 2153 | 3939 | 5725 | 784CIP2B_40 | 924 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| 389 | 2175 | 3961 | 5747 | 784CIP2B_62 | 1809 |
| 390 | 2176 | 3962 | 5748 | 784CIP2B_63 | 1868 |
| 391 | 2177 | 3963 | 5749 | 784CIP2B_64 | 1898 |
| 392 | 2178 | 3964 | 5750 | 784CIP2B_65 | 1926 |
| 393 | 2179 | 3965 | 5751 | 784CIP2B_66 | 1965 |
| 394 | 2180 | 3966 | 5752 | 784CIP2B_67 | 1967 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| 1235 | 3021 | 4807 | 6593 | 784CIP2B_925 | 8395 |
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| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
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| 1659 | 3445 | 5231 | 7017 | 784CIP2D_7 | 4004 |
| 1660 | 3446 | 5232 | 7018 | 784CIP2D_8 | 4700 |
| 1661 | 3447 | 5233 | 7019 | 784CIP2D_9 | 4703 |
| 1662 | 3448 | 5234 | 7020 | 784CIP2D_10 | 4774 |
| 1663 | 3449 | 5235 | 7021 | 784CIP2D_11 | 4894 |
| 1664 | 3450 | 5236 | 7022 | 784CIP2D_12 | 4918 |
| 1665 | 3451 | 5237 | 7023 | 784CIP2D_13 | 5159 |
| 1666 | 3452 | 5238 | 7024 | 784CIP2D_14 | 7443 |
| 1667 | 3453 | 5239 | 7025 | 784CIP2D_15 | 8673 |
| 1668 | 3454 | 5240 | 7026 | 784CIP2D_16 | 8679 |
| 1669 | 3455 | 5241 | 7027 | 784CIP2D_17 | 8727 |
| 1670 | 3456 | 5242 | 7028 | 784CIP2D_18 | 8734 |
| 1671 | 3457 | 5243 | 7029 | 784CIP2D_19 | 8756 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|---|--|
| 1672 | 3458 | 5244 | 7030 | 784CIP2D_20 | 8818 |
| 1673 | 3459 | 5245 | 7031 | 784CIP2D_21 | 8844 |
| 1674 | 3460 | 5246 | 7032 | 784CIP2D_22 | 8846 |
| 1675 | 3461 | 5247 | 7033 | 784CIP2D_23 | 8912 |
| 1676 | 3462 | 5248 | 7034 | 784CIP2D_24 | 8918 |
| 1677 | 3463 | 5249 | 7035 | 784CIP2D_25 | 8918 |
| 1678 | 3464 | 5250 | 7036 | 784CIP2D_26 | 8941 |
| 1679 | 3465 | 5251 | 7037 | 784CIP2D_27 | 8941 |
| 1680 | 3466 | 5252 | 7038 | 784CIP2D_28 | 8951 |
| 1681 | 3467 | 5253 | 7039 | 784CIP2D_29 | 8951 |
| 1682 | 3468 | 5254 | 7040 | 784CIP2D_30 | 9007 |
| 1683 | 3469 | 5255 | 7041 | 784CIP2D_31 | 9012 |
| 1684 | 3470 | 5256 | 7042 | 784CIP2D_32 | 9013 |
| 1685 | 3471 | 5257 | 7043 | 784CIP2D_33 | 9025 |
| 1686 | 3472 | 5258 | 7044 | 784CIP2D_34 | 9053 |
| 1687 | 3473 | 5259 | 7045 | 784CIP2D_35 | 9054 |
| 1688 | 3474 | 5260 | 7046 | 784CIP2D_36 | 9054 |
| 1689 | 3475 | 5261 | 7047 | 784CIP2D_37 | 9113 |
| 1690 | 3476 | 5262 | 7048 | 784CIP2D_38 | 9134 |
| 1691 | 3477 | 5263 | 7049 | 784CIP2D_39 | 9152 |
| 1692 | 3478 | 5264 | 7050 | 784CIP2D_40 | 9152 |
| 1693 | 3479 | 5265 | 7051 | 784CIP2D_41 | 9211 |
| 1694 | 3480 | 5266 | 7052 | 784CIP2D_42 | 9223 |
| 1695 | 3481 | 5267 | 7053 | 784CIP2D_43 | 9223 |
| 1696 | 3482 | 5268 | 7054 | 784CIP2D_44 | 9231 |
| 1697 | 3483 | 5269 | 7055 | 784CIP2D_45 | 9236 |
| 1698 | 3484 | 5270 | 7056 | 784CIP2D_46 | 9236 |
| 1699 | 3485 | 5271 | 7057 | 784CIP2D_47 | 9303 |
| 1700 | 3486 | 5272 | 7058 | 784CIP2D_48 | 9309 |
| 1701 | 3487 | 5273 | 7059 | 784CIP2D_49 | 9314 |
| 1702 | 3488 | 5274 | 7060 | 784CIP2D_50 | 9326 |
| 1703 | 3489 | 5275 | 7061 | 784CIP2D_51 | 9339 |
| 1704 | 3490 | 5276 | 7062 | 784CIP2D_52 | 9348 |
| 1705 | 3491 | 5277 | 7063 | 784CIP2D_53 | 9376 |
| 1706 | 3492 | 5278 | 7064 | 784CIP2D_54 | 9382 |
| 1707 | 3493 | 5279 | 7065 | 784CIP2D_55 | 9407 |
| 1708 | 3494 | 5280 | 7066 | 784CIP2D_56 | 9414 |
| 1709 | 3495 | 5281 | 7067 | 784CIP2D_57 | 9439 |
| 1710 | 3496 | 5282 | 7068 | 784CIP2D_58 | 9485 |
| 1711 | 3497 | 5283 | 7069 | 784CIP2D_59 | 9493 |
| 1712 | 3498 | 5284 | 7070 | 784CIP2D_60 | 9501 |
| 1713 | 3499 | 5285 | 7071 | 784CIP2D_61 | 9526 |
| 1714 | 3500 | 5286 | 7072 | 784CIP2D_62 | 9526 |
| 1715 | 3501 | 5287 | 7073 | 784CIP2D_63 | 9551 |
| 1716 | 3502 | 5288 | 7074 | 784CIP2D_64 | 9557 |
| 1717 | 3503 | 5289 | 7075 | 784CIP2D_65 | 9568 |
| 1718 | 3504 | 5290 | 7076 | 784CIP2D_66 | 9588 |
| 1719 | 3505 | 5291 | 7077 | 784CIP2D_67 | 9597 |
| 1720 | 3506 | 5292 | 7078 | 784CIP2D_68 | 9615 |
| 1721 | 3507 | 5293 | 7079 | 784CIP2D_69 | 9628 |
| 1722 | 3508 | 5294 | 7080 | 784CIP2D_70 | 9649 |
| 1723 | 3509 | 5295 | 7081 | 784CIP2D_71 | 9652 |
| 1724 | 3510 | 5296 | 7082 | 784CIP2D_72 | 9660 |
| 1725 | 3511 | 5297 | 7083 | 784CIP2D_73 | 9662 |
| 1726 | 3512 | 5298 | 7084 | 784CIP2D_74 | 9725 |
| 1727 | 3513 | 5299 | 7085 | 784CIP2D_75 | 9746 |
| 1728 | 3514 | 5300 | 7086 | 784CIP2D_76 | 9777 |
| 1729 | 3515 | 5301 | 7087 | 784CIP2D_77 | 9787 |
| 1730 | 3516 | 5302 | 7088 | 784CIP2D_78 | 9790 |
| 1731 | 3517 | 5303 | 7089 | 784CIP2D_79 | 9842 |
| 1732 | 3518 | 5304 | 7090 | 784CIP2D_80 | 9842 |
| 1733 | 3519 | 5305 | 7091 | 784CIP2D_81 | 9848 |

| SEQ ID NO: of full- length nucleotide sequence | SEQ ID NO: of full- length peptide sequence | SEQ ID NO: of contig nucleotide sequence | SEQ ID NO: of contig peptide sequence | Priority docket number_ corresponding SEQ ID NO: in priority application | SEQ ID NO: in U.S.S.N. 09/488,725 |
|--|--|---|---|---|--|
| 1734 | 3520 | 5306 | 7092 | 784CIP2D_82 | 9867 |
| 1735 | 3521 | 5307 | 7093 | 784CIP2D_83 | 10010 |
| 1736 | 3522 | 5308 | 7094 | 784CIP2D_84 | 10011 |
| 1737 | 3523 | 5309 | 7095 | 784CIP2D_85 | 10052 |
| 1738 | 3524 | 5310 | 7096 | 784CIP2D_86 | 10057 |
| 1739 | 3525 | 5311 | 7097 | 784CIP2D_87 | 10085 |
| 1740 | 3526 | 5312 | 7098 | 784CIP2D_89 | 10139 |
| 1741 | 3527 | 5313 | 7099 | 784CIP2D_90 | 10142 |
| 1742 | 3528 | 5314 | 7100 | 784CIP2D_92 | 10165 |
| 1743 | 3529 | 5315 | 7101 | 784CIP2D_93 | 10173 |
| 1744 | 3530 | 5316 | 7102 | 784CIP2D_94 | 10173 |
| 1745 | 3531 | 5317 | 7103 | 784CIP2D_95 | 10273 |
| 1746 | 3532 | 5318 | 7104 | 784CIP2E_1 | 3121 |
| 1747 | 3533 | 5319 | 7105 | 784CIP2E_2 | 3628 |
| 1748 | 3534 | 5320 | 7106 | 784CIP2E_4 | 3673 |
| 1749 | 3535 | 5321 | 7107 | 784CIP2E_5 | 4018 |
| 1750 | 3536 | 5322 | 7108 | 784CIP2E_6 | 4467 |
| 1751 | 3537 | 5323 | 7109 | 784CIP2E_7 | 4865 |
| 1752 | 3538 | 5324 | 7110 | 784CIP2E_8 | 4916 |
| 1753 | 3539 | 5325 | 7111 | 784CIP2E_9 | 4923 |
| 1754 | 3540 | 5326 | 7112 | 784CIP2E_10 | 4926 |
| 1755 | 3541 | 5327 | 7113 | 784CIP2E_11 | 4962 |
| 1756 | 3542 | 5328 | 7114 | 784CIP2E_12 | 4963 |
| 1757 | 3543 | 5329 | 7115 | 784CIP2E_13 | 4964 |
| 1758 | 3544 | 5330 | 7116 | 784CIP2E_14 | 4988 |
| 1759 | 3545 | 5331 | 7117 | 784CIP2E_15 | 5835 |
| 1760 | 3546 | 5332 | 7118 | 784CIP2E_16 | 7682 |
| 1761 | 3547 | 5333 | 7119 | 784CIP2E_17 | 7682 |
| 1762 | 3548 | 5334 | 7120 | 784CIP2E_18 | 7699 |
| 1763 | 3549 | 5335 | 7121 | 784CIP2E_19 | 7707 |
| 1764 | 3550 | 5336 | 7122 | 784CIP2E_20 | 7707 |
| 1765 | 3551 | 5337 | 7123 | 784CIP2E_21 | 7752 |
| 1766 | 3552 | 5338 | 7124 | 784CIP2E_22 | 8357 |
| 1767 | 3553 | 5339 | 7125 | 784CIP2E_23 | 9065 |
| 1768 | 3554 | 5340 | 7126 | 784CIP2E_24 | 9324 |
| 1769 | 3555 | 5341 | 7127 | 784CIP2F_1 | 2976 |
| 1770 | 3556 | 5342 | 7128 | 784CIP2F_2 | 3559 |
| 1771 | 3557 | 5343 | 7129 | 784CIP2F_3 | 4021 |
| 1772 | 3558 | 5344 | 7130 | 784CIP2F_4 | 4474 |
| 1773 | 3559 | 5345 | 7131 | 784CIP2F_5 | 4566 |
| 1774 | 3560 | 5346 | 7132 | 784CIP2F_6 | 4705 |
| 1775 | 3561 | 5347 | 7133 | 784CIP2F_7 | 4707 |
| 1776 | 3562 | 5348 | 7134 | 784CIP2F_8 | 4712 |
| 1777 | 3563 | 5349 | 7135 | 784CIP2F_9 | 5008 |
| 1778 | 3564 | 5350 | 7136 | 784CIP2F_10 | 5009 |
| 1779 | 3565 | 5351 | 7137 | 784CIP2F_11 | 5015 |
| 1780 | 3566 | 5352 | 7138 | 784CIP2F_12 | 5015 |
| 1781 | 3567 | 5353 | 7139 | 784CIP2F_13 | 7724 |
| 1782 | 3568 | 5354 | 7140 | 784CIP2F_14 | 7725 |
| 1783 | 3569 | 5355 | 7141 | 784CIP2F_15 | 8828 |
| 1784 | 3570 | 5356 | 7142 | 784CIP2F_16 | 8830 |
| 1785 | 3571 | 5357 | 7143 | 784CIP2F_17 | 9739 |
| 1786 | 3572 | 5358 | 7144 | 784CIP2F_18 | 9896 |

TRADOC:1416247.1(%CS7011.DOC)

TABLE 7

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--|--|--|
| 5359 | 337 | 1131 | AHLSARLSALILDEVAILPAPQNLVSLSTNMKHLMLMWSPVIA PG ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTGEPEDVTDIT A TVPNLNRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIP L VLALFAFVGFMILLVVPLFVWKMGRLLQ/YLLLPRGSSQTPW KITQF |
| 5360 | 2 | 1115 | PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLK CVASGHPRPDITWMKDDQALTRPEAAEPKKKWTLSLKNLRPED SGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLTGTHFVNTVD FGGTTSFQCKVRSVDKPVIOQLKRVYGAEGRHNSTIDVGGQK VVLPTGDVWSRPDGSYLKLLITRARQDDAGMYICLGANTMGYS FRSAFLTLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL GTL LLWLCAQKQKPTPAPAPPLPGHRPPGTARDRSGDKDLPSL AALSAGPGVGLCEEHGSFAAPQHLLGPGVPVAGPKLYPKLYTGHS TPHTYTHPPFSCQLNSSHS |
| 5361 | 3 | 925 | HEGSISSANILLDDQFQPKLTDFAHAHFRSHLEHQSC T INMTSS SSKHLWYMP E EYIRQGLSIKTDVYSFGIVIMEVLTCGRVVLDD PKHIQLRDLRLRELMKRGDLSCLSLDKKVPCCPRNFSKLFCL AGRCAATRAKLRPSMDEV LNTLESTQASLYFAEDPPTSLKSFRC PSPLFLENVPSIPVEDDESQNNLLPSDEGLRIDRMTQKTPFEC SQSVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIIVPSQD LRPYKVNIDPSSZAPGHSCSRSPVSSSCSKFSWDEYEYQYKKE |
| 5362 | 2 | 4879 | SCQVEGCTRTYNSQSISGKHKMTAHPDQYAAFKMQRKSKKQKA NNLNTPNNGKFVYFLPSPVNNSNPFSTQTKANGNPACSAQLQH VSPPIFFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL FFSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA VFPSQVNVANNFSSTNAQSSAPEKVKKDRGRGTGKERKPKHKN RAKWPAILRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQBLQSNQPSLLASMLSTNAVNLLQPPQOSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTSVSQEGSEII IQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQRTSNTSKTSSIECSSLVPVPTNDLLKTVEN GLCSSSFPNSGGPSQNFSTNSRRSVISGPQNTRSSHNLNKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSV E IPTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNF EKT LEIIKTAMNSQILEVKSGSQAGETSQNAQINYNIQLPVSVNTV NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITV IQPVSE MINIQFNDKVNKPFVCQNGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTTRNSNLRACQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKE SQ PALELRAETQNTHSNVAVIEKQLIEKKSPDKTESLQVITVTS EQCNTNALTNTQTKGRKIRRHKKKEEKKRKKPVQSLEFPTRY SPYRPRYCVHQGCFAFTIQNLILHYQAVHKSDDLPAFSAEVEE ESEAGKESEETETKQTLKEPRCQVSDCSRIFOAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKDCCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPQENMSSKANQEKSXKRGTKHSRCGKBGI KMPKTKRKKKNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGTSTVVTSESNIIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDS DTCVSESND NSRTTATVSQKEVEKNE*DEMDELTELFITKLINE DSTSVETQA NTSSNVSNDFQEDNLQSERQKASNLKRVNKEKNVSQNKKRKVE KAEPASAAELSSVRKEEETAVAIQITIEHPASFDWSSFKPMGFE VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNRKNIDKTAV TSGNHVCPCKESETFVQFANPSQLQCSNDNVKIVLDKNLKDCTEL |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--|--|---|
| 5363 | 8066 | 703 | <p>VLKQLQEMKPTVSLKKLEVHSNDPDMVMKDISIGKATRGQY</p> <p>RLCCTGGGEGTGPASGKRGPAATTSLVLCIPSPVPPVFPPTLWP PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPRLNML RGP GPG LLL LLA V L C L G T A V P S T G A S K S K R Q A Q M V Q P S P V A V S Q S K P G C Y D N G K H Y Q I N Q W E R T Y L G N A L V C T C Y G G S R G F N C E S K P E A E T C F D K Y T G N T Y R V G D T Y E R P K D S M I W D C T C I G A G R G R I S C T I A N R C H E G G Q S Y K I G D T W R R P H E T G G Y M L E C V C L G N G K G E W T C K P I A E K C F D H A A G T S Y V V G E T W E K P Y Q G W M M V D C T C L G E G S G R I T C T S R N R C N D Q D T R T S Y R I G D T W S K D N R G N L L Q C I C T G N G R G E W K C E R H T S V Q T T S S G S G P F T D V R A A V Y Q P P H P Q P P P Y G H C V T D S G V V Y S V G M Q L A * K T Q G N K Q M L \ C T C L G N G V S C Q E T A V T Q T Y G G N S N G E P C V L P F T Y N G R T F Y S C T T E G R Q D G H L W C S T T S N Y E Q D Q K Y S F C T D H T V L V Q T R G G N S G A L C H F P F L Y N N H Y T D C T S E G R R D N M K W C G T T Q N Y D A D Q K F G F C P M A A H E E I C T T N E G V M Y R I G D Q W D K Q H D M G H M M R C T C V G N G R G E W T C I A Y S Q L R D Q C I V D D I T Y N V N D T F H K R H E E G H M L N C T C F G Q G R G R W K C D P V D Q C D S E T G T F Y Q I G D S W E K Y V H G V R Y Q C Y C Y G R G I G E W H C Q P L Q T Y P S S S G P V E V F I T E T P S Q P N S H P I Q W N A P Q P S H I S K Y I L R W R P K N S V G R W K E A T I P G H L N S Y T I K G L K P G V Y E G Q L I S I Q Q Y G H Q E V T R F D F T T T S T S T P V T S N T \ V T G E T T P F S P L V A T S E S V T E I T A S S F V V S W S A S D T V S G F R V E Y E L S E E G D E P Q Y L V L P S T A T S V \ N I P \ D L L P G R K Y I V N V Y Q I S E D G E Q S L I L S T S Q T T A P D A P P D P T V D Q V D D T S I V V R W R S P Q A P I T G Y R I V Y S P S V E G S S T E L N L P E T A N S V T L S D L Q P G V Q Y N I T I Y A V E E N Q E S T P V V I Q Q E T T G T P R S D T V P S P R D L Q F E V E T D V K V T I M W T P P E S A V T G Y R V D V I P V N L P G E H G Q R L P L S R N T F \ A E N T G L S P G V T Y Y F K V F A V S H G R E S K P L T A Q Q T T K L \ D A P T N L Q F V N E T D S T V L V R W T P P R A Q I T G Y R L T V G L T R R G Q P R Q Y N V G S V S K Y P L R N L Q P A S E Y T V S L V A I K G N Q E S P K A T G V F T T L Q P G S S I P P Y N T E V T E T T I V I T W T P A P R I G F K L G V R P S Q G G E A P R E V T S D S G S I V V S G L T P G V E Y V Y T I Q V L R D Q Q E R D A P \ I V N K \ V V T P L S P P T N L H L E A N P D T G V L T V S W E R S T T P D I T G Y R I T T T P T N G Q Q N S L E E V V H A D Q S S C T F \ D N L E V P G L E Y N V S V Y T V K D D K E S V P I S D T I P A V P P P T D L R F T N \ I L G P D T M R V T W \ A P P P S I D L T N F L V R Y S P V K N E G R M L Q S L S I F F L S D N \ A V V L T N L L P G T E Y V V S V S S V Y E Q H E S T P \ L R G R Q K T G L D S P \ T G I D F S \ D I T A \ N S F T \ V H W \ I A P R A \ T P I T G Y R I R \ H H P E H F \ S G R P R E D R \ V P H S R N S I T L T N L T P G T E Y V V S I V A L N G R E E S P L L I G Q Q S T V S D V P R D L E V V A A T P T S L L I \ S W D A P A V T V R Y Y R I T Y G E T G G N S P V Q E F T V P G S K S T A T I S G L K P G V D Y T I T V Y A V T G R G D S P A S S K P I S I N Y R T E I D K P S Q M Q V T D V Q D N S I S V K N L P S S S P V T G Y R V T T T \ P K N G P G \ P T K T K T A G P D Q T E M T I E G L Q P T V E Y V V S V Y A Q N P S G E S Q P L V Q T A V T N I D R P K G L A F T D V D V D S I K I A W E S P Q G Q V S R Y R V T Y S S P E D G I H E L F P A P D G E E D T A E L Q G L R P G S E Y T V S V V A L H D D M E S Q P L I G T Q S T A I P A P T D L K F T Q V T P T S L S A Q W T P P N V Q L T G Y R V R V T P K E K T G P M K E I N L A P D S S S V V V S G L M V A T K Y E V S V Y A L K D T L T S R P A Q G V V T T L E N V S P P R R A R V T D A T E T T I T I S W R T K T E T I T G F Q V D A V P A N G Q T P I Q R T I K P D V R S Y T I T G L Q P G T D Y K I Y L Y T L N D N A R S S P V I D A S T A I D A P S N L R F L A T T P N S L V S W Q P P R A R I T G Y I I K Y E K P G S P P R E V V P R P R P G V E A T I T G L E P G T E Y T I Y V I A L K N N Q K S E P L I G R K K T D E L P Q L V T L P H P N L H G P E I L D V P S T V Q K T P F V T H P G Y D T G N G I Q L P G T S G Q Q P S V G Q Q M I F E B H G F R R T T P P T T A T P I R H R P R Y P P N V G Q E A L S Q T T I S W A P F Q D T S E Y I I S C H P V G T D E E P L Q F R V P C T S T S A T L T G L T R G A T Y N I I V E A L K D Q Q R H K V R E E V V T V G N S V N B G L N Q P T D D S C F D P Y T V S H Y A V G D E W E R M S E S G F K L L C Q C L G F G S G H F R C D S S R W C H D N G V N Y K I G E K W D R Q E N G Q M M S C T C L G N G K G E F K C D P H E A T C Y D D G K T Y H V G E Q W Q K E Y L G A I C S C T C F G G Q R G W R C D N C R R P G G E P S P E G T T G Q S Y N Q Y S Q R Y H Q R T N T N V N C P I E C F M P L D V Q A D R E D S R E</p> |
| 5364 | 8066 | 703 | <p>RLCCTGGGEGTGPASGKRGPAATTSLVLCIPSPVPPVFPPTLWP</p> <p>PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPRLNML</p> <p>RGP GPG LLL LLA V L C L G T A V P S T G A S K S K R Q A Q M V Q P S P V A V S</p> |

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|------------|--|--|--|
| | | | <p>QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESEK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGWET CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRG EWKCEHRTSVQTTSSGSGPFTDVRRAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFFYSCCTTEGRQDGHLCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGR DNMKWCGTTQNYDADQKFGFCFMAAHEEICTTNEGVMYRIGDQW DKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQCIVDITYNVN DTFHKRHEBGMNLCTCFGQGRGRWKCDPVDQCDSETGTFFQI GDSWEKYVHGVRVYQCYCYGRGIGEWHCQPLQTPSSSGPVEVFI TETPSQPNSHPIQWNAQPSHISKYILRWPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTTSTST PVTSTNT\VTGETTFFSPLVATSESVTEITASSFVSVWSASDTV SGFRVEYELSEEGDEPQYLVPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVVIQQUETITGTPRSDTVSPRDLQFVEVTDV KVTIMWTFPESAVTGYRVDVIPVNLPGHEGQRLPLSRNTF\AEN TGLSPGVITYYFKVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRQPRQYVNGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETITVITWTPAPRIGFKLGVRPSQGEAPREVTSDSGSIV VSGLTPGVEVYTIQVLRDQGERDAP\IVNK\VVTPLSPPTNLH LEANPDGTGLTVSWERSTTPDITGYRITTTPTNGQQNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN\ILGPDTRMTW\APPPSIDLTNFLVRYSVPKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSVEYQHESTP \LRGRQKTGLDSP\TGIDFS\DTA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTGTEYV SIVALNGREBSPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRITYGETGGNSPVQEPVPGSKSTATISGLKPGVD YTITVAVTGRGDSPASSKPIISINYRTEIDKPSQMVDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQQQVSRVRYTSSPEDGHELFAPADGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS SVVVSGLMVAATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRR ARVTDATETITISWRKTETITGQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDLP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVQGMIFEEHGRRTTPTTATPIRHRPRPYPPNVGQE ALSQTTSWAPFQDTSYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGQGRWRCNCR RPGGEPSPEGTTGQSYNQYQRYHQRTNTNVCPIECFMPPLDVQ ADREDSRE</p> |
| 5365 | 8066 | 703 | <p>RLCCTGGGEGTGPASGKRGPAATSLVLCPISVPPVFPPTLWP PPSWRRQPPGGIRDFSRRLREANLVATCLPVRASLPHRLNML RGPGLGLLAVLCLGTAVPSTGASKSKRAQOMVQPSVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESEK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGWET CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR</p> |

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|------------------|---|--|--|
| | | | <p>ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICITGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETA VTQTYG GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ KYSFCTDHTVLVQTRGGSNGALCHFPFLYNHNYTDCSTSEGR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDOW DKQHDMMHMRCTCVNGRGEWTCIAYSQLRDQCI VDDI TYNVN DTFHKRHEEGHMLNCTCFQGGRGWKCDPVDQCDSETGTFFYQI GDSWEKVVHGVRYQCYCYGRGIGEWHCQPLQTPSSSGPVEVFI TETPSQPNSHPIQWNAQPSHISKYILWRPKNSVGRWKEATIP GHLSYTIKGLKPGVVEGQLISIQYGHQEVTRFDFTTSTST PVTSTNT\VTGETTFFSPLVATSESVTEITASSFVSVWSASDTV SGFRVEYELSEEGDEPQYLVLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEGGEQSLILSTSQTTPADAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSSTELNLPETANSVTLSDLQPGVQYN ITYAVEENQESTPVVIQOETTGTPRSDTVPSRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIVPNLPGEHQRLLPLSRNTF\AEN TGLSPGVITYYFKVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYVNGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTS DSGSIV VSGLTGVEVYVTIQVLRDQGERDAP\IVNK\VVTPLSPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQNSLEEV HADQSSCTF\DNLEVPGLYVNSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN\ILGPDTRMTW\APPSIDLTLNPLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVS VSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DATA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYVV SIVALNGREESPLLIQGSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRITYGETTGNSSPVQEFVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPI SINYTEIDKPSQM QVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGDQTEMTI EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQQVSRVRYTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPATDLKFT QVTPTSLSAQWTPPNVQLTG YRVVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRR ARVTDATETITISWRTKETITIGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTNPNLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDLEP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SQQQPSVGGQMI FEEHGFRRTPPTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIIISCHPVGTDDEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREVVTVGNSVNEGLNQPT DDSCFDPTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQENGQMMSCCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGQGRGWRCNCR RPGGEPSPGTTGQSYNQYSQRYHQRTNTNVNCPICFMPPLDVQ ADREDSRE</p> |
| 5366 | 8066 | 703 | <p>RLCCTGGGEGTPGASGKRGPAATTSVLVCIPSVPPVPFPTLWP PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML RGPFGGLLLAVLCLGTAVPSTGASKSKRQAQQMVQPSPVAVS QSKPGCYDNGKHQINQWERTYLGNALVCTCYGGSRGFNCESS PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGRIS CTIANRCHEGGQSYKIGDTWRPHEGTGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGGMMVDCCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICITGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETA VTQTYG GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ</p> |

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|------------------|---|--|--|
| | | | <p>KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCSTSEGR</p> <p>DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW</p> <p>DKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQCIVDDITYNVN</p> <p>DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFTYQI</p> <p>GDSWEKYVHVGRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI</p> <p>TETPSQPNSHPIQWNAQPSHISKYILRWRPKNSVGRWKEATIP</p> <p>GHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTTSTST</p> <p>PVTSNT\VTGETTTPFSPLVATSESVTEITASSFVSVWSASDTV</p> <p>SGFRVEYELSEEGDEPQYLVLPLSTATSV\NIP\DLLPGRKYIVN</p> <p>VYQISEDGEQSLILSTSQTTPADAPPDPTVDQVDDTSIVVRWSR</p> <p>PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN</p> <p>ITIIYAVEENQESTPVVVIQOETTGTTPRSDTVPSRDLQFVEVTDV</p> <p>KVTIMWTPPEAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN</p> <p>TGLSPGVTYFYKVFVAVSHGRESKPLTAQQTTL\DAPTNLQFVN</p> <p>ETDSTVLVRWTPPRAQITGYRLTVGLTRRQPRQYVNGVPSVSKY</p> <p>PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN</p> <p>TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIV</p> <p>VSGLTPGVEYVYTIQVLRDQGERDAP\IVNK\VTPLSPPTNLH</p> <p>LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQNSLEEVV</p> <p>HADQSSCTF\DNLEVPGLYVNSVYTVKDDKESVPISDTIIPAV</p> <p>PPPTDLRFTN\ILGPDTRMTW\APPPSIDLNLFLVRYSPVKNE</p> <p>GRMLQSLSIFFLSDN\AVVLNLLPGTEYVSVSVVYBQHESTP</p> <p>\LRGQKTGLDSP\TGIDFS\DATA\NSPT\VHW\IAPRA\TPI</p> <p>TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYVV</p> <p>SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD</p> <p>APAVTVRYRITYGETGGSNPVQEFVTPGSKSTATISGLKPGVD</p> <p>YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS</p> <p>ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI</p> <p>EGLQPTVEYVSVYAQNPSGESQPLVQATVNTIDRPKGLAFTDV</p> <p>DVDSIKIAWESPOGQVSRVRYVYSSPEDGIHELFPAPDGEEDTA</p> <p>ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT</p> <p>QVTPTSLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS</p> <p>SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRR</p> <p>ARVTDATETTITISWRKTETITGQVDAVPANGQTPIQRTIKP</p> <p>DVRSYTTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS</p> <p>NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP</p> <p>RPGVTEATITGLEPGTEXTIYVIALKNNQKSEPLIGRKKTDEL</p> <p>QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT</p> <p>SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE</p> <p>ALSQTTISWAPQDTSYIISCHPVGTDDEPLQFRVPGTSTSAT</p> <p>LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNEGLNQPT</p> <p>DDSCFDPTYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD</p> <p>SSRWCHDNGVNYKIGEKWDRQENGQMMSCCTCLGNGKGFEKCDP</p> <p>HEATCYDDGKTYHVGEQWQKEYLGAICSCTCGGQRGWRCDNCR</p> <p>RPGGEPSPEGTTGQSYNQYSQRVHQRTNTNVCPIECFMPDLVQ</p> <p>ADREDSRE</p> |
| 5367 | 235 | 3591 | <p>KKILNMLCKKNIVIEYLADILYEYLYGFCPSGIKKYLIHVLRL</p> <p>ILELWMTRLLEKSVSLQTQYLLLIIVKILSWFPKGEMRHHLQIM</p> <p>EVMMRKQDS/RIVNGNSEQQLOKELADVLMDPPMDQPGKEKLV</p> <p>KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ</p> <p>GDSEASSPFTPVADEDSVVFSLTYLGCASVNAPRSEVEALRMM</p> <p>SILRSQCQISLDVTLSPVNVSEGIIVRLDPQINTETIANYPYIKI</p> <p>LFVCRGHDGTPESDCFAFTESHYNALFRIHVFRCEIQEAVSRI</p> <p>LYSFATAFRRSKQTPLSATAAPQTPDSDIFTFSVSLIEKEDDG</p> <p>KGYFSAVPKDKDRQCFLRQGDKKIVYVQQTINKELAIERCF</p> <p>GLLLSPGKDVRNSDMHLLDLESMDGSSDGKSYVITGSWNPKSPH</p> <p>FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLETKVRVCS</p> <p>NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCL</p> <p>ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDEDEEDNDEPLL</p> <p>SGSGDVSKECAEKILETWGELLSKWHLLNVRPKQLSSLVRNGV</p> <p>PEALRGEVWQLLAGCHNNHDLVEKYRILITKESPDQSAITRDIN</p> |

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|------------|--|--|---|
| | | | RTFPAHDYFKDTGGDQDLSLYKICKAYSVDDEETGYCQGSFLA AVLLHMPPEEQAFSVLVKIMPDYGLRELFKQNFEDLHCKFYQLE RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVPH IDLLLCBGSIVIFNVALGLLKTSKDDLLLTDFEGALKFFRVQL PKRYRSEENAKKLMELACNMKISQKLLKYEKEYHTMREQQAAQ EDPIERFERENRRLEQANMRLEQENDDLAHELVTSKIALRKDLD NAEEKADALNKEMLMTKQKLIDAEEEKRRLEESAHLLKMCRRRE LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR QKVVDCERCREFPNKEGRVKGISSTKEVLDEDTDEKETLKNQL REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K KTWFNRTLSSIKTATGVQGKETC |
| 5368 | 573 | 2014 | GAAAGAADPRGSLGGRTMLDFAIFAVTFLALLVGVAVLYLYPAS RQAAGIPGITPTEKDGNLDPDIVNSGSLHEFLVNLHERYGPVVS FWFGRRLVSLGTVDLVKQHINPNKTLT/LF*NHAEVLIKVSIN WWQCE*KP\QRKKLYENGVTDSLKSNFALLKLPEELLDKWLVS PETQH\VLPSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG TVWSEIGKGLDGLDKNMTRKKQYEDALMQLESVLRNIIKERK GRNFSQHIFIDSLVQGNLNDQILEDMSIFSLASCIITAKLCTW AIWFLTTSEEVQKKLYEINQVFGNGPVTPEKIEQLRYCQHVLC ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETFLVYALGVVLQDP NTWPSPHKFPDPRFDDDELVMKTFSSLGFSGTQCEPELRFAYMVT TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREBAWITVSKRY |
| 5369 | 1 | 6622 | PRSLCFSLWAAEAVLADGGLRRRRRLLRGTMSASFVNGASLED CHCNLFCLADLTGIKWKYVWQGPSAPILFPVTEEDPILSSFS RCLKADVLG/VWRRDQRPERR\/*IFWGGEDP/VLLTLFTMTY QKKMECGRMDPMNAVLCFKAVHNLRLCLMNRNFRVIGKWF VKPYEKDEKPKINKSEHLSCSFTFFLHGDSNVCTSVINQHQPVY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWKQFYPISSCCLKEMSEKQEDMDWEDDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTPSPVGSTHCSSSCGLGVHQPASTRDP MSSVTLTPTPSPEEVQTVDPQSVQKWKVSSVSDGFSNDSTSHH GGKIPRKLANHVVDVWQECNMNRQNKRYSSASSGGLCEEATA AKVASWDFVEATQRTNCSCLRHKNLKSRLNAGQQQAPSIGQQQQ ILPKHKTNEKQEKSEKPKRPLTPFHHRVSVSDVGM\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHTEMANSPO PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDELVPSPKM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEDEANLAWKYYK FPKKKDVLELPPQLPSDKFDDFVGFQGESVTSVTELMVQCKK PLKVSDELVQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLNLFNSDEDEL PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSKIDFSYVYKPCNCQILVGCMSFAPLKTLPSSQY LPLIKLPEECIYRQSWTVGKLELLSSGSPSMFPIKEGDGNSMDQE YGTAYTPQHTSCGMPSSAPPSSNGAGILPSPSTPRFPTPTPT RTPRTPRGAGGPASAQGSVKYENS DLYSPASTPSTCRPLNSVEP ATVPSIPEAHSYLVNLLSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPPGAADQDPFKSGVISNWWVRVEERDCNDCYLA LEHGRQFMDNMSGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLDIAIQKRTVRPWGVQGPLTWQGFHKMAGRGSYG TDESPEPLIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRL TDGIMRVGSTASKKLSKLVAEWFSQAADGNNEAFSKLKYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSILITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTASTSSSSS SNLNSGVSSNKLSPFPFPGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPDGDSDH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ |

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|------------|--|--|---|
| | | | TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF TQCRRLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC TDLYGELLETCIINIDVPNRARRKSSARKFGLQKLWEWCLGLV QMSSLPWRVVGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM CRMCGISAADSPSILSACL VAMEPQGSFVIMPDSVSTGVSFGRS TTLNMQTSQNLTPQDTSCTHILVFPPTSASVQVASATYTTENLDL AFNPNNDGADGMGIFDLDLTDGDDLDPDIIINILPASPTGSPVHSP GSHYPHGGDAGKGQSTDRLSTEPHEEVPNIIQQPLALGYFVST AKAGPLPDWFWSACPAQYQCPLFLKASLHLHVPSVQSDELLHS KSHPLDSNQTSDVLRVFLQYQYNALSWLTCDPATQDRRSCLPIH FVVLNQLYNFIMNML |
| 5370 | 1226 | 716 | RWSRKLRLRRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN ANDVETVQQLLEDGADPCAADDKGR TALHFASCNQNDQIVQLLL DHGADPNQRDGLGNTPLHLAACTNHVPVITTLRGGARVDALDR AGRTPLHLAKSKLNLQEGHAQCLKAVR/HGGEADHPYAEVGSV APRAT*AARCSGVFPSPSRNLGSAPWSRSSCTIWSLPLHEAKCR AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACSTLPVG GCISWL |
| 5371 | 1331 | 167 | IAAMLWKL LLSQSCLRLCSFRKMRSPPKYRPFACFTYTTDKQS SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMKKLRI/P LQELGADETAVASILERCEAIVCSPTAVNTQRKLWQLVCKNE ELIKLIEQFPESFFTIKDQENQKLVQFPQELGLKNVVISRLLT AAPNVFHNPEVKNKQMVRIQESYLDVGGSEANMKVWLLKLSQ NPFI LLNSPTAIKETLEFLQEQGFTSFELQLLSKLKGFLFOLC PRSIQNSISFSKNAFKCTDHDLLKQVLKCPALLYSVPVLEERM QGLLREGISIAQIRETPMVLELTPQIVQYRIKLNSSGYRIKDG HLANLNGSKKEFEANFGKIQAQKVRPLFNPVADPLNVEE |
| 5372 | 51 | 857 | SPGAQFLWAAPDMPDPLFSAVQGGDEILHKALCFPCPWLGRGGM FLRLILFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR RKANCRQLGEKGPCQRRVSVTHNLWLLSFLRRWNGSTAITDDTLG DPLTITLRLNLPDAGLYQCQSLHGSEADTLRKVLVEVLADPLD HRDAGDLWFPGLDLRASRMPMWSTASPGASWKEKSPSHPLPSFS SWPASFSSRF*QPAPSGQLQPGMDRSQGHHPVNWTVAMTQGISS KLCQG |
| 5373 | 2814 | 346 | VKKT KSI FNSAMQEMEYVENIRKFGVFNYSFFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKNFDMTASPKILMSKPVLSGG TGRRI SLSDMPSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLDNRKAEMDLKELSESVOQQSTPVPLISPQRQ IRSRFQLNLDKTI ESCKAQLGINEISEDVYTAVEHSDSEDESEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGRAKPS PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSTVTVTAPAPATGSPVKKQRPLLPKE\TAP AVQRCSTGSSSTVQKKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIGKTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQL\SEMKNH LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAQVDETCKKQWC ANFKKBAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ \QADAE\VNTETLNKSSQSSSSSTQSAPSETASA\SKEKETS EKSKEGSLDLSGSRTPSSILGNSQGS DHSR\SNKSSWSSS DEKRGSL\TRSDHN\TPSTQHGRLPLPGKESRAGTFLGTSK |
| 5374 | 2814 | 346 | VKKT KSI FNSAMQEMEYVENIRKFGVFNYSFFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKNFDMTASPKILMSKPVLSGG TGRRI SLSDMPSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLDNRKAEMDLKELSESVOQQSTPVPLISPQRQ IRSRFQLNLDKTI ESCKAQLGINEISEDVYTAVEHSDSEDESEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP |

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|------------|--|--|--|
| | | | TNPVEIKEELKSTSFASEKADPGAVKDKASPEPEKDFSGKAKPS PHPIKDKLKGKDETDSPVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKESPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSTVTVPAPAPATGSPVKQRPLLPKE\TAQ AVQRSCGTSSSTVQKEITOSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQL\SEMKN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAQVDETKKKQWC ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCQTOSATAPO \QEADAE\VNTETLNKSSQSSSSSTQSAPSETASA\SKEKETSA EKKESGSTLDLGSRETTPSSILLGSNQGSDHSR\SNKSSSSS DEKRS\TRSDHN\TPSTQHGRSLPLPGKESRAGTPFLGTSK |
| 5375 | 2907 | 1116 | HIFLAEEEPMLERRCRGLAMGPAQPRLLSGPSQESPTLGKES RGLRQQGTSVA\QSGAQAPGRAHRCACHRRHFGWVA\LWLHTR RCQA\RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH LCCGQFRGWVALVLHLRAHSAKAGPFACPKMADAFWRRKAAS SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV SRRP*ERGEPAKVFWGPRPRGPPPTGDTPPGPGGDAVDRPF\QCA CCGKRFRHK\PNLIRSHAACSTGERPHQ/CSRECG\KRFTNKP LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS AQAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP QDPIEAPPSLYSCDDCGRSFRLERFLRAHQHQHTGERPFTCAEC GKNFGKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN SAEPNAPRFGPFVCPDCGKAFRHKPYLAHRPIATPAEKPVYCP DCRKAFSQKSNL\VSHRIHTGERPYACPDCCDRSFSQKSNLITH RKSHIRDGAFCACICGQTFDDEERLLAHQKKHVDV |
| 5376 | 4504 | 591 | VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGRGTVAIVYGATLFBATGKWVGVLDEAKG KNDGTQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRLKPKKAPTARKTTTTRPKPTRP ASTGVAGASSSLGPSASAGELSSSEPSTPAQTPLAAPIIPTP VLTPGAVPPLPSPSKEEEGLRAQVRDLBEKLETLRKRAEDKA KLKELEKHKIQLEQVQEWKSKMQBQADLQRRLEKARKAKEAL EAKERYMEEMADTADAIEMATLDKEMAEEAESLQOEVEALKER VDELTDLLEILKAEIEEKSGDGAASSYQLKQLEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMKKNQLELVVRQQRERLQEEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRERLTVG DLEAMNEMNDELQENARETELELRQOLDMAGARVREAKRVAA QETVADYQQTICKYRQLTAHLQDVNRELTNQOEASVERQQQPPP ETFDKIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLMPRLICKAELIRKQAEKFESENCE RPLRGAGAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQR LD\VYKKVGSGLYPEMSAHERSLDFLIELLHKDQLDETUNVEPLT KAICYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVALEELAFKASEQIYGTTPSSSPYECLRQSCNII ISTMNK\LVAMQEGEYDAERPSPKPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKSLKIKGEELSEANVRLTLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAEKQLRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPLVKDPSLLQQLISAMRLHISQLQHENSIL KGAQMKASLASLPLHVAKLSEHGPGSELPAVALYRKTSQLEET LNQLSTHVVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVKEL KDEVLKETVSQRPGATVPTDFATFPSSAFPLRAKEEQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQQLHQLHSRLIS |
| 5377 | 762 | 1106 | DVPCRVLPAAEQEKQTLTSCGESGEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGGWGGQYIFIFRGMREWEBQ |
| 5378 | 2009 | 664 | QASGTTLRPLPDLPQLKREATSRNRALKPRGRLVMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSSEVDLTR |

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|------------|--|--|--|
| | | | SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFITLKWKMLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRPQHTIMAGNVVTGEMV EELILSGADI IKVGIGPGSVCTTRKKTGVGPQLSAVMECADA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFGKDVEHTIRDILGGIRSTCTYVGAALKELSRRTTIFIRVTQQ VNPIFSEAC |
| 5379 | 2009 | 664 | QASGTTLRPLPDLPLQKREATSRNRALKPRGRVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSREVDLTR SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFITLKWKMLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRPQHTIMAGNVVTGEMV EELILSGADI IKVGIGPGSVCTTRKKTGVGPQLSAVMECADA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFGKDVEHTIRDILGGIRSTCTYVGAALKELSRRTTIFIRVTQQ VNPIFSEAC |
| 5380 | 2 | 2050 | PSRAGGAERGAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESQKPCALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSTIGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSSKKLIRQAAPRRPPRGRTRPAPGGCQIP RGPI\EQVYQEI\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLSEDAQRFYQDLIKGIEYLYHQII H\RDIKPSNLLVGEDGHIKIADPGVSNFEGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVEI KLHPWVTRHGAEPPLSEDNCTLVEVTEEBVENSVKHIPS LATV ILVKTMIKRKSFNGPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWVGTPLPFPPLSTSWL PDLVGAAGSHFCFLNIALLRYSHTM |
| 5381 | 2 | 2050 | PSRAGGAERGAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESQKPCALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSTIGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSSKKLIRQAAPRRPPRGRTRPAPGGCQIP RGPI\EQVYQEI\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLSEDAQRFYQDLIKGIEYLYHQII H\RDIKPSNLLVGEDGHIKIADPGVSNFEGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVEI KLHPWVTRHGAEPPLSEDNCTLVEVTEEBVENSVKHIPS LATV ILVKTMIKRKSFNGPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWVGTPLPFPPLSTSWL PDLVGAAGSHFCFLNIALLRYSHTM |
| 5382 | 1536 | 203 | GARGSQQDAPALQEAERVGPRAQPARGRMTKARLFRLLVLVLS VFILLIIVYWSAGAAHYLHTSFSRPHTPPLTPGDRDRDE LTADSDVDFDLKFLSAGVKQSDLPKRETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFPTKERPF DIPNSELSHLIVDDRHAICYVPKVACTNWKRVMLVLSGSLH RGAPYRDPLRIPREHVHNASAHLTNKFWRRYGKLSRHLMKVKL KYYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRRAHAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAFFNEH WRQVYRLCHPCQIDYDFVGKLETLDDEAAQLQLLQVDLAAPLP |

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|------------|--|--|--|
| | | | PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP ENLLRD |
| 5383 | 45 | 5250 | <p>VERLLGCRNSKRTWRMLISKNPWRRLQGISFGMYSAEELKKLS</p> <p>VKSITNPRYLDLSGNPSANGLYDLALGPADSKEVCSTCVQDFSN</p> <p>CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCTPRAVI</p> <p>HLLLCQLRVLEVGAQAVYELERILSRFLEENADPSASEIREEL</p> <p>EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC</p> <p>PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ</p> <p>IGKRGYLTPTSAREHLSALWKNEGFFLNLYFSGMDDDGMESEFVN</p> <p>PSVFFLDPLVPPSRSRPVSRLGDQMTNGQTVNLQAVMKDVVL</p> <p>IRKLLALMAQEQLPEEVATPTTDEEKDSLAIIDRSPLSTLPGQ</p> <p>SLIDKLYNIWIRLQSHVNIIVFDEMDKLMMDKYPGIRQILEKKE</p> <p>GLFRKHMGMKRVDAARSVICPDYINTNEIGIPMVFATKLTYP</p> <p>QPVTWNVQELRQAVINGPNVHPGASMVINEDGSRALSADVMT</p> <p>QREAVAKQLLTPATGAPKPGQTKIVCRHVKNQDILLNRQPTLH</p> <p>RPSIQAHRARILPEEKVLRRLHYANCKAYNADFDGDEMNAHPQS</p> <p>ELGRAEAYVLACTDQQLVLPKDGQPLAGLIQDHMVSGASMTTRG</p> <p>CFFTREHYMELVYRGLTDKVGKRVKLLSPSILKPPPLWTGKQVVS</p> <p>TLLINIIPEDHIPLNLGKAKITGKAWVKETPRSVGFNPDSMC</p> <p>ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCEYIYGGETSGKV</p> <p>LTCARLFTAYLQLYRGFTLGVEDILVKPKADVQRORIIESTH</p> <p>CGPQAVRAALNLEAASYSYDEVRGKWQDAHLGKDQDFNMIDLKF</p> <p>KEEVNHYSEINKACMPFGLHRQFPENTLQMLVQSGAKGSTVNT</p> <p>MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG</p> <p>RFLTGIKPPPEFFHFCMAGREGLVDTAVKTSRSGYLQRCIKHLE</p> <p>GLVVQYDLTVRSDSGSVVQFLYGEDGLDIPKTFQLQPKQFPFLA</p> <p>SNYEVIMKSQHLHEVLSRADPKKALHHPRAIKKQSKHPNTLLR</p> <p>RGAPLSYSQKIQEAVKALKLESENENRGR/RPWDS/G/RMLRMWY</p> <p>ELDEESRRKYQKAAACPDPSLSVWRPDIYFASVSETFETKVDD</p> <p>YSQEWAAQTEKSEKSELSLDRLLRLQL/KWQRLCEPGEAVG</p> <p>LLAAQSIGEPSTQMTLNTFFHAGRGEMNVTGIPRLREILMVAS</p> <p>ANIKTPMMSVPLVNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ</p> <p>ESFCMEKQNKQFQVYQLRFQFLPHAYYQOEKCLRPEIDILRFMET</p> <p>RFFKLLMESIKKNNKASAFRNVNTRATQRDLNAGELGRSRG</p> <p>EQEGDEEEEGHIVDAEAEEDADADAKRKEKQEEVDYSEEE</p> <p>EEREGEENDDDEDMQERNPHREGARKTQEQDEEVGL/GH*GGPV</p> <p>PSRPPDAAPETHPQPGAPGA/EAMERRVQAVREIHFFIDDYQYD</p> <p>TEESLWCQVTVKLPLMKINFDMSSLVSVSLAHGAVIYATKGITRC</p> <p>LLNETTNKNEKELVLNTEGINLPELFKYAEVLDLRLRLYSNDIH</p> <p>AIANTYIGIEAALRVISKEIKDVFAVYGIADVPRHLSLVADYMC</p> <p>EGVYKPLNRFGIRSNSSPLQMTFETSQFLKQATMLGSHDEL</p> <p>SPSACLVGKVVRRGGTGLFELKQPLR</p> |
| 5384 | 196 | 886 | <p>QSCGQRLPTVL*L*GPPGSCPCILSLF/PGRPHALPEIRPYINI</p> <p>TILKDGKDGDPGMGLPGYMGREGPGQPGQSGKDGKMGSPG</p> <p>APCOKRFFAFSVGRKTALHSGEDFQTLFVRVFNLDGCFDMAT</p> <p>GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS</p> <p>ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDYITF</p> <p>SGHLIKAEDD</p> |
| 5385 | 326 | 799 | <p>LMVPRTKKEAPAPPKAEAKAKAL/KAKKAVLKDVHSHKKNKIHM</p> <p>SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHVIKFPPLTTE*A</p> <p>VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ</p> <p>SDGERKAYVRLAPDYDALVVATKIGIT</p> |
| 5386 | 326 | 799 | <p>LMVPRTKKEAPAPPKAEAKAKAL/KAKKAVLKDVHSHKKNKIHM</p> <p>SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHVIKFPPLTTE*A</p> <p>VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ</p> <p>SDGERKAYVRLAPDYDALVVATKIGIT</p> |
| 5387 | 2 | 2117 | <p>FVVAASGGCWFVLGERRAGSLLSASYGTFAFPMGMVLFGRRNAIA</p> <p>SDDLVPFGFELVVRVLWVIGILTLYLMHRGKLDCAAGALLSSY</p> <p>LIVLMILLAVVICTVSAIMCVSMRGITCNPGPRKMSKLLYIRL</p> <p>ALFFPEMVWASLGAAWVADGVQCDRTVVNGIATVVVSWIIIAA</p> <p>TVVSIIVFDPLGGKMAPYSSAGPSHLDSHSSQLNLGLKTAAT</p> |

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|------------|--|--|--|
| | | | SVWETRIKLLCCCGKDDHTRVAFSSSTAELFSTYFSDTDLVPSD IAAGLALLHQQDNIRNNQEPAPQVCHAPGSSQEAADLDAELKNC HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGCCRSKNPQTMT/M VGGDQLQL/CTSAPILHTRAAVQGLHPRQLPWTRFTLPFLVA LDHRKESVAVVAVRGTMQLDVLTDLSAESEVLDEVEVDRLAH KGISQAARYVYQRLINDGILSQAFSAIEPYRLVIVGHSLSGGAA ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIIVSLVLG KDVIPRLSVTNLEDLKRIRLVVAHCNPKPKYKILLHGLWYELFG GNPNLPTLEDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSSDPL DSSPKYPLYPGRRIHLEQEGASGRFGCCSAAHYSKAKSHAE FSKILIGPKMLTDHMPDILMRALDSVSDRAACVSCPAQGVSSV DVA |
| 5388 | 1569 | 753 | TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSAIDST SSSMQSPVSNQSLLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFOEKFSPGSHQQLLEYK ILEHLQTKN |
| 5389 | 1569 | 753 | TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSAIDST SSSMQSPVSNQSLLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFOEKFSPGSHQQLLEYK ILEHLQTKN |
| 5390 | 217 | 1332 | EDPRKLMEKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAFKRIRLRPRYLDRDSEVDTRTTIQGEEI SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWFLYVHPDLQLNKQLIQRVESLGFKALVIT LDTFVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPI TSLCWNDSLWFSITRLPIILKGILTKEDELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNLTNEFHTSMA\ LTGCRSVAEINRNVLVQFSRL |
| 5391 | 1 | 1292 | VKKAAGRSRGPPTAGGQRCEAPGTMERRLGVRWVKNRGSF QPPVCNKLHQEQKLMVFGVGNTRKDYHIEEGEEVYQLEBDM VLRVLEQGHKRDVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYVVDMDVLFKWFYCKDLGTOLAPIIQEFFF SEQYRTGKPIPDQLLEKPPFLSTRSIMPEMSLDWLDSHREL QAGTPLSLFGDTYETQVIAYGQSSSEGLRQNVVWLWQLEGSV VTMGRRLSLGPMWDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTCSTSTPRRPSIKAS |
| 5392 | 1 | 1623 | IRGSNAQKVVGASGSGGAGPQDPAGPGGVPAALAAVLAGCBPR CAAPCPLPALSRCRGAGSRGSRGGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRMGCI EVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSKKAPNKALASVLGKSNLRF GMSISIHISTDGLSLSPATRQVIANHMPSSISPAAGGDTMTD YVAYVAKDPIINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYNIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPLRDACSLPDWDVGSTGAP PGDGYVQADARGPPDHEEHLVNTQGLDAPEPEDSPKKDLDFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWSPPTTRAPVAPTEEQ LRQEPWYHGRMSRRAERMLRADGDFLVRDSVTNPGQYVLTGMH AQPKHLLLVDPBGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP |
| 5393 | 2 | 982 | GGDSAGMTMETQMSQNVCPRLNLWLLQPLTVLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAQP/ERSDSIQWFHNG |

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|------------|--|--|---|
| | | | \NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTV LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFPQNGK SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV QVPSMGSSSPMGIIIVAVVIATAVAIIVAAVVALIYCRKKRISAN STD PVKAAQFEPFGROMIAIRKRQLEETNNDYETADGGYMTLNP RAPTD DDKNIYLTLPNDHVNNSN |
| 5394 | 2 | 982 | GGD SAGMTMETQMSQNVCPNRLWLQPLTVLLLASADSQAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAQP/ERSDSIQWFHNG \NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTV LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFPQNGK SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV QVPSMGSSSPMGIIIVAVVIATAVAIIVAAVVALIYCRKKRISAN STD PVKAAQFEPFGROMIAIRKRQLEETNNDYETADGGYMTLNP RAPTD DDKNIYLTLPNDHVNNSN |
| 5395 | 3135 | 531 | RASDAKNQEGLLNTRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWD DPNFNFSSSTSKMQESP KL PQQSYNFDPTCDESVD PFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDLNKPAAKKKTPLKTDTRFVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP SEAIETAPEGSFASADALLSRLAHPVSLCGALDYLEPD LAEKN PPLFAQKLQREAAHPTDVSISK TALYSRIGTAEVEKPAGLLFQO PDLSALQIARAEIITKEREVSEWKDYEESSRREVMEMRKIVAE YEKTI AQMIEDEQREKSVS\HQT VQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKKEVLEGF RKNEEVLKRC AQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELI AKMGKS |
| 5396 | 3135 | 531 | RASDAKNQEGLLNTRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWD DPNFNFSSSTSKMQESP KL PQQSYNFDPTCDESVD PFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDLNKPAAKKKTPLKTDTRFVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP SEAIETAPEGSFASADALLSRLAHPVSLCGALDYLEPD LAEKN PPLFAQKLQREAAHPTDVSISK TALYSRIGTAEVEKPAGLLFQO PDLSALQIARAEIITKEREVSEWKDYEESSRREVMEMRKIVAE YEKTI AQMIEDEQREKSVS\HQT VQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKKEVLEGF RKNEEVLKRC AQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELI AKMGKS |
| 5397 | 3135 | 531 | RASDAKNQEGLLNTRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWD DPNFNFSSSTSKMQESP KL |

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|------------|--|--|---|
| | | | <p>PQOSYNFDPDTCDSEVDPPKTSSTPSSPSKSPASFEIPASAME ANGVDGDGLNPKAKKKKTPLKTDTPRVKKSFKRSLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD YPQPSDLSTFVNETHFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEN PPLFAQKLQREAAHPTDVSISKALYSRIGTAEVEKPAGLLFQQ PDLSALQIARAEIITKEREVSEWKDKYEESSREVMEMRKIVAE YEKTIQMIEDEREKESVS\HQTVOQLVLEKEQA\LDLNSVEK \SLADLFRRYEKMEVLEGFKNNEVLKRCQEQYLSRVKKEEQ YQALKVHA\EEKLDRANAE\IAQVRGKAQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAMGKS</p> |
| 5398 | 56 | 5426 | <p>SGEVCRMESNFQEGVPRFSYVFSADPIARPSEINFDGIKLDLS HFESLVAPNTEANSFESKDYLVQCLIRPFTQSEKELESEGCVH ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPFGLGPAT TQKEFPQGCIMHP\VKDLLKGQSRIFTYGLTNSGKTYTFQGT ENIRILPRTLNVLPDSLQERLYTKMNLKPHRSRYRLSSEQEK EEIASKSALLRQIKEVTVHNSDDTLYGSLTNSLNISEFEESIK DYEQANLNMANSIKFSVWVSFFETIYNEYIYDLFVPVSSKFQKRK MLRLSQDVKGYSPFKDLQWIOVSDSKAYRLKLGKIKHQSVAF KLNNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLCLAGSER TMKTQNEGERLRETGNINTSLTLGKCINVLKNSEKSKFQOHVP FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS AIAQKVCVPDTLNSQEKLFPGPVKSSQDVSLDSNNSKILNVKR ATISWENSLEDLMEDEDLVEELENAEETD/VGETKLDEDLDK TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE EVTQEFTOYWAQREADFKETLLQEREILEENAERRLAIFKDLVG KCDTREBAKDICATKVETERATACLELKFNQIKAEAKTKGEL IKTKEELKKRENESDLIQELETSSNKIITQNRKIKELINIIDQ KEDTINBFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKDSKSKICSERKRVNENELQDEPPAKKGSIHVSSAITEDQKK SEEVPRNIAETDIRVLQENNEGLRAFLLTIENELKNEKEKAE LNKQIVHFQQLSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK SKNQEQBEKIMKLSNEIETATRSITNNVSIKLMHTKIDELRTL DSVSQISNIDLLNLRDLNSGSEEDNLPNTQLDGLGNDYLVSKQV KEYRIQBPNNRENSFHSSIEAIWEECKEIVKASSKSHQIEELEQ QIEKLQAEVKGKDBNNRLKEKEHKNQDLDLKEKETLIQQLKEE LQEKNTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE TQKVERSHSAXLEQDILEKESIILKLEARNLKEFQEHQDSVKNT KDLNVKELKLEETITLNNLQDMKHLQLKEEEEEETNRQETEK LKEELSASSARTQN\LNADLQKEEDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK EQLINQKVEEAIQQYERACKDLNVKEKIIDMRMTLEEQEQTV EQDQVL\BAKLEEVERLATELDRWRVKNDLETQNNQRSNKEHE NNTDVLGKLTNLQDELQSEQKYNADRKKWLEKMLITQAKEA ENIRNKEMKKYADRERFPPKQNNEMEILTAQLTEKDSDLQKWRB ERDQLVAALIEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI MDIKPKRISSADPKLQTEPLSTSFEISRNKIEDGSVVLDSEV STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEEEDLVKCNKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIGVNLATKKKEGTLOKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVASKENVSQPKRAKRLYTSE ISSPIDISGQVILMDQMKESDHQIIKRRLRTKTAK</p> |
| 5399 | 705 | 230 | <p>GPMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDNGELDFSTFLTINMHMQIKQEDPKKE ILLAMLVMDKEKGYVMASDLRSKLTSLGKLTTHKEV\DDLFRE \ADIEPNGKVYDEFIHKITSYLDGTY</p> |
| 5400 | 931 | 248 | <p>SHCSSGMEIPTNYPASRAALVAQNYINYQQGTTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQKVNCTAEVLYPSTGQE TAPEVNTFTBGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN</p> |

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|------------|--|---|--|
| | | | FGNVSPMTLVHLAWVACGYIIWQNSTEDTWYKMKVIQTQVQVQRNDDFIELDYTILLHNIASQEIIPWQMQLVWHBPQYGTQVKVHNSRLPKEVQLE |
| 5401 | 3 | 1360 | TGWSYGPPTTSLAFLAPRDFPPFPKLLIHPQAVVRLSCGAGSMGSGAAAEWRNWNASWEGSSSLSGCSMGCFKDDRIVFTWTFSTYFMEKWAPRQDDMLFYVRRKLAISGSESGADGRKAAEFVEVEVYRRDSKKLPGLGDPDIDWEESVCLNLIQLKLDYMTCAVCTRADGGDIHIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\VFSDMTVGKGMVCVELVADSKTNTFQGVIFQGSIRYEALKKVYDNRVSVAAARMAQ\MSFGFSKYSNMEF\VR\MKGPQGGHAEMAVSRVSTGDTSPCGTEEDSSPASPHERVTSFSTPPTPERNNRPAFFSPSLKRVPRNRIAEKKSHSANDSEEFFREDDGGADLHNATNLRSLSGTGRSLVGSWLKLNADGNFLLYAHLTYVTLPLHRI LTDILEVRQKPILMT |
| 5402 | 3445 | 1563 | GECEFMAAVVQNDLVFEFASNVMEDEQLGDPAIFPAVIVEHVPGADILNSYAGLACVEEPNDMITESSLDVAEEETIDDDDDITLTVEASCHDGETIETIEAAEALLNMDSPGPMLEKRIINNIFSSPEDDMVVAPEVTHVSVTLTGIPVEMETQQVQEKYADSPGASSPEQPKRKKGRKTKPPRPDSPATTPNISVKKKNDGKGNITLYLWEFLLALLQDKATCPKYIKWTQREKGIKFLVDSKPVSRLLWRKHKNKP\DMNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDEDPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLKPGNSKAAKPKDPVEVAQPSVLRVTQPTQSPYPTQLFRTVHVQPVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSPRNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAI PSSQPMTVLKENVMLQSQKAGSPPSIVLGPAPV\QQVLT SNVQTCINGTVSV\ASSPSFS\ATAPVVTFLFLGSSQLVAHPPGTVITSVIKTQETKTLTQVEKKESEDHLKENTEKTEQQPQPYVMVSSSNGFTSQVAMKQNELLEPNSF |
| 5403 | 3445 | 1563 | GECEFMAAVVQNDLVFEFASNVMEDEQLGDPAIFPAVIVEHVPGADILNSYAGLACVEEPNDMITESSLDVAEEETIDDDDDITLTVEASCHDGETIETIEAAEALLNMDSPGPMLEKRIINNIFSSPEDDMVVAPEVTHVSVTLTGIPVEMETQQVQEKYADSPGASSPEQPKRKKGRKTKPPRPDSPATTPNISVKKKNDGKGNITLYLWEFLLALLQDKATCPKYIKWTQREKGIKFLVDSKPVSRLLWRKHKNKP\DMNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDEDPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLKPGNSKAAKPKDPVEVAQPSVLRVTQPTQSPYPTQLFRTVHVQPVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSPRNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAI PSSQPMTVLKENVMLQSQKAGSPPSIVLGPAPV\QQVLT SNVQTCINGTVSV\ASSPSFS\ATAPVVTFLFLGSSQLVAHPPGTVITSVIKTQETKTLTQVEKKESEDHLKENTEKTEQQPQPYVMVSSSNGFTSQVAMKQNELLEPNSF |
| 5404 | 187 | 1111 | LPVTLIFAKMKTQLSTLLLLLVPLIKPAPPTQQDSRIIYDYGTDNFEESIFSQDYEDKYLDGKNIKEKETVIIIPNEKSLQQLQKDEAITPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAYLYARPNKIKKLT\AKDFADIPNLRLDFTGNLIEDIEDGTFSKLSLVEELSLEAENQLLKLPLVLPKLTFLNAYNKIKSRGIKANAFKLNNTFLYLDHNALESVPLNLPESLRVILHGFNNIASITDDTFCKANDTSYIRDRIEERLEGNPIVLGKHPNSFICLRLPIGSYF |
| 5405 | 2199 | 1220 | QNSRSLHMDPQNQHSGSSSLVVIQPPSLDSRPRLDYERETIPTA ILSLDQIKAIRGSNEYTEGSPVVRKPAPTAPRQEKHERTHEIIPINVNNNYEHRTSHLGHAVLPSNARGPILSRSTSTGSAASSGSSASSASQGLGRSPTRPVPGRHSERAIPTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKGECTAPRTLPSCLACNRQCLCSAESMVEYGTMCML\VKGIFYHCSNDDGDSYSDNPCCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRCYDWIHRPGCRCKNSNTVYCKLESCPSRGGQKPS |
| 5406 | 279 | 2732 | RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQLYRNVMLENY |

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|------------|--|--|---|
| | | | RNLVFLG/ITAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVD CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLFKCECGKSFCLSHLAQHKKIHTRVNFCCKEKGKAF NCPSIITKHKRINTGKPYTCERCCKVFNWSSRLTTHKKNYTRY KLYKCEECGKAFNKSSILTTHKIIRTGEKFKYCKEAKAFNQSS NLTEHKKIHPGKPKYKCECGKAFNWPSTLTTHKRINTGKPYT CECGKAFNQFNLTHKRINTA\EFYKCTECGEAFSRS\SNL TKHKEIHTKPKYKCECGKAFKWSKLTTHKLTHGKPKYKCE KCGKAFNCPSSIITKHNRINTGKPYTCECGKAFNWSRLTTHK KNYTRYKLYKCECGKAFNKSSILTTHKKIHTKPKYKCECGK AFKWSKLTTHKIHTGKPKYKCECGKAFNHFSLTTHKRINT GKPKYKCECGKAFNQSSNLTHKKIHTGKPKYKCECGKAFNQ SSNLTHKKIHTGGKPKYKCECGKAFNQFSTLTTHKIHTGKPK YKCECGKAFKWSSTLTTHKIHTGKPKYKCECG\KAFKLSST LSTHKIHTGKPKYKCECGKAFNRPSNLIEHKKIHTGKPKYK EECGKAFNYSSHLNTHKRINTGKPKYKCECGKAFNQYSSNLTH NKIHTGKPKYKPEDVTILTTPQTFNSIK |
| 5407 | 3 | 659 | RPRRRQSSCCTGWLGLLRAAPRFRRTETDMEQKGLAVLIL AIIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAAEKNTWF KDGKMI GFLTEDKKKWNLGSNAKDPGRMYQCKGSQNKSKPLQVY YRMCQNCIELNAATISGFLFAETVSIFDLAVGVYFIAGTGMEFR QS\RASDKQTLTP\NDPAPTQPLKDPKMTQVSHLQGN\QLRRN |
| 5408 | 2745 | 6128 | QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVSVRPQGPDRDPKDSRDAKREQGS APRPVPASRGGKTLCKGYRQAPPQPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAHEHCE VRNKDMSWPEEMSFIANSSKIDRHKVPTKGTGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRTIAYAPRPNFGQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAEAWDNHLRRNRS IVVDLFHGLRSQVKCKTCGHSVRFPDPFNFLSLPLPMDSYMHL EITVIKLDGTTVPVRYGLRLNMDEKYTGKQLSDLCGLNSEQIL LAEVHGSNINKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTFSSSPSTNEMFTLTNGDLPRPIFIPNGMPTVPCGTEK NFTNGMVNGHMPSLPDSPTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKDLVDVAVIQVSRLASPLPPQEASNH AQDCDSMGYQYFPTLRVQKDGNSCAWCPWYRFRGCKIDCGE DRAFIGNAYIADVWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYCSKCKTHCLATKLDLWR LPPILI IHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCOHKPLTPQGDSEPRILAREVKVDAQSSAGEEDVLSKS PSSLSANI ISSPKGSPSSSRKSGTSCPSKSNSSPNSPRTLGRS KGRRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH LVGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVYTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMEDFESDY\EKYCVLQ |
| 5409 | 2745 | 6128 | QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVSVRPQGPDRDPKDSRDAKREQGS APRPVPASRGGKTLCKGYRQAPPQPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAHEHCE VRNKDMSWPEEMSFIANSSKIDRHKVPTKGTGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRTIAYAPRPNFGQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAEAWDNHLRRNRS IVVDLFHGLRSQVKCKTCGHSVRFPDPFNFLSLPLPMDSYMHL EITVIKLDGTTVPVRYGLRLNMDEKYTGKQLSDLCGLNSEQIL LAEVHGSNINKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP |

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|------------|--|--|--|
| | | | TQTFSSSPSTNEMFTLTNGDLPRPFIIPNGMPNTVVPQGTENFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTLEYFLSSQKNRPSLFPMPLIVPCTVHTRKKDLYDAVWIVQVSRLASPLFPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFRGCKIDCGE DRAFIGNAYIAVDWHTALHLRYQTSQERVVDEHESVEQSRRRAQ VEPINLDSCLRAFTSEEELGENEMYCCKCTHCLATKKLDLWR LPPILIIHLKRQFVNGRWIKSQKIVKFPRESFDPFAFLVPRPD ALCOHKPLTPQGDSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISPPKGPSSSRKSGTSCPSSKNSSPNSPRTLGRS KGRRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVYTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQIDYAFPLPK TDGKKMADTSSMEDFESDY\EKYCVLQ |
| 5410 | 2 | 710 | LRFPQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY VHQNFSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNLDSKLSLPNG KPVSVLLANKCDQGDVLMNGLKMDQFCKEHGFVGFETSAK ENINIDEASRLVKHILANECDLMESIEPDVVKPHLTSTKVASC SG\CAKILVGTFAGVW |
| 5411 | 1302 | 289 | TGPAAAGRRKALGSFGKPSVPTGLRAARRRRTRPSAPAAPSVC GKRRES DAGAGGERASVRTGSGRRGRTMAGDSEQLQNHQPN GGEPLIGVSGGTASGKSSVCAKIVQLLQNEVDYRQKQVVL S QDSFYRVLTSEQAKALKGQFNFDPHDAFDNELILKLTKEITEG KTVQIPVYDFVSHSRKEETVTVYPADVLFEGILAFYSQER/IR DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLR FV KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH |
| 5412 | 3180 | 313 | QGISNFFHKEANFWFEVSGYLISPLRSPFVDFALEWSLMASPNW KMEGESSRFEIHTPVSDKKKKKCSIHKERPKQKHSHEIFRDSLLV NEQSQITRRKKRKKDFQHLISSPLKKSRI CDETANATSTLKKRK KRRYSALEVDEEAGVTVVLDKENINNTPKHFRKDVVDVVCV DMS IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQ R KAASWESQRA\RD TLPQSEFPPTQESWLSVGGGEITELP\ASA HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV GLDDETPQLLGP THKKSKKKKKKSNH QEFESLAMPEGSQVGS EVGADMQES\RPVAGLHGETAGIPAPAYKNKSKKKKKSNHQEF EAVAMPESLESAYPEGSQVGS EVGTVEGSTALKGFESNSTKKK SKKRKLT SVKARVSGDDFSVPSKNSSTLFDSVEGDGAMMEEG VKSRPRQKKTQACLASKHVQEAAPRLEPANEZHNVEAEDSEIRY LSADSGDADSDADLGS AVKQLQEFIPNIKDRATSTIKRMYRDD LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD KLLYTD RYPEEKSVITNLKRRYSFRLHIG\RN IARPWKLIYYRA KKMFDVNNYKGRYSEGDTEKLKMYHSL LGNDWKTIGEMVARRSL SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQBLK BVD SKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS KWT EILT KRM TNGRR IY YGMNALRAKVS LIERLYEINVEDTNEI DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTPEIIDYL YETTLPLLKEKLEKMEKKGTKIQTAPAAPKQVFPFRDIFYYEDD SEGGGHRKRKRPRRHAWFTPIVPLWEAKAGWII |
| 5413 | 3753 | 1304 | RFPAGVAPRRAMANVSKVSWSGRDRDDEEAAPLLRRRTARPGGG TPLLNGAGPGAARQS PRSALFRVGHMSSVKLDDELLEP\DM DPF HPFPKEIPHNEKLLSLKYESLDYDENSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKRVIKGNID KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ IKCFLNGVKIPHVVRLKTLVIKVGSVILSVVGGGLAVGKEGPMIH SGSVIAAGISQGRSTSLKRPDKIFEYLRDTEKRDVFSAGAAAG VSAAPGAPVGGVLFSLBEGASFWNQFLTWRIFASMISTFTLNF VLSIYHGNMWDLSSPGLINPGRFDSEK MAYTIEIPVFIAMGVV GGVLGAVFNALNYWLTMFIRIYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAFAFFNTPEK |

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|------------|--|--|--|
| | | | SVVSLFHDPPGSGYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP SLLLGAAGWRLFGISLSYLTGAAIWADPGKYALMGAAQGGIV RMTLSLTVMMEATSNVTYGFIMLVMTAKIVGDVFIIEGLYDM HIQLQSVFPLHWEAPVTSHTLTAREVMSTPVTCLRRREKVGIV DVLSDTASNHNHGFVVEHADDTPARLQGLILRSQILVLLKHKV FVERSNLGLVQRRLRLKDFRDYAPRFPPIQSIHVSQDERECTMD LSEFMNPSFYTVPQEAASLPRVFKLFRALGLRLHVVDNRNQVVG LVTRKDLARYRLGKRGLEELSQAQT |
| 5414 | 2130 | 390 | GVASAWDRALFSPLLSPTSRSVFRTSPPRCVSTETGRRDRARVPS QWCSVLQGLKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCCQGPGRTRSP RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNMDRFTV AGVLPDIEQFFNIGDSSSGLIQTTFISSYMLAPVFGYLGDRYN RKYLMCGGIAFWSLVTLGSSFIPEGHFWLLLLTRGLVGVGEASY STIAPTLLADLFVADQRRSRLSIFYFAIPVGSGLGYIAGSKVD MAGDWHWALRVTPGLGVVAVLLLFLVVREPPGAVERHSDLPPL NPTSWWADLRALARNPSFVLSSSLGFTAVAFVTGSLALWAPAFLL RSRVVLGETFPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIATYIF IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD AGSPYLIGLISDRLRNWPSPFLSEFRALQFSLMLCAVFGALGG AAFLGTAHLH |
| 5415 | 693 | 2986 | IPPKTKLELQKH\LTTLT\NQEQTIFEEVQKLRPRNEQRENE IISFLRCLFEBKQKEHIHIGEMKQTSQMAENIGSELPPSATRF RLDMLKNXAKRSLTESLESILSRGNKARGLQEHISISVDLDSLS STLSNTSKEPSVCEKEALPISESSFKLLGSSDLSSDSHSLPE EPAPLSPQQAFFFFRANTLSHFPIECQEPQPARGSPGVSRQKLM RYHSVSTETPHERKDFESKANHLGDSGGTPVKTTRHRSWRQIFL RVATPQKACDSSSRDYEDYSELGELPPRSPLEPVCEGDPFGPPPE EKKRTSRELRELWQKAILQQIILLRMEKENQKLQASENDLLNKR LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIIPDMEKMHSAVGQ GVP\RHHRGEIWKFLAEQFHLKHQFPKQKQPKDVPYKELLQLT SQQHAILIDLGRTPFTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGVCQGLSFVAGILLHMESEEEAFKMLKFLMFMGLRQKQYRPM IILQIQMYQLSRLLDYHRLYNHLEBEHIGPSLYAAPWFLTMF ASQFPLGFVARVFDMLFLQGTETVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIKQLQAYEVEYH VLQEEIDSSPLSDNQMDKLEKTNSLRKQNLDDLLEQLQVANG RIQSLIATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD |
| 5416 | 27 | 4074 | KSQLECFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNITIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSNSDDNKQCPNPLIARSQVTSTFISKPPPLETSLPFLTIP ENRQLPPPSPOLPKHNLHVTKTLMETRRRLEQERATMQMTPEGF RRPRLASFGMGTTSSLSLPSFVGSGNHNPAKHQLQNGYQGNQDYG SYAPAAPTTSSMGSSIRHSPSSGISTPVTNVSFPHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRLVSQKLNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAENMNDIVVYHRGSRSCKDAAVGTLVEMRNCVSVTE AMLGVMTEADKEIELQQQTIESLKEKIVRLEVQLRETTTHDREMT KLKQELQAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGIQCPECKNKVVGPELPMNWIIVKER VEMHRCAGRSVEMCDKSVSEVSVCTGSNTESVNDLTLTKT NLNLKEVRSIGCGDCSDVDTVCSPEKASRGVNTEAVSQVEAAV MAVPRADQDSTDLQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQQAFLGMMTGLDHYIERIQKLLAEQQ TLAENYSELAEAFGEPSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCCKGGLQSGSPLSSQTSQPE |

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|------------|--|--|---|
| | | | QEVGTSEGKPISSLDAPPTQEGTLPVNLTDQIAAGLYACTNN ESTLKSIMKKKDGKNSGAKKNLQFVGINGGYETSSDDSSSD ESSSESDDCEDVIEYPLEEEEEDEEDTRGMAEGHHAVNIEGL KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEAEKDMRIVEELFCGCDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPPGPTHRSFD |
| 5417 | 27 | 4074 | KSQLCFPGWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGTNIKRLNIQKRRKPSVPCBPRTTSGQQGIWSTES LSSSNSDDNKQCPNFIARSQVSTSPISKPPPLETSLPFLTIP ENRQLPPSPQLPKHNLHVTKTLMETRRRLQERATMQMTPEGF RRPRLASFGGMGTTSSLPFVSGSNHNPAAKHLQNGYQGNQDYG SYAPAAPTTSSMGSSIRHSPSSGISTPVTVNSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAENMNDIVVYHRGSRSCDKAAVGLVEMRNCVSVTE AMLGVMTRADKEIELQQQTIESLKEKIYRLEVQLRETTDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMGVSH MDLVDTCVGTSVETNSVSGISQPECKNKVVGPELPMNWIVKER VEMHDCAGRSVEMCDKSVSVEVSVCTGNSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSDVDVTCSPKECASRGVNTAEVSVQAAV MAVPRADQDSTDLQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTAVAGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQAPLGMGTGLDHYIERIQKLLAEQQ TLLEAENYSELAEAFEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCCKGGLQSGSPSSQTSQPE QEVGTSEGKPISSLDAPPTQEGTLPVNLTDQIAAGLYACTNN ESTLKSIMKKKDGKNSGAKKNLQFVGINGGYETSSDDSSSD ESSSESDDCEDVIEYPLEEEEEDEEDTRGMAEGHHAVNIEGL KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEAEKDMRIVEELFCGCDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPPGPTHRSFD |
| 5418 | 24 | 1133 | SVPRAGGDMETGAELYDQALLGILQHVGNVDLRLVLFGLYLR KTDIFYRLLRHPSDRMGFPFGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRKKEEEEAKTVSAAAEKEPVPVPVQEIETDSTTEL DGHQVEVEKVPPGPVKEMAHGSQAEAPGAVAGAAEVPR\EPPI LPRIQEQQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVKHVVK GKQVSVALSSSSIRVAMLEENGERVLMGKLTHTKINTESSLWSL EPGKCVLVNLSKVGEYWNAILLEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLGKQSQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF |
| 5419 | 1395 | 259 | GTHPLDPLVSRSTVQGPLMTMACPGMSDTEESPFGLPRAAEEG SESEACEAFGRKKEEGRRSDTSGFGRSRKHKNVWVWHPERADA KDFASLPQC/LGP/DCVRPAQPSKSKYCSDDCGMKLAANRIYEL PQRIQQWQSPCIAEHEGKLLERIRREQQSARTRLQEMERRPH ELEAII LRKQAVREDEESNEGSDDTDLQIFCVSCGHFINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADVCGCPVLRDVPFELTGDFCRLPK RQCNRYHCWEKLRRAEVDLERVRVWYKLDLFEQERNVRTAMTN RAGLLALMLHQTIQHDLPTTDLRSSADR |
| 5420 | 117 | 1733 | NEAGGACPFKGGASGRLYLSPLRPRVSVAGCEERPLGWVWLGG GGFLPARPPRAQRHLGFSHAQSMEDPYEVLVSREQLFHERIR |

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|------------|--|--|---|
| | | | ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRGV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYLLP YLYSCISFLGVLLLVCTPLGLARMF SVTGKLLVKPRLLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELLHRQVLALQTORVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGFAGVIQVVLIFYLMVSSVVG F YSSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGL TRFDLLGDGFRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFATAV RAE LIRAFGERE |
| 5421 | 117 | 1733 | NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGVWVVLGG GGFLPARPPRAQRHLGFSAEQSMAPDYEVLSVREQLPHERIR ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRGV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYLLP YLYSCISFLGVLLLVCTPLGLARMF SVTGKLLVKPRLLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELLHRQVLALQTORVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGFAGVIQVVLIFYLMVSSVVG F YSSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGL TRFDLLGDGFRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFATAV RAE LIRAFGERE |
| 5422 | 3 | 1263 | SCGESLPTWLAGASRPGIGRKGAGGGRGGSSPAQVLLSPGPVF KAGCNWHLSDQAGVQRCDLGSSQPPPLGFRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR TVFVSERELDWAKVMVEKSRMGVVPPTQVEQLLYAKLYDSAF HPDTGEKMNIVGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQV NQSFNALVNYTNRNAASPTSVRQMAISYFTATTAVATAVGMNM LTKKAPPLVGRWVPPAAVAAANCNIPMMRQQELIKGICVKDRN ENEIGHSRRAAIGITQVVISRITMSAPGMILLPVIMERLEKLH FMQKVVL/SAPLQVMSGCFLIFMVVACGLFPQKCELPVSYL EPKLQDTIKAKYGELEPYVYFNKGL |
| 5423 | 3186 | 905 | GVSMALGEEKAEAEASEDTKAQSYGRGSCREERELDIPGPMSEGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQFQASD ANREPVAERSEPALSGLPATMGSGDLLLLSGESQVEKTKLSSSE EFPQTLSPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVG LGPRPQWSPQVPSGSDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPKNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVLDLSFVSVPASTLKS P TNVSPNCPAEATALPFSGPREPSLKQWPSRVQKQGMGLASW SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSRPREKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSLSVLSISTLVTLPTGDIKQSPLEVSDSDG PASFFSSSSSQLPFGAALQSGDPEGQNPCLFRSFVRAHDSAG EGSLSGSSQALGVSSGLLKTRPSLPARLDRNPFSDPDVEGQLPRK GGEQKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGT PAR SNLTSK\SSLQLYRQFKDIDEHQSLTESVLQKEILLQCLE NTPVLEDDVLGRIAKQSGELESADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV |
| 5424 | 3186 | 905 | GVSMALGEEKAEAEASEDTKAQSYGRGSCREERELDIPGPMSEGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQFQASD ANREPVAERSEPALSGLPATMGSGDLLLLSGESQVEKTKLSSSE EFPQTLSPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVG LGPRPQWSPQVPSGSDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPKNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVLDLSFVSVPASTLKS P TNVSPNCPAEATALPFSGPREPSLKQWPSRVQKQGMGLASW |

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|------------|--|--|--|
| | | | <p>SQIATSTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSRPPEKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSSLVSYLGSISTLVTLPTGDIKQSPLEVSDDSG PASFPSSSSQSQLPFGAALQSGDPEGQNPCLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK GGEQKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTTPAR SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVLGRIAKQSGELESADRLYDSILASLDMLAGCTLIP DKKPMAMEHPCEGV</p> |
| 5425 | 1086 | 115 | <p>GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLT NSYWRVSTVHGNVITNTIFENLWFSCATDSLGVYNCWEFFPML ALSGYIQACRALMITAILGFLGLLLGIAGLRCTNIGGLELSRK AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSPLYPGT KYELGPALYLWGSASLISILGGLCLCSACCCGSDDEPAASARRP YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA PKKRGPGRGFFPYSNLRGRPRPVVAPPRPRPVLSHSGPSQAK NCSWEVAYLPSEAGSLIF</p> |
| 5426 | 42 | 3435 | <p>ATSSQSLGRADPPRGGTMERSPGEGSPSPMDQPSAPSDPTDQF PAAHAKPDGSGGQFAGPGAAGEALAVLTSFGRRLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLDDDEQL TAKTLYMSHRELPAWVSFPDVEKAELNKKIQAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPPFVGAUSMFFIRRPDLINWTGMTNLLDIPGLSSLSLSD TMIMDSIAAPLVLPNRLVPLVPLDQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVVMHVEVPGQIEVEVFDKDPDKDDFLGRMKLDVGVK LQASVLDDWFPLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG VSSRPDPSPSAAILVVYLDRAQDLPMVTSELYPPQLKKGKNEPNP MVQLSIQDVTQESKAVYSTNCPVWEAFAFRFLQDPQSQELDVQV KDDSRALTGLALTPLARLLTAPELILDQWFQSSSGPNSRLYM KLVMRILYLDSSIECFPTVPGCPGAWDVDSNPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLLLAGRSFRSHVVREDLNPRWNEVEFVITVSPGQLEVEVF DKDLDDKDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPTPTAAELEEVQVNSLIQTQKSAELAAALLSIYMERAE LPLRKGTKHLSPYATLTVGDSHKTITISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGVLLRAQLGILVSQHSQVGAHSHSYSHSSSSLSSEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTWYYSE ERKLVSIVHGCRSLRQNGRDPDPYVSLLLLPDKNRGTRKRTSQ KKRTLSPEFNERFEWELPLDEAQRRLDVSVKSNSSFMSSREREL LGKVQLDLAETDLSQGVARWYDLMNDKDKGSS</p> |
| 5427 | 42 | 3435 | <p>ATSSQSLGRADPPRGGTMERSPGEGSPSPMDQPSAPSDPTDQF PAAHAKPDGSGGQFAGPGAAGEALAVLTSFGRRLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLDDDEQL TAKTLYMSHRELPAWVSFPDVEKAELNKKIQAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPPFVGAUSMFFIRRPDLINWTGMTNLLDIPGLSSLSLSD TMIMDSIAAPLVLPNRLVPLVPLDQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVVMHVEVPGQIEVEVFDKDPDKDDFLGRMKLDVGVK LQASVLDDWFPLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG VSSRPDPSPSAAILVVYLDRAQDLPMVTSELYPPQLKKGKNEPNP MVQLSIQDVTQESKAVYSTNCPVWEAFAFRFLQDPQSQELDVQV KDDSRALTGLALTPLARLLTAPELILDQWFQSSSGPNSRLYM KLVMRILYLDSSIECFPTVPGCPGAWDVDSNPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLLLAGRSFRSHVVREDLNPRWNEVEFVITVSPGQLEVEVF DKDLDDKDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL</p> |

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|------------|--|--|---|
| | | | ERLTTPRTAAEEVLQVNSLIQTQKSAELAAALLSIYMERAE LPLRKGTKHLSPYATLTVGDSHKTITISQTSAPVWDESASF LIRKPHTESLELQVRGEGTGVLSLSLPLSELLVADQLCLDRWFTL SSGQGVLLRAQLGILVSQHSQVGAHSHSYSHSSSSLSSEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTWYSE ERKLVSIHGCRLRQNGRDPDPYVSLLLLPDKNRGTRKRTSQ KKRTLSPEFNERFEWELPLDEAQRRLDVSVKNSFSREREL LGKVQLDLAETDLSQGVARWYDLMDNKKDKGSS |
| 5428 | 3 | 1839 | SSRSERLSACAIAPPWLVSSRPAPQALQRPQGMVEDGAELED LVHFSVSELPSRGYGVMEIIRRGKLCVTLKIGDHKFSAHRI LAASIPYPHAMFTNDMECKQDEIVMQGMDPSALEALINFAYNG NLAIQDQNVQSLMGASFLQLQSIKDACCFTLRERLHPKNCGLV RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLLPLEDVLLE VSRDELNVKSEEQVFEAALAWRYDREGRGTF\RLNLSNIRLL FCRPQFLSDRVQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP AFRTRPRCCTS IAGLIYAVGGLNSAGDSLNVVEVDFDIANCWER CRPMTTARSRGVAVVNGLLYAGGYDGLRLSTVQAYNTETDT WTRVGSMMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSVETYSPE TDKWTVTVMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH YNHHTATWHPAAGMLNKRCHGAASLGSKMFVCGGYDGSGLFSI AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGV TGQSNL\SSVGDVLTPETDCTWFM\APMACHEGGVGVGCIPLLT I |
| 5429 | 828 | 202 | RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF AQRERFHRFQPTYPYLQHEIDLPTISLSDGEBPPPYQGPCTLQ LRDPEQQLELNRESVRAPPNRTIFDSLDLMSARLGGPCPPSSNS GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQSSGPPSL LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL |
| 5430 | 441 | 1507 | QKRKRKRKRKTKTKTQPKMHNSTSWAIFTGLAALCLFQGVVRS GDATFPKAMDNVTVRGESATLRCTIDNRVTRVAVLNRSITLYA GNDKWCLDPRVLLSNTQTOYSIEIQNVVDVDEGPYTCVQTDN HPKTSRVHLIVQVSPKIVEISSDISINEGNISLTCIATGRPEP TVTWRHISPKAVGVSEDEYLEIQGITREQSGDYECASNDV\A APV\VRVKVTVNYPPYISEAKGTGVFVGQKGTQCEASAVPSA EFQWYKDDKRLI/EGKKGVKVENRPFSLKLIFFNVSEHDYGNFT CVASNKLGHNTASIMLFPGPAVSEVSNGTSSRRAGCVLLPLLV HLLKLF |
| 5431 | 2 | 1312 | AAAAPGSRRRRPLDRPHMAHGYEAPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGFY SDGEISICMEHMDGGSLLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPPIPP DAKELEAIFGRPVVDGEGEPHSISPRPRPPGRPVSGHGMDSRP AMAFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEVDVAGWLCKTLRLNQPGTPTRTAV |
| 5432 | 2 | 1312 | AAAAPGSRRRRPLDRPHMAHGYEAPPPAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGFY SDGEISICMEHMDGGSLLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPPIPP DAKELEAIFGRPVVDGEGEPHSISPRPRPPGRPVSGHGMDSRP AMAFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEVDVAGWLCKTLRLNQPGTPTRTAV |
| 5433 | 360 | 1885 | SVQEDKVGFEPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LFGWPSLVFVFNEDYFKDLGCPDAGPIGNATGQADCKAODERF SLIFTLGSFMNFMFTPTGYIFDRFKTTVARLIAIFFYTTATLI |

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|------------|--|--|--|
| | | | IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI ITLYNGAPDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC STHFPPDAPGAHPIPTAPQLQLWPVPEWHHKGREG/QQLSMKT GSYSQRRSSFFQRRKRPGQGRSRNSAPSGATL/CSRRFAWHLVWL SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL CAPWNGLLMDRLKQYKQKEARKTGSSTLAVALCSTVPSLALTSL LCLGFALCASVPILPLQYLTPILOVISRSPFLYGSNAFLTLAFL SEHFGKLFGLVMALSAVVSLLQFPITFLIKGSLQNDPFYVNVMF MLAILLTFHFPFLVYRECRTWKESPSAJA |
| 5434 | 66 | 652 | RYAALIISLIQHKLWNRNQHCSRVCIMSPAQSAGLNWLF/GSGK HGPFILGCSQYPACDYVRPLKSSADGHIVKVGQVCPACGANLV LRQGRFGMFIGCINYPECEHTELIDKPDETAITCPQCRTHLVQ RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT AQGVKHFCAKQCGKPVSAE |
| 5435 | 4704 | 1597 | PGDSSQRLAEMSNAKERKHAKKMRNOPTNVTLSGGFVADRGVKH HSGGKPFQQAQKQEPHPTSRQRQTRVNPVHSLPDPEVNEQSSSK GMFRKKGWKGAGPEGTSEIPIKYITASTFAQARAAEISAMLKAV TQKSSNSLVFQTLFRHMRRRAMSHNVKRLPRRLQEIQAQKAEKA VHQKKEHSKNKCHKARRCHMNRNRTLEFNRRQKKNIWLETHIWHAK RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYCCLE LKGKEEELKALSGMCNIDTGLTFAAVHCLSGKRQGSLLVLYRVN KYPREMLGPVTFIWKSRTPGDPSESRLWIHLHPTLKQDILEE IKAACQCVBPIKSAVCIADPLPTPSQEKSCTELPDEKIGKKRRR KDDGENAKPIKKIIGDGTDRDCLPYSWISPTTGIIISDLTMEMN RFRILGPLSHSILTEAIIKAASVHTVGEDTEETPHRWIETCKKP DSVSLHCRQEAIFELLGGITSPAETIPAGTILGLTVGDPRINLPQ KKSALPNPEKQDNEKVRQLLEGVVVECTHSFIWNQDICKSV TENKISDQDLNMRSELLVPGSQLILGPHESKIPILLIQPGVK TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVVRVGLKESAVH SQYKRSPNVPDPPDCPAGMLFAEEQAKNLEKYKRRPPAKRPN YVKLGTLPFCPPWEQLTQDWESRVQAYEEPSVASSPNGKESDL RRSEVP/CAPMPKKTHQPSDEVGTSIEHPREAEVMDAGCQESAG PERITDQEAENHVAATGSHLCVLRSRKLLQLSANCSPSSDS RGGRRAPGRGQGLTREACLILGHFPALVWVSLLSKGSPE PHTMICVPKEDFLQLHEDWHYCGPQESKHSDFRSKILKQKEK KKREKRQKP\GRASSDGPAGEEPVAGQEAALTGLWGSGLFRVTL HCSRTLLGFVTQGDFFMAVGCGEALGFVSLTGLLDMLSQPAAQ RGLVLLRPPASLQYRFARIAIEV |
| 5436 | 1781 | 635 | ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFGLPYSGKSR RAEELRVALAAEGRVYVDDAAVLGAEDPAVYGDSAREKALRG ALRASVERRLSRHDVVILDSINYIKGFRYELY\CLARAARTPLC LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA GSSVLRELHTADSVVNGSAQADVPELEREBSGAARSPALVTPD SEKSAKHGSGAFYSPELLEALTFRFEAPDSNRNRWDRPLFTLVGL EEPLPLAGIRSALFENRAPPHQSTQSQPLASGSFLHQLDQVTS QVLGLMEAQKSAVPGDLLTLPGTTEHLRFRTRPLTMAELSRRLR QFISYTKMHPNNENLPQLANMFLQYLSQSLH |
| 5437 | 739 | 1672 | CQEAASEFGGPLHTPAMFLRLGGWLPRPWGRRKPMRPDPPEYPE PRRDSSSENSGSDWDSAPETMEDVGHPKTKDGSALRVSRASE PSKEEPQVEQLGSKRMDSLKWDQPISTQESGRLEAGGASPKLR WDHVDGGTRRPGVSPGGL\GVPGPGAPLEKPGRREKLLGWLR GEPGAPSRYLGGPEECQISTNLTLLHLELLASALLALCSRPLR AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG KGL |
| 5438 | 2443 | 1152 | TKPRKRRHQPASQRQRPWSSDSTGDLARGKGRKEENKGS DRV LAPPSLRPMMQCSEARQGPRLRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYLLPFGALRPLSRVGRVPSRVVALYKS VPTRLLSRAWGRNLNQLPHWLRRPVSYLWTFGVNMKEAAVE DLHHYRNLSFEFFRRLKQARPVCGLSVISPDSGRILNFGQVK NCEVEQVKGVTYLSLESFLGPRMCTEDLPFPPAASCDSFKNLVT |

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|------------|--|--|---|
| | | | REGNELYHCVIYLA PGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVL TGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSGSYNDFS FVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL |
| 5439 | 2443 | 1152 | TKPRKRRHQPASQRQRPWSSDSTGDL LARGKGRKEENKGS DRV LAPPSLRPMQCSEARQGP ELRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYLLPFGALRPLSRVGRFPVSRVALYKS VPTRLLSRAWGRNLQVELPHWLRPVYSLYIWTFGVNMKEAAVE DLHHYRNLSSEFFRRKLKPQARPVCGLSVISP SDGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTEDLPFP PAASCD SFKNQLVT REGNELYHCVIYLA PGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVL TGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSGSYNDFS FVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL |
| 5440 | 693 | 253 | EPIPVTPDHLVMTTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA MLGAPHNPAPPMSTVIHIRSETSVPDHV VWSL FNTLFMNTCCLG FIAFAYSVKSRDRKMVG DVTGAQAYASTAKCLNIWALILGIFMT ILLIIIPVLVQAQR |
| 5441 | 2 | 2054 | CRDGGKNGFMVSPMKPLEIKTQC SGPRMDPKICPADPAFFSFIN NSDLWVANIETGEERRLTFC HQGLSNVLD DPKSAGVATFVIQEE FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVSP ALEERKTDSYRYPRTGSKNPKIALKLA EFQ TDSQGIKIVSTQKE LVQPPSSLPFKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVL PPALFIPSTENEEQ\RLASARAVFRNVQPYVYVEVTNVWINVH DIFYPPQSEGEDEL CFLRANECKTGFC HLYKVTA VLK SQGYDW SEPFSPGEGEQLTNAIWN EETKL VYFQGT KDTPLEHHLYVVS YEAAGEIVRLTTPGF SHSCMSQNFDMFVSHYSSVSTPPCVHVY KLSGPD DPLHKQPRFWASMM EAAKIFHFHTRSDVRLYGM IYKP HALQPGKKHPTVLVYGGPQVQLVNNSFKGIKYLRNLTLASLGY AVVVIDGRGSCQGRGLRFE GALKNQMGQVEIEDQVEGLQFVAEKY GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVMW AYDTGYTERYMDVPENNOHGYEAGSVALHVEKLPNEPNRLILH GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL |
| 5442 | 1 | 3474 | CGQSRRRSPDMPEAKPAKAPKGDAPK GAPKEAPPKEAPAE APKEAPPEDQSPTAE EPTGVFLKKPDSVSVETGKDAVVAVKNG KELPDKPTIKWFKGKWE LGSKSGARFSFKESHNSASNYTTVEL HIGKVVLGDRGYRLEV KAKDTCDS CGFNIDVEAPRQDASGQSL ESFKRTSEKSDTAGELDFSGLLKREVVEEKKKKKKDDDDLG IPPEIWELLKGAKKSEY EKIAFYQGITDLRGMLKRLKKAKVEVK KSAAF TKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNQGEIK PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV KEPPVLIVTPLEDQQV FVGDRVEMAVEVSSEGAQVMMKDGVEL TREDSEFKARYRFPKDGKRHILIFSDV VQEDRGRYQVITNGGQCE AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWKY NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDTFVPDGYAL GSLSAKLNFL EIKVEYVPKQ\EP PKIPLGFASGGKTSENAD/IV VVAGNKLRLDV\ SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE KRVDSS FVIESAQREDEGRYTIKVTNP IGEDVASIFLQVVDVP DPPEAVRITSVGEDWAILVWEP PMYDGGKPV TGYLVERKKKGSQ RWMKLNFEVFTETT YBESTKMIEGILYEMRVFAVNAIGVSQPSMN TKPFMPIAPTSEPLHLIVEDVTD TTTTLKWRPPNRI GAGGIDGY LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGYN IAGRSEPATLAQPV TIREIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQ GKPRPVVWTKGGAPLDSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYFRVY TENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVV VAGYSAALNCAVRGHKPKPV VWMKNKMEIREDPKFLITNYQGVLT LNI RRPSPFDAGTYTCRAV NELGEALAECKLEVRVPQ |

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|------------|--|--|--|
| 5443 | 66 | 1003 | SRGQLDAGQSSEQHGGNRQPEQSRSSSSSSSSSPRRSRSAEPA MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKT NKIEEFLBEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS RPEANEALERGLLKTQLKLDYLNLSPLPDEIDENSMEDIKFSTR KFLDGNEMTLADCNLLPKLHIVKVVAKKYNFDIPKEMTGIWRY LTNAYSRDEFTNTCPDKEVEI\AYS DVAKRLHQVKSRLLEKVS FMSSP |
| 5444 | 2 | 344 | SGPIGVTGAQMAKWLRLDYLSFGGRRPPPPQPTPDYTESDILRAY RAQKNLDFEDPY*DSESRLEPDAGPGDSKNPGDAKYGSPKHRL IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHAPPDDG YMEPYDAQWVMSLPGRGVQLYDTPYEEQDPETADGPPSGQKPR QSRMPQEDERPADBYDQPEWKKDHISRAFAVQFDSPEWERTPG SAKELRRPPRSPQPAERVDPALPLEKQPFHGLNRADAESLL SLCKEGSYLVRLSETNPQDCSLSLRSSQGLHLKFARTRENQVV LGQHSPPFPSPVPELVHYSSRLPVQGAHLALLYPVVTQTP*Q *PDWGDRRPNQVATGLPELWGAEPASAAHPGLHRRHRHPEGLP RAEKPLRGPLLGLREPLGAGPRCPWGLQEPRRQCVWFSSQAPAH QGGGCGYGGSQGSGRPRGGAGSRH |
| 5445 | 2364 | 486 | ILSRGFLGSVEICIQPLPASEPVLLLTWARRRRWRETSRREPT TLRAQSVCPWWI*ETRMNRSIPVEVDESEYPQQLKPIPEYSP EESEPPAPNIRNMAPNSLSAFTMLHNSSGDFSAHSTLKLANKH QRVSRQVTCRLTQVLEDSQSCFRRHPLGKAPFSGCSAVSEP ASESVVGLPAEHQFSFMEKRNQWLVSQLSAASPDTHGDSKSD QSLPNASADSLGGSQEMVQRPQPHRNAGLDLPTIDTGYDSQPQ DVLGIRQLERPLTSCYCPQDLPLPLRSREFPQFEPQRYPACA QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDPYRAAYQQVIQ ALPGQPLPGASVRGLHPVQKILNYPSPWDQEEERPAQRDCSFP LFRHQDQPHHQPNNRAGAPGESLECPAELRPQVPQPPSPAAPVR PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLV NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIIVASPKYQ DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMMFRFIPVLF PNAKKEHVPTWLQNTVYVSWPKNKNILLRLLREEEYVAPPRGP LPTLQVVPL |
| 5446 | 972 | 161 | SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGO TLDVKCDYTLKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP VQVGRILLEDYHDHGLLRVRMNLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTGSGNSNSTQNVYKIPPTTKALCLPT TFRVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA GGFLSKSLVFSVLPFAVTLRSFVP*AHPTRMSSDFQPHPSGSCA KGGRR |
| 5447 | 207 | 617 | MTARTLSLMASLVAYDDSDSEATEHAGSFNATGQQKDTSGVAR PPGQDFASGTLDPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWPGKEPQVTFPIKEPSCSLWTSHPVASHMPLAAA RFKQVKLSRNFPKSSFHAQSESETVGKNGSSPQKKCEDCVVPY TPRRLRQRQALSTETGKGDVEPQGPAPGRAPAPLVVGPVSEF IQPYLNSHYKETTVPKVLPHLRGHRGPVNTIQWCPVLSKSHML LSTSMKTFKVVNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL SGGDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIPLCG GFSSEMKAWDIRTGKVMRSYKATIQOTLDILFLREGSEFLSSTD ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREP FLAQTNNGYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCESPG GDLVTGSADGRVLMYSFRTASRACTLQHTQACVGTITYHPVLP SVLTCSSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL KSPSPSKSLVLLCGRAMFPQATCPWQLPALSK |
| 5448 | 194 | 1833 | MASKVTDIVVYQKKIGAYDQOIWEKSVEQREIKGLRNKPKKTA HVKPDLDIVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF RWLQVTSKVIFFWLLVLVYLQVAAIVLFCSTSSPHSIPLTEVI GPIWMLLLGTVHCQIVSTRTPKPLSTGGKRRRLKRAAHLEH HREGDSSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLS GSKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHQPQCT |

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|------------|--|--|---|
| | | | IRPEETAWNTGTLRNGPSKDTQRTITNVSEVSSEEGPETGYSL RRHVDRTSEGVLNRKSHHYKKHYPNEDAPKSGTSCSSRCSRR QDSEARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLCVAERTYKQVGIM*TSEGVLNRKSHHYKKHYPNEDAPK SGTSCSSRCSRRQDSEARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI WEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLCVAERTYKQVGIM |
| 5449 | 194 | 1833 | MASKVTDIAVWYQKKIGAYDQQIWEKSVEQRRIKGLRNKPKKTA HVKKPDLIDVDLVRGSFAKAKPESPTSLTTKGIVRVVFPPFF RWLQVTSKVIFFWLLVLYLLQVAAIVLCSTSSPHSIPLTEVI GPIWMLLLGTVHCQIVSTRTPKPLSTGGKRRRKLKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLS GSKAKNSIDKSTETDNGYVSLDGKKT VKSGEDGIQNHQPQCT IRPEETAWNTGTLRNGPSKDTQRTITNVSEVSSEEGPETGYSL RRHVDRTSEGVLNRKSHHYKKHYPNEDAPKSGTSCSSRCSRR QDSEARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLCVAERTYKQVGIM*TSEGVLNRKSHHYKKHYPNEDAPK SGTSCSSRCSRRQDSEARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI WEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLCVAERTYKQVGIM |
| 5450 | 8136 | 1242 | GQQFASFFG*NHPEVTVMALTDIDLQLQFMSQPEALLLLAAG PADHLLQLYSGHLQVRLVLGQEBELRLQTPAETLLSDSI PHTVV LTVVEGWATLSVDGFLNASSAVPGAPLEVYPGLFVGGTGLGLP YLRGTSRPLRGCLHAATLNGRSLRLPLTPDVHEGCAEEFASDD VALGFSGPHSLAFAFPWGTQDEGTLEFLLTQSRQAPLAFQAGG RRGDFIYVDIFEGHLRAVVEKGGQTVLLHNSVPVADGQPHEVSV HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA AGCRLEEEYEDDAYGHYAFSTLAPAEAWPAMELPEPCVPEPGL PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAE LRK SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD GSEDTSDQLVLEVSVTARVMPSCLRGQTYLLPIQVNPVNDPP HIIFFHGSMLVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT SSGLPVERRDQPEPATEFSCREAGSLVYVHCGGPAQDLTFR VSDGLQASPPATLKVVVAIRPAIQIHRSTGLRLAQSAMPILPAN LSVETNAVGGQDVSVLFRVTGALQFQELQKHSTGGVEGAEWATQ AFHQRDVEQGRVRYLSTDPQHAYDTVENLALVQVQBSILSNL SFPVTIQRATVWMLRLEPLHTQNTQOETLTTHALEATLEEAGPS PPTFHYEVVQAERKGNLQOGTRLSDGOGFTQDDIQAGRVTYGA TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV LLVVEGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG TQDKTTMVTSTFNEDLLRGLRVYQHDDSETTEDDIPFVATRQGE SSGDMAWEEVRGVFRVAIQPVNDHAPVQTI SRI FHVARGRRLL TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVPPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQDLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMSRGALADEPPS LDPVQSFSQEAVDTRGVLYLHRSRPEAWSDAFSLDVASGLGAPLE GVLVELEVLPAAIPLEAQNFVSVEGGSLTLAPPLLRVSGPYPPT |

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|------------|--|--|---|
| | | | LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVBEQLIRYV HDGSETLTDSEVFLMANASEMDRQSHPVAFVTVLPVNDQPPILT TNTGLQMWEGATAPIPAEALRSTDDGSGSEDLVYTIEQPSNGRV VLRGAPGTEVRSFTQAQLDGGVLVLFSHRGTLDDGGFPFRLLSDEH TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS SAGTDPQLLLYRVVRGQPLGRFLFAHQDSTGEALVNFTQAEVYA GNILYEHMPPEPFWEAHDTELEQLSSPPARDVAATLAVAVSFE AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSQ RSEHDVLFQVTQFPSRGQLLVSEEPHAGQPHFLQSOLAAGQLV YAHGGGGTQQDGFHRAHLQGPAGASVAGPQTSEAFITVRDYN ERPPQPQASVPLRLTRGSRAPISSRAQLSVVDPDSAPGEIEYEQ RAPHNGFLSLVGGGLGPVTRFTQADVDSGRFAFVANGSSVAGIF QLSMSDGAAPPLPMSLAVDILPSAIEVQLRAPLEVPPQALGRSSL SQQLRVVSDREPEAAVRLIQGPQYGHLLVGGRPSTAFSQFI DQGEVVFATNFSSSHDHFRLALARGVNASAVNVTVRALHIV WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLEGPGRHR VVRVPRARTEPGGSQLEVEQFTQDDLEDGRLGLEVGRPEGRAPGP AGDSLTLLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASPEPAVAKGGFLSFLEANMFVS IIPMLVLVLLALLLPLLFYLRKRNTGKHDVQVLTAKPRNGLA GDTETFRKVEPGQAIPLTAVPGQGGPPGGQPDPELLQFCRTFNP ALKNGQYVW |
| 5451 | 1 | 2274 | RDSSEQGRGTDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR KNSEPGSPHSLEALRDAAPSQGLNLFLLFTKMLFI FNF LFSPLP TPALICILTFGAALFLWLTITRFPQVPLPLDLNNSQSVGIEGGARK GVSQKNNDLTSCCFSDAKTMYEVFQRGGLAVSDNGPCLGYRKPNQ PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW IISELACYTSMVAAPLYDTLGPEAIVHIVNKADIAMVICDTPQ KALVLIGNVEKGFPTSLKVIILMDPFDDDLKQRGEKSGIEILSL YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN IVSNAAAFKLCVEHAYEPTPDDVAISYLPPLAHMFERIVQAVVYS CGARVGFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFELQKGIIRHDSFWDKLI FAKIQDSL GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAQGTECTGGCT FTLPGDWTSGHVGVPLACNYVKLEDVADNMNYFTVNNEGEVCIK TNVFKGYLKDPEKTQEALDSGWLHTGDI GRWLNPNGTLKI IDRK KNIFKLAQGEYIAPEKINIYNSQPVLQIFVHGESLRSSSLVGV VVPDPTDVLPSFAAKLVGKGSFEELCQNQVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEFFSIENGLLTPTLKAARGELSKYFRTQ IDSLYEHIQD |
| 5452 | 1833 | 1138 | SRVPSLCLSLSLSPSPREP VAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSLCLALSVLLLAQLSDAANKFEDVRCKICPPYKENS HIYNKNISQKDCDCLHVPEPMPVRGPDVEAYCLRCECKYEBRSS VTIKVTII IYLSILGLLLYMVYLTVEPILKRRLFGHAQLIQS DDDIGDHQPPFANAHDLARSRSRANVLNKVEYAQQRNKLQVQE RKSVFDRHVLS |
| 5453 | 111 | 1520 | PSIPAAVPQSAPPEPHREETVTATATSQVAQPPAAAAAPGEQAV AGPAPSTVPSSSKDRPVSPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAVCELODRKLTKEERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKCIVLVTELMSTGTLKTYLKRKFKVMKIKVL RSWCRQILKGLQLHTRTPPI IHRDLKCDNIFITGPTGSGVIGD LGLATLKRAFSKSVIGTPEFMAPEMYEKEYDESVDVYAFGCM LEMATSEYPYSECNAAQIYRRVTSVVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLNLHAFQEETGVRVELAEBDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRREORQL* |
| 5454 | 111 | 1520 | PSIPAAVPQSAPPEPHREETVTATATSQVAQPPAAAAAPGEQAV AGPAPSTVPSSSKDRPVSPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAVCELODRKLTKEERQRFKEEAEMLKGLQHPNI |

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|------------|--|--|---|
| | | | <p>VRFYDSWESTVKGKKCIVLVTLMSTGTLKTYLKRPVKMKIKVL RSWCRQILKGLQLHTRTPPIIHRDLKCDNIFITGPTGSGVKIGD LGLATLKRAFAKSVIGTPEFMAPEMEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLGKGYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKRQRL*</p> |
| 5455 | 1359 | 377 | <p>LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ WVRGKAYLRNAVVIITGATSLGKCEAKVFYAAGAKLVLCGRNG GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAIL QCFGYVDILVNNAGISYRGTIMDTTVDVDRVMETNYFGPVALT KALLPSMIKRRQGHIVAIISSIQGKMSIPRSAYAASKHATQAFF DCLRAEMEYQIEIVTVISPGYIHTNLSVNAITADGSRYGVMDDT TAQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRITLAPG LFFSLMASRARKERKSKNS</p> |
| 5456 | 2 | 2332 | <p>CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPKHSFGACG TEVMDMPQRPSPLEEVKGNIELKRPLIKAPSQPLSGSRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPVPSLTTPVQTQGGTTA QKVSCKTGPSTAIATGLKNQKVPVAVPVQKSGTSGVPPMAGG KKPSKRPAPDLKGLCDLNAELKRCRERTQTLDQENQQLQDQLR DAQQVQKALGTERTTLEGLAKVQAQAEQGGQELKNLRACVLEL EERLSTQEGVLQELQKKQVELQEERRGLMSQLEEKERRLQTS ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRLHNLQ QELKGNIRVFCRVRPVLPGEPPTPPGLLFPSPGPGSDPPTRL SLSRSDERRGTLGAPAPPTRHDFSFDRVFPSPGSGQDEVFEEIA MLVQSALDGYVPCIFAYGQTGSGKTFMEGGPGGDPQLEGLIPR ALRHLFSVAQELSGQGWTSYFVASVYIYNETVRDLLATGTRGK QGGECEIRRAGPGSEELTVTNARYVPVSCKEVDALLHLARQNR AVARTAQNERSRSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG SERLDPLGALGPGERERLRETQAINSSSLTGLVIMALSNKESH VPYRNSKLTLYLLQNSLGGSAKMLFVNISPLEENVSESLNSLRF ASKVEPSVLFGTASNRKWKTDPDLCVCCVCCVCCVCCVCCV MSMYRVRGGRVAGGCFIGWRAPCPRAIK</p> |
| 5457 | 2 | 1540 | <p>DDFVERRRWRTRTCLVRSPPHVPVCGHACSWNGGSLDPLKGT LLRSAERLMRKVKLLRLDKENTGSWRFSLSNSEGAEARMATGTP TADRGDAATDDPAARFQVQKHSWDGLRSIIHGSRYSGSLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLSWKQMLDHPQATPHHGVSREEELLRERKRLGVFGI TSYDFHSEGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDPPKSAGVATFVIEEFDRFTGYWNCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPT GSKNPKIALKLAEFQTDSSQKIVSTQEKELVQPFSSLPKVEYI ARAGWTRDGKYAWAMFLDRPQWLQVLVLPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLLDQCS</p> |
| 5458 | 6642 | 4022 | <p>FVPGLEPQWEPAPQPSATMSAPSEEEYARLVMEAPFWLRAEV KRLSHELAEATTREKIQAAEYGLAVLEEKHQLKQFEELEVDYEA IRSEMEQLKEAFQQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLQELQELKQLRNVLTNTQSENERLASVAQELKEINQV QRRLRDDIKYKFREARLLQDYSELEENISLQKQVSVLRNQ VEFEGLKHEIKRLEETEYLSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAAELVNGFEHGGAKLPLDNKTSTPKKEGLAPSPSPLSV DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSDHEDG DYVEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAA HAEKGRYEAEGQALTEKVSLEKASRQDRELLARLEKELKVS DVAGETQGSLSVAQDELVTFSLEELANLYHHVCMCNETPNRVML DYYREGQGGAGRTSPGGRTSPGARRSPILLPKGLLAPAEAGRA DGGTGDSSSPGSSPLSPSPLSDPRRPMNIYNLAIIRDQIKHLQ AAVDRTTELSRQRIASQELGPAVDKDEALMEEILKLSLLSTK</p> |

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|------------|--|--|--|
| | | | REQITTLRTVLKANKQTAEEVALANLKSXYENEKAMVTETMMKLR NELKALKEDAATFSSLRAMPATRCDEYITQLDEMQRQLAAAEDE KKTLSLLRMAIQKQLALTQRLELLELDHEQTRRGRAKAAPKTK PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD |
| 5459 | 316 | 1262 | RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLIVFKKASS KGPKRLEKFSDEAAAYFRCHYKVTENNVKNVARLPKSTKKHAI GIYFNDTSKTFACESDLEADWCKVLQMECVGTRINDISLGE DLLATGVVEREQSERFNVYLMPSPLNGCYMGECALQITYEYICLW DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCTEGELFIF QTRDGEAIYQKVHSAALAAIEQHERLLQSVKNSMLQMKMSERAA SLSTMVPLPRSAWQHITRQHSSTGQLYRLQDVSSPLKLHRTET PAYRSEH |
| 5460 | 45 | 2097 | RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSDDGNKKS ASEGSSSKSGSGNSGKGGNQLRCPKCGDLCTHVETVSSSTRFVK CEKCHHFFVVLSEADSKKSIKEPESAAEAVKLAQQKPPPPPK KIYNYLDKYVVGQSPAKKVLSSVAVYNHYKRIYNNIPANLRQQA VEKQTSLSLTPRELEIRREDEYRFTKLLQTAGISPHGNALGASMO QQVNVQIPQEKRGGEVLDSSHDDIKLEKSNILLGPTGSGKTL AONTLAKCLDVFAICDCTTLTQAGYVGEDI ESVIAKLLQDANY VEKAQQGIVFLDEVKIGSVPGIHQLRDVGGEGVQQGLLKLLEG TIVNVPEKNSRKLGRGETVQVDTTNILFVASGAFNGLDRIISRR NEKYLGFPTPSNLGKRRRAAAAADLANRSGESNTHQDIEEKDRL LRHVEARDLIEFGMIEPEFVGRPLVVVPLHSLDEKTLVQILTEPR NAVIPQYQALFSMDKCELNVTEALKAIRLALERKTGARGLRS IMEKLLLEPMFEVPPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES SEEEYDSGVVEEGWPRQADAANS |
| 5461 | 1481 | 160 | INPPPPPKSPCGRRARKWRRRRRFGAPEAAVMELPSGPGPERLFD SHRLPGDCFLLLVLLLYAPVGFCLLVLRFLGIHVLVSCALPD SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLSNHVTPFDH NIVNLLTTCSTPLNSPPSFVCWSRGFMENNGRGELVESLKRFC ASTRLPPTPLLLFPPEEATNGREGLLRFSWFFSIQDVVQPLTL QVQRPLSVSVTSDASWVSELLWSLFVPFTVYQVRNLRPVHRQL EANEFEALRVQQLVAKELGQTGTRLTTPADKAHMKRQRHPRLRP QSAQSSFPSPGSPDPVQLATLAQRVKEVLPVPLGVIRDLAK TGCVDLTITNLEGAFAVMPEDITKGTQSLPTASAKFPSSGPV TPQFTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD |
| 5462 | 663 | 3353 | KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA RLNGSFPASPLTNSRGSVHTVSFLQLIGLTRESVTIEAQELSL SAVKDLVCSIVYQKFPCEGFFGMYDKILLFRHDMNSENILQLIT SADEIHEGDLVEVLSALATVEDFOIRPHTLYVHSYKAPTFCDY CGEMLWGLVRQGLKCEGCGLNHYKRCAPKIPNNCSGVRKRRLSN VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI WMEKVMVCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDIDIPMDIN NDINSDSSRGLDDTEPSPPEDKMFFLDPSDLDERDEEAVKTI SPSTSNIPLMRVVQSIIKTKRKSSTMVKEGMMVHYTSRDNLRK RHYWRDLSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIIITDTMVYFVGENNGDSSHNPLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGDHDKDLSTSISVSNQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHKRTGRDVAIKVIDKM RFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERFVVMK LHGDMLEMILSSEKSLRPERITKFMVTQILVALRNLFKNIVHC DLKPEVLLASAEPPQVKLCDFGFARIIIGKSPRRSVVGT PAYLAPEVLRSGYNRSLDMSVGVIIYVSLSGTFPNEDEDINDQI QNAAFMYPPNPWREISGEAIDLINLLQVKMKRYSVDKSLSH WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP KHFIAPNPDDMEEDP |
| 5463 | 237 | 1012 | LLSVTMTTSRCSHLPEVLFDCTSSAAPVVKTVEDCGSLVNGQPQ YVMQVSAKDQQLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL |

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|------------|--|--|---|
| | | | LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR PLVEWLRNPGPQHEKRTLFQDMVCFITPLATISGWLCLRGAV DHLHFSSRLAEAVGLIALTVALFTIYLPWTLVSFRYHCRLYNEWR RTNQVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV |
| 5464 | 195 | 677 | SPSMNPRKKVDLKLITVGAIGVGKTSLLHQYVHKTFYEEYQTTL GASILSKIIILGDTTLKLQIWDTGQQRVSRMVSTFFYKSGDGI LAFDVTDLSEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPDQSRSRCC |
| 5465 | 5278 | 3348 | KGDPPREFIRVHREALECDYVSAHLHEWIDLIFGYKQGGPAAVEA VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHLDNLRPSLTPV KELKEPVGQIVCTDKGILAVEQNKVLIPTWNKTFANGYADLSC RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC VWEMGTSKEKAKTVTLQALLGHTDTVTATASLAYHIIVSGSR DRTCIWDLNKLSTLTLRGRHAPVSALCINELTGDIVSCAGTY IHVWSINGNPVSVNTFTGRSQIICCCMSEMNEWDTONVITG HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ DEDSSDSEADEQSIQDPKDTSPQPSSTSHRPRASCRATAAWC TDSGSDSSRRWSDQLSLDEKDGFI FVNYSEGQTRAHLQGPLSH HPNPIEBVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHPA EVTALGISKDHSLILVGDSRGRVFSWSVSDQPGRSAADHWVDE GGDSCSGCVRFSLTERRHHCRCNGQLFCQKCSRFQSEIKRLKI SSPVVVCQNCYYNLQHERGSEDPGRNC |
| 5466 | 3 | 992 | HACAHASAHASGRLVVRWRKRSSVMGIQTSPLVLLASLGVLVTL LGLAVGSYLVRSSRPQVTLDPNEKYLRLLDKTTVSHNTKRF RFALPTAHTLGLFPVGKHIYLSRIDGSLVIRPYTPVTSDEDDQ YVDLVIKVYLKGVHPKFPEGGKMSQYLDLKVGDVVEFRGPSGL LTYTGKGFNIQPNKSPPEPRVAKLGMIAAGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIIILREDEELQARYPNRFLW FTLDHPPKDWAYSKGFVTADMIREHLPAAGDDVLVLLCGPPPMV QLACHPNLDKLGYSQKMRFTY |
| 5467 | 2103 | 4 | GEALRVGTGRCDRLPDPQARIFIQKKDLEEDSVTAAHLKSRG RSPRKIDQCNSSNMVHGSVTFRDVAIDFSQBEWECLQPDQRTL YRDVMLENYSHLISLAGSSISKPDVITLLEQKEPVMVVRKETS RRYPDLLEKYGPEKVSPENDTSEVNLPKQVIQISTTLGIEAFY FRNDEYRQFEGQYQEGNINQKMSIYEKLPHTPHASLICNT HKPYECKEKGKYSFGSGLNIQHQS IHTGKPKYCKEKGKAFQLH IQLTRHQKFTGKTFECKEKGKAFNLPTQLNRHKNHTVKKLF ECKEKGKSFNRSSNLQHQSIHAGVKPYQCKEKGKAFNRGSNLI QHOKIHSNEKPFVCKEKGMAFRYHYQLIEHCQIHTGKPFCKE CGKAFTLTLKVRHQIHTGKPFCKEKGKAFSLNLQNRHKN IHTGKPFCKEKGKSFNRSSNLVQHQS IHAGIKPYECKEKGK FNRGAHLIQHQIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG DKPFECQDCGKAFNRSSSLVQHQS IHTGKPKYCKEKGKAFRLY LQLSQHQKTHTGKPFCKEKGKFFRRGSNLNQHRS IHTGKPF ECKEKGKAFRLHMLIRHQKLHTGKPFCKEKGKAFRLHMLI RHQKLHTGKPFCKEKGKVFSLPTQLNRHKNHTGKAS |
| 5468 | 225 | 2976 | SFLTDLFQSLAQLENLCKQLYETDTTTLQAEKALVEFTNSPD CLSKCQLLLERGSSSYQLLAATCLTKLVSRINNPLPLEQRIDI RNYVNLNLYLATRPKLATFVTOALIQLYARITKLGFDCQKDDYVF RNAITDVTRFLQDSVEYCIIGVTILSQTNEINQVSATAFLIEA DTTHPLTKHRKIASSFRDSSLDFITLSCNLLQASGKNLNLND ESQHGLLMQLLKLTHNCLNDFIGTSTDESSDDLCTVQIPTSWR SAFLDSSTLQSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL VCRVLQMLNLTDSRLAQAGNEKLELAMLFFEQFRKIYIGDQVQ KSSKLYRRLSEVLGLNDETMLSVFIGKIITNLKYWGRCEPITS KTLQLLNDLSIGYSSVRKLVLKSAVQFMLNHTSEHPSFLGINN QSNLTDLMCRRTTFYALGRLLMVDLGEDEDEQYEQFMLPLTAFA AVAQMFSTNSFNBQEAARTLVGLVRDLRGIAFAFNAKTSFMMLF EWIYPSYMPILQRAIELWYHDFACTTFLVCLKMAELVHNRSQRLQ |

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|------------|--|--|---|
| | | | FDVSSPNIGILLFRETSMKMTMYGNRILTLGEVFKDQVYALKLKG ISICFMSMLKAALSGSYVNFVFRLYGDDALDNLQTFIKLLLSI PHSDLLDYPKLSQSYSLLEVLTQDHMNFIALEPHVIMYILSS ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ ESDRFLHIMQQHPMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG LILLNEKYFSDLRNSIVNSQPFQQAAMHLCFENLMEGIERNLL TKNRDRFTQNLASAFREVNDMSKNSTYGVNSNDMMMS |
| 5469 | 134 | 2653 | DOEFETSLVPWHLPMGWLCGSLLPVSVCLVLQVASSGNMKVLQ EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLEAHTC VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSKPS EHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPDPNLYNHLTYAVN IWSENDPADFRIYNYTYLEPSLRIAASTLKSGISYRARVRAWAQ CYNTTWSEWSPSTKWHNSYREPFQHLGLGVSVSCIVILAVCLL CYVSIKIKKEWWDQIPNPARSLVAIIQDAQGSQWEKRSRQG EPAKCPHWKNCCLTKLPCPLEHNMKREDPHKAAKEMPFQSGSK SAWCPVEISKTVLPESISVVRVCLPEAPVECEEEEEVEEEKQ SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGFCQDQ MGESCLLPSPGSTSAHMPWDEFPSSAGPKEAPPWGKEQPLHLEPS PPASPTQSPDNLTCTETPLVIAGNPAYRSFNSLSQSPCPRELQ PDPLLARHLEVEPEMPCVPQLSEPTTVQPEPETWEQILRRNV LQHGAAAAPVSAPTSGYQEFVHVEQGGTQASAVVGLGPPGEAG YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDP PVPVPLFTFGLDREPPRSPQSSHLPPSSPEHLGLEPGEKVEDMP KPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGQ QTPVMASPCCGCCCGDRASPPTTFLRAPDPSGGVPLEASLCPA SLAPSGISEKSKSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM RVS |
| 5470 | 17 | 1418 | TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMDSF KNVGLVFNKSRDRTKAVLCMVVAGATAAVFHTLIAYSDLGYYI INKLHHVDES VGSKTRRAFLYLAAFPMDAMAWTHAGILLKHXY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPIILSLYMG LVRCTTLCGLYYKNIHDIIPDRSGPELGGDATIRKMSLFWWPLA LILATQIRSRPIVNLVSRDLGSSAATEAVAILTATYVGHMP YGLWTEIRAVYPAFDKNPNPNKLVSTSNVTAAHIKKFTFVCM LSLTLCFVWFMTPNVSEKILIDIIGVDFAFELCVPLRIFSPF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIVLIALSVLPLVL GVHGATLGVSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPTTEVTDIVEMRENE |
| 5471 | 1868 | 658 | RSSAPPGPQRAAAATAAAAAAGVMAAAAAAGGGGGEPRTTEGV GPGVPGEVEMVKGQPFDPVGPRTYQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFQHTYQRTLREIQILLRFRHENVIGIRDILR ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKI CDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLSKGYTKSIDIWSVGCILAEMLS NRPIFPKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAAWAKLPKSDSKALDLDRLMTFNPKNKRITVEEALAHF YLEQYYDPTDEPVAEPEPTFAMELDDLPERLKLIFQETARFQ PGVLEAP |
| 5472 | 1469 | 753 | LYVMARYLSDEEVAVSIDRLCKANGRSFSPFPGTVRIIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQDGFHR GSDKMPGRVVTLLDHEGCTWGVAYVQVQGEQVSKALKYLVNREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTQALALV |
| 5473 | 3 | 2119 | FMNVKLLIQDLEDIEQRPVMDAQYKIIITTAHLITKESPOQEG KMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLELEKQMTS FYDSLKGKINEIITVLREAQSSALFKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLNVLKHFQDTRLQRIADIHVAFQSMVKK TGDWKKHVETNSRLMKKFESRAELEKVLRIAQEGLEBKGDPEE LLRRHTEFFSQDQRLNLAFLKACDELTDILPEQEQQGLQEA VRLKHQWKLQGEAPYHLHLKIDVEKNRFLASAECELTEDRET |

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|------------|--|--|---|
| | | | KLMPQEGSEKIIEHRVFFSDKGPVHLCERLQLIEELCVKLPV RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS EFSSWISTNETQLKGIGEAIDTANHGEVRAVEEIRNGVTNRG ETLSWLKSRLLKVLTEVSSSENAQKQGDDELAKLSSSFKALVTL EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQABKILDT NLFEAQQLLLHHQKTKRISAKKRDVQQQIAQAQQGEGGLPRG HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTEIAVQAEN LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYVIDK S |
| 5474 | 2 | 780 | TPDVRQLQASRRGI AVASWCSPRWFAGEEMAFVKSGLLRQSTI LKRWNKNWDLWSDGHLIYYDDQTRQNI EDKVHMPMDCINIRTG QECRDTPPDGKSKDCMLQIVCRDGTISLCAESTDDCLAWKFT LQDSRTNTAYVGSAMVTDTSVSSPPPYTAYAAPAPEVGRSL LQQAQYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYQQ PANQVIIRERYRDNDSDLALGMLAGATGMALGSLFWVF |
| 5475 | 2 | 506 | ARGWLESLSLTCTTPPPSSPLLHSPETFIHTMPPNLTGYR VSQKNMEDYLQALNISLAVRKIALLLKPKDKEIEHQGNHMTV STFRNYTVQFDVGVFEEDLRSVDGRKQCQITVWEEHLVVCVQ GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR |
| 5476 | 192 | 1457 | SDSMSLLDCFTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYELQVEIGRFPDNLTSVHLARHTPTGL VTIKITNLENCNEERLKLKAVILSHFRHPNITTYWTVFTVG SWLWVISPFMAYGASQLRITYPEGMSETLIRNIFGAVRGLN YLHQNGCIHRISIKASHILISGDGLVTLGSLSHLSLVKHGQRH AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSIDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPYSPDLDISIFPQSESERMKNS SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQDDPEKRPSASSLLSHVFFKQMKESQDSILSLPPAYNKPISI SLPPVLPWTEPECDPPEKDSYWEF |
| 5477 | 3 | 1044 | RGNSRLRYSHDELQPLPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLEKAAEMLSQLDLFSRNEDEEIASTDLYLLV PAFQGALTMKQVNP SKRLDHLQRAREHF INYLTQCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQROAKIQRKQKKELE HRLSAMKSAVESGQADDERVREYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIKAAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG |
| 5478 | 2 | 835 | KTVRIWVPNVKGESTVFRHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTVDFHPSGTCLAAAGMDNTVKVW DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVWKS NFDIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP |
| 5479 | 2 | 835 | KTVRIWVPNVKGESTVFRHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTVDFHPSGTCLAAAGMDNTVKVW DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVWKS NFDIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP |
| 5480 | 444 | 1952 | LSLSRMEEAELVKGRQLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKALREKWLLDGISSGKEQEEMKQKQNDQHQIQVLEQSI LRLEKEIQDLEKAEQISTKEAILKKLKSIBRTTEDIIRSVKV EREERAESIEDIYANIPDLPKSYIPSRRLKEINEEKEDDEQNR KALYAMEIKVEKDLKTGSTVLSSIPLPSDDFKGTGIVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNKSPTEYH EPVYANPPYRPTTPQRETVPFPNFOBRKIKITNGLGIGVNESI HNMGNLSEERGNFNHISPIPPVPHPRSVIQAAEKLHTPQKR |

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|------------|--|--|---|
| | | | LMTPEESNVMDKAPSPKPRLSPRETI FGKSEHQNSSPTCQE DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT GYDGIHAELVVIDDEEEDEGEAEKPSYHPIAPHSQVYQPAKP TPLPRKRSEASPHEKHKHS |
| 5481 | 3 | 1422 | NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLLHESQPQPALRV VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV QGLNEAGDDLEAVAKFLDSTGSRDLYRRYADTLFDILVAGSMLA PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK YLEKAFEDEMKKLLFLKAFSETEQTKLAMLSGILLNGTLTPAT ILTSLFTDSLVEGIAASFVKLFKAWMAEKDANSVTSRLRKAN LDKRLLELPVNRQSVDFHAFKYFTDAGLKELSDFLRVQQSLGTR KELQKELQERLSQECPIKEVVLYVKEEMKRNLDLPETAVIGLLWT CIMNAVWVNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL OKVQVEYCYDNIHFMAFQKIVLVFYKADVLSEEAALKWYKEAHV AKGKSVFLDQMKKFVWELQNAEESESEGEEN |
| 5482 | 1492 | 528 | THVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSRL BGLQEKDGGPYSCSVNVQDKQKSRGHSIKTLELNVLVPPAPS CRLQGVPHVGANVTLSQCSPRSKPAVQYQWDRQLPSFQTFPAPA LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVLEVSTGP GAADVAGAVVGTGLVGLGLAGLVLLYHRRGKALEEPANDIKEDA IAPRTLWPWKSSDTISKNGTLSSVTSARALRPPHGPFRPGALTP TPSLSSQALPSPRLPTTDGAHPQPIPIPGGVSSGLSRMGAVP VMVPAQSQAQGLV |
| 5483 | 1 | 788 | FFFFGCRAGRGNESDYRKLEEMHQRFLVSESKDDLQRLRLTRA ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL KLQENKQLRKETESLRKIALEAQKAKVKISTMEHEFSIKERG FEVQLREMBDSNRNSIVELRHLLATQQKANRWKEETKKLTESA EIRINNLKSELSRQKLHTQELLSQLEMANEKVAENKILIEHQE KANRLQRRLSQAEERAASASQOLSIVITVQRRKAASLMNLENI |
| 5484 | 3 | 1997 | IMADMEDLFGSDADSEAEKDSDSGSDSDSDQENAAAGSNASGS ESDQDERGDSGQPSNKLFGDDSEDEGASHHSGSDNHSERSDN SEASERSDHEDNDPSDVDQHSQSEAPNDDDEGHRSDGGSHHSE AEGSEKAHSDDEKQWREDKSDQSDDEKIQNSDDEERAQGSDEDK LQNSDDDEKMQNTDDEBRPQLSDDERQQLSEEEKANSDDERPVA SDNDEKQNSDDEEQQLSDDEKMQNSDDERPOASDEEHRHSD EEEQDHKSESARGSDSEVLRMKRKNATASDSEADSDTEVPKD NSGTMDLFGGADDISSGSDGEDKPPTPGQFVDENGLPQDQQEE PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVPEPRFPDQYYE DEFDEEMLEDEGRTRLKLVKVENTIRWRIRRDEEGNEIKESNAR IVKWSGDSMSLHLGNEVFDVYKAPLOGDHNHLEFIRQGTGLQGQA VFKTKLTFRPHSTDATHRKMTLSLADRCSTQKIRILPMAGRD PECQRTMIKKEEERLRASIRRESQQRMRREKQHQGLSASYLE PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE EDKAQRLKAKKLTSDVVRPNLFNSRGLSCTQEPPTALNEELTDQ AGTN |
| 5485 | 161 | 1074 | KRKILSSMMDSEAEKRPILTSSKQDISPHITNVGEMKHLYCG CCAAFNNVAITFPIQKVLFRQOLYGIKTRDAILQLRRDGFNLY RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPFATSGVAA VLAGTTEAIFTPLERVQTLQDQKHHDKFTNTYQAFKALKCHGI GEYRGLVPILFRNGLSNVLFGLRGPIKEHLPTATTHSAHLVN DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFVKFQKI WLERDRKILINLFRGAHLNHYHRSLSISWGINATYEFLLKVI |
| 5486 | 1404 | 142 | IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR PAGKEAQKGPLLFDLLPASSTDSGSGGPLLFDLLPASSGDS GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVKCASSV IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRSY FAVFDGHGGIRASKFAAQNLHQNLIKRPKGDVISVEKTVKRCL LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLSKEHNPTQYERMRIQKAGGNVR DGRVLGVLEVSRISIGDQYKRCGVTSVPDIRCQLTPNDRFILL |

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|------------|--|--|--|
| | | | ACDGLFKVFTPEEAVNFILSCLEDEKIQTREKSAADARVEAAC NRLANKAVQSGSADNVTVMVVRIGH |
| 5487 | 535 | 182 | AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTALALLLAGLITA LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK CKCKSSQKQHSFVPEKAIPLITPGSATTC |
| 5488 | 1072 | 259 | AMAASGEFQRQWQEEVAAVVVVGSCTDLVSLTSRLPKTGETH GHKFFIGFGGKGANQCVQARLGAMTSMVCKVKGDSFGNDYIEN LKQNDISTEFTYQTKDAATGTASIVNNEGQNIIVIVAGANLLL NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL FNPAPAIADLDLPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE AALVLLKRGCCQVVIITLGAEGCVVLSQTEPEPKHIPTKVKAVD TTVSFKI |
| 5489 | 81 | 893 | GKGPVAAFIDQSNIFLTDPKIFLGQWREPEPKMPLLLLGETEPLK LEHDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIARKKQGEVVGFLANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGTEAQKEGSEDFG NLPEAQEKNEEEGETATEETEELAMEGAEGEAEETAEGEPEP GEDEDS |
| 5490 | 81 | 893 | GKGPVAAFIDQSNIFLTDPKIFLGQWREPEPKMPLLLLGETEPLK LEHDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIARKKQGEVVGFLANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGTEAQKEGSEDFG NLPEAQEKNEEEGETATEETEELAMEGAEGEAEETAEGEPEP GEDEDS |
| 5491 | 204 | 1194 | GSAPRLSLGPTGAQARDPDWARPPSRPYTQSKEDRPDTEGRSE QGDMASSFLPAGAITGDSGGELSSGDDSGEVFPSPHSEIETSC LAELFEKAAHLQGLIQVASREQLLYARYKQVKVGNCTNPKP SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKLDPGWNPQI PEKKGEANTGFGGPPVISSLYHEETIREEDKNIFDYCRENNIDH ITKAISKNVVDVNVKDEEGRALLHWACDRGHKELVTLLQHRAD INQDNEGQTALHYASACEFLDIVELLQSGADPTLRDQDGLCP EEVTGCKTVSLVLQRHTTGKA |
| 5492 | 3 | 1896 | ASKNPLSAVCTTGTIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE QLKIDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM RNINRGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGGP IDPEDAPESI TRAVASLPPEQMFELMKQMKLCVQNSHQEARNML LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSL SVSVSGPGPGPGPLCPGPNVLNQQNPAPQPQHLARRPVKDI PPLMQTPIQGGIPAPGPPIPAAVPGAGPGSLTPGGAMQPQLGMPG VGPVPLERGQVQMSDPRAPIPRGPVTPGGPLPPRGLLGDAPNDPR GGTLLSVTGEVEPRGYLGPPHQGPPMHASGHDRGPSSHEMRG GPLQDPRLLIGEPRGPMIDQRLPMDGRGGRDSRAMETRAMETE VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGFPVSSRGP MTGGIQGPGPINIGAGGPPQGPQVPGISGVGNPGAGMQGTGIG GTGMQAGIQGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ PSSFSPPQSQVTPQDQEKAAALIMQVLQTLADQIAMLPPEQRQSI LILKEQIQKSTGAS |
| 5493 | 1 | 1876 | RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPPTPVYREKEDMYDEIIELKKSILH VQKSDVDLMRTKLRLLEENSRKDRQIEQLLDPSRGTDVFRVTLA EKRPDASWVINGLQRIKLEQQCKEKDGTISKLTDMKTTNLC BMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLRSVQELTEENQSLKEDLDRVLSTSPITISKTQGYVW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLAASSAL HRQPRGRDNKDHERLARGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKLEECAREGEERREEREVLREEIQTLSKQLQELQEM KKEEKEDCEPVPHKAQELPAPTSSSRHCEQDWPDPSSBGLPFR RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR |

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|------------|--|--|---|
| | | | GHLTRTKLLASKAHGSEPPSVPLPDQSSPVPRVPSFIAQATGS PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASRRRSASAT HGDASSPPFLAALPDPSPSGQAVAPLPGDDVNSDDSDDIVIAP SLPTKNFPV |
| 5494 | 71 | 536 | RSKAKIGTPTREVPSTDMKVRRESSSSLTTHRPAPSPATPRLTGT RRVLLGVSBGTGCADAMELVLFCLSLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFSVGLILLILSRCKCSFNQKPRAP GDDEEQVENLITANATEPQKAEN |
| 5495 | 273 | 2168 | DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG ELRPASLVLPRLSLAPAFERFCQVNTGPLPLLGQSEPEKWMLEPP QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL GCSFSLLEEALAKGLPRRDPAGHSQAGAYKTTVPCVTHAGFCPP LVVTMRPIPKDKLEGLVLRACCSLGGEQGPVHMGDPPELLGIKEL SKPAYGDAMVCPPEVVPVFWPSPLTSLGAVSSCETPLAFASIPG CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ KIRELES MIGIDPGNRGIGHLLCKDELLKASLSLHARSVLIT GPPTHFNHEPPEETDGPAGVALVAFLOALEKEVAIIVDQRAWN LHQKIVEDAVEQGVLTQIPILTYQGGSEAAQAFCKNGDPQT PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDFIDDLFLAACK IPGISSTGVGDGNGELGMGVKEAVRRHIRHGDVIACDVEADFA VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGSPRAPGDA WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNT AEMIQLVDVTTAQV |
| 5496 | 3 | 2408 | QDTKMHEIYKGNITPQLNKNLTLSAATDVWAVYFSQFWIDYEG MKSCKGRPISEFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT SQSESSDLAGRLKRKKLLKEYYSTSEPLTNGGQKPPSSSDTFFR FSPSSSEADIHLLVHVHKKHVMQINHYQYLLLLFLHESLILLSE NLRKDVAVTGPASQTSICIGILLRSALALLHPVDQANTLK SPVSESVPVVDYLPTEGDFLSKKRQISRDINRIRSVTVNH MSDNRSMSVDLSHIPKDPPLLFKSASDTNLQKGISFMDYLSDKH LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE DSNILSFDSDGNQNILSSTLTSGKNETIESIFKAEDLLPEASL SENLDISKEETPPVRTLKSSQSSLSGKPKERCPPNLAFLCVSYKN MKRSSSQMSLDTISLDSMILEEQLES DSGSDSHMFLEKGNKNS TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS VVVKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ CHIKNFSTEPLTSSLMNIQHFLDEDETATVMFMKIQVSNKINL KDDSPRSSTVSLPAPVTVHIDHLVVERSDDGSFHIRDHMLNT GNDLKENVKS DSVLLTSGKYDLKKQSVTQATQTS PGVPWPSQS ANFPEFSFDFTREQLMEENBSLKQELAKAKMALAEAHLEKDALL HHIKMTVE |
| 5497 | 1821 | 3308 | SISKLLKRRSNIDAYLLSNSCAFFAPRLFLSLASQIIREQQSPNV CFIYKYSGFPSLEQCCHFVSPHSSCYINFFSFPFVFCQLSN GFSHYLSSESHVGPTGAGLFPCLPASRLPRVTSVHLPDYAH YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREP PNGGGPTTASGPPAAEEAQRPRSMTVSAAATRPGEEMEACEELA LALSRGLQLDQRRSRSLQCSSGYSTQTTTPCCSEDTIPSQVS DYDYFSVSGDQEQADQEQFDKSSSTIPRNSDISQSYRRMFQAKRPA STAGLPTTLGPAMVTPGVATIRTPSTKPSVRRGTIGAGPIPIK TPVIPVKTPTVPDLPGVLPAPPDGPPEERGEHSPSPSVGEGPQG VTSMPSMMWGGQASVNPPLPGPKPSIPEHRQAIPESAEDQER EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKKLKT TTNDRSAPRFS |
| 5498 | 2434 | 1492 | ILTHQEIFTGKPCBCGKASIOMSHLSQKIIYSGENPFACKVCG KVFSHKSNLTHEHFHTREKPFECNECGKAFSQKQYVIKHQNT TGEKLFECNECGKSFQKENLLTHQKHTGKPFECCKCGKAFI QKSNLIRHQRHTTGKPFVCKECCGKTFSGKSNLTHEKIHIGEK PFKCECGTAFGQKKYLIKHNHTGKPFYECNECGKAFSQRST LIVHVRHSGDKPYECNVCAGKAFSSSSLTVHVRSHSTGKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH |

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|------------|--|--|--|
| | | | QKIHTH |
| 5499 | 324 | 926 | GFGQIGRGHKITTYPPSPRKSGRKGMAQSQGWVKRYIKAFCKGF FVAVPVAVTFLDRVACVARVEGASMQPSLNPQGSQSSDVLLNH WKVRNFEVHRGDIVSLVSPKNPEQKIIRVIALEGDIVRTIGHK NRYVKVPRGHIWVEGDHGHGSFDSNSFGPVSGLLHAHATHILW PPERWQKLESVLPPELPPVQREEE |
| 5500 | 1978 | 1286 | KPDWRLQNLFPRLYLWRSRFRGFGHLKKRLQMDFKIEHTWDGFP VKHEPVFIRLNPGRGVMMDISAPFFRDPPAPLGEPPGKPFNELW DYEVVEAFFLNDITEQYLEVELCPHQHLVLLLSGRRNVWKQEL PLSPRVSRGETKWEKAYLPWSYPPNVTKFNSFAIHGSKDKRS YEALYPVQHELOQGOQKPDFHCLEYFKSFNFNTLLGEEWKQES DLWLIEKCDI |
| 5501 | 2927 | 2226 | CRFPVSARVAPGHQAVGGSGRRPARVEVVDAAARPSRRPFLP AATMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFFNVIA SGQFSEDMIPTVGFNMNRKVTKGNVTIKIWDIGGQPRFRSMWERY CRGVNAIVYMIDAADREKIEASRNELHNLDDKPKLQGIPLVLG NKRDLPNALDEKQKLEKMNLSAIQDREICCYSSCKEKNIDIT LQWLIQHSKSRSS |
| 5502 | 3 | 824 | NSAFPVWVPERTALLTCLGAAPGSSREAPGIAGPPNSTAMSKL GKFFFKGGSSSKSRAAPSQEAFLVRLRETEMLGKKQEVLENRIQ REIALAKKHGTQNKRAALQALKKKRFEKQLTQIDGTLSTIEFQ REALENSHTNTEVLRLNMGFAAKAMKSVHENMDLNKIDDLMQEIT EQQDIAQEISEAQSQRVGFDDDFDELMAELELEQEELNKKM TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT |
| 5503 | 216 | 654 | KGVRRGRVRSDESDSHLGYFKMSFLPKLTSKKEVDQAIKSTA EKVLVLRFRGDEDPVCLQLDDILSKTSSDLSSKMAIYLVDDVQDT AVYTYFDISYIPSTVFFNGQHMKVYDGGEDPALRSIKAVRRT SPAGTLGKEKPVNS |
| 5504 | 58 | 3563 | QLSFSFQAPVTFDDITVYLLQEEWVLLSQQKELCGSNKLVAPL GPTVANPELFRKFGRGPEPWLGSVQGRSLLEHHPGKKQMGYMG EMEVQGPTRSGQSLPPQKKAYLSHLSTGSGHIEGDWAGNRKRL LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL IEGYTGPFKVTETLYHAKSKAHMFCVNALAARDPIWAARFRSIR DPPGDVLASPELPTADCFIFYPPGFLGGFDSMAELLPSRAEL EDPGDGAI PAMYLDICISDLRQKEITDGIHSSDINILYNDAVE SCIQDPSAEGLSSEVPVVEELPVVFEDEVAVYFTREENGMLDKR QKELYRDVMRMNYELLASLGPAAPKDLISKLERRAAPWIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARAS CSSSICEGDPRIKRTYRPRSIRQSWFGQFPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVTETLYHEVSKAHLRCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAHRSRLN DFEKILQLLQSTGTIVLGKYRNRCTQFIKYISETLKRILEID VRNSPCVSVLLDSSDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDPFRKPGWVVLGTDGSAMLSR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLKVKCDRH IRTVKFYQSSNKRNLNELQEGAAPLEQEIIRLKDNLAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLDPLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKKEEFNASFKDGRHLGICLDKLEVAEQRFQADRRTV LTGIEYLQORFDADRPQLKNMEVFTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEALLBEWLGLKTAQHLFPFSLMCKNAL AQHCRFPFLSKLMAVVVCPISTSCCERGFKAMNRJRTDERTKL SNEVLNMLMTAVNGVAVTEYDPPQAIQHWYLTSSGRFRFSHYVT CAQVPARSPASARLRKEEMGALVVEEPRTPQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS |
| 5505 | 3312 | 1219 | NCSPRSLSAAKMNRRNNKLPNLPQLQNLKIKRDPAYIEEFLQ QYNHYKSNVEIFKLQPNKPSKELAEVMPMAQISHCYPEYLSNF PQEVKDLLSCNHTVLDPLRMTFCKALILLRNKNLINPSSSLEL FFELFRCHDKLLRKTLYTHIVTDIKINAKHKNNKVNVLQNF |

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|------------|--|--|--|
| | | | YTMRLDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK VTKILVAALTFFLGKDEDEKQSDSEEDDGPTARDLLVQYATG KKSSKNKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPODFA EKLLKQLECCKERFEVKMMLNLSRLVGIHELFLNFYFPFLQR FLQPHQREVTKILLFAAQASHHLVPEIIQSLLMTVANNPVTDK NSGEVMTVGINAIBITARCPLAMTEELLQDLAQYKTHKDKNVM MSARTLIHLFRTLNPQLQKKFRGKPTASIEARVQYEGELDAK DYIPGAEVLEVEKEENAENEDGWESTSLSEEDADGEWIDVQH SSDEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM AQMRELDAAPGKSQKRKYIEDSDDEEPRGELLSLRDIERLHKK PKSDKETRLATAMAGKTDRKEFVRKTKTNPFSSSTNKEKKKQK NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK |
| 5506 | 1 | 1531 | FRGDLCCGQGGGSAFEGGGSSAWPAPAHPLPEREREREALCPGRS CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFYRWAVVV LAAPPSLGAGGETPEAPPESWTQLWFRRPVVNAAGYASFMVPGY LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVFLAPRT EAAETTPMWQALKLLFCATGLQVSYLTWGLQERVMTRSYGATA TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY SFASLSNVLSWQYEALEKFSFPTQVLAKASKVIPVMLMGKLV SRRSYEHWEYLTATLISIGVSMFLSSGPEPRSSPATTLISGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFSCFLTGVSL LEQGALLEGTRFMGRHSEFAAHALLSICSACGQLFIPYITIGQF GAAVPTIIMTLRQAFALLSCLLYGHTVTVVGGLGVAVVFAALL LRVYARGRLKQRGKKAVPVESPVQKV |
| 5507 | 3704 | 1271 | PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGFGTAAGKK VAVADVQFGPMRFHODQLQVLLVFTKEDNQCNGFCRACKAGFK CTVTKEAQAVLACFLDKHHDIIIDHRNPRQLDAELCRSIRSS KLSENTVIGVVRRVDREELSVMPPISAGFTRRVVENPNIMACY NELLQLEFGEVRSQKLKLRACNSVFTALENSEDAIEITSEDRFIQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWQGIYAKKNGDNIQQNVKIIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRKGSLDVKAVASRAT EVSSQRRHSSMAIHSMTIEAPITKVINIINAAQESSMPVTEA LDRVLEILRTTELYSPQGAQDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSNNIITPISLDDVPPRIARAMENEYWDPI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHVDVHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMILI KCADVSNPCRPLQYCIWAARISEEYFSQTDEEKQQLGVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMOHLDDNF KYWKGLDEMKLRLRPPPE |
| 5508 | 1151 | 691 | LSSVFSRRSASMFAVGCSMGPFLLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLGQTVGESQELREKFW EFYKADWCWPAAQFVNFLFVPPQFRVTYINGLTGLWDYLSYL KYRSPVPLTPPGCVALDTRAD |
| 5509 | 1238 | 619 | RKSRGQCNALSASGPAAAAAAMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRLVLRRLQRRREDYTRYNQLSRAVRELARLRDL ERDQFRVRASAAALDKLYALGLVPTRGSLLELCPVTASSFCRRR LPTVLLKLRMAQLQAQAVFVEQGHVRVGPVVDPAFLVTRSM EDFVTWVWSSKIKRHVLEYNEERDDFDLEA |
| 5510 | 96 | 1195 | PAGAHSSGSSEPLEVEPGRGRVGRVKGRLQASGSAPGRSKM AEGERQPPDSSBEAPPATQNFIPKKEIHTVPDMGKWKRSQAY ADYIGPILTLNEGKGGKLTFFYRVSEAIEKLVALNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEBAENLVATVPTHAAVAP EVAVYLKESVGNSTRIDYGTGHEAAFAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNIISAVPWSKVNQGLIRMYKAECLKFPVIQHF KFGSLPIHPVTSG |

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|------------|--|--|---|
| 5511 | 276 | 1980 | KLSRVNLNPPENLITSISAVPISQKEEVADFQLSVDSLLEKDNH HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKNRELTLK TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKPHVG HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL FGYEEKLQSNPLQHLFEVYVQVNKEAADKSVAKAAQEFFQRLE LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK SQEVLKLLSKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT SLYATRDLAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI MGYDWAERCQHVFPVGVQGMKTRRGDVTFLVDLNEIQLRMLQN MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFWSWR VFQSRGDTGVFLQYTHARLHSLLEETFGCGYLNDFNTACLQEPQS VSIQLHLLRFDEVLYKSSQDFQPRHIVSYLLTLHLAAVAHAKTL QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM |
| 5512 | 120 | 1015 | DPSLLLTITVTGVTVLVVLKSMNSRRREPITLQDPEAKYPLPL IEKEKISHNTRFRFLGPSFDHVLGLPVGNVYQLLAKIDNELVV RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK IGETIFFRGRGRLFYHGPNGNLGIRPDQTSSEPKTLADHLGMIA GGTGITPMLQLIRHITKPSDRTRMSLIIFANQTEEDILVRKELE BIARTHDPQDFLWYTLDRPPIGWKYSSGFVTADMIKEHLPFPAK STLILVCGPPPLIQTAAHPNLEKLGTYQDMIFTY |
| 5513 | 2 | 837 | ARWRLPSDSPRIIPAGAETPGRGSCRNYLPSSSPFPEPSSPFS PPTSRRGGPGSRDMSDEESQDRQLKIVVLGDGASGKTSLTTC FAQETFGKQYKQTIGLDFLRITLPGNLNVTLQIWDIGGQTIG GKMLDKYIYGAQGVLLVYDITNYQS FENLEDWYTVVKKVSESE TQPLVALVGNKIDLEHMRITKPEKHLRFCEQENGFSHFVSAKTG DSVFLCFQKVAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS RTVNPPRSSMCAVQ |
| 5514 | 1295 | 449 | VNRPSWIMGNFRGHALPGTFFFIIGLWCTKSILKYICKKQKRT CYLGSKTLFYRLLEIGITIVGMALTMAGBQFIPGGPHMLLYD YKQGHWNQLLGHWHFTMYFFGLGVADILCFTISSLPVSLTKL MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAF EPLVRNNVLELLRSSLIILQGSWFFQIGFVLYPPSGGPAWDLN DHENILFLTICFCWHYAVTIVIVGMNYAFITWLKVSRLKRLCSS EVGLLKNAEREQESEEM |
| 5515 | 1572 | 260 | FVRLVGRGDCDPLLSVCLTTPPLYEGLSGGGEKTAVIDLGEAF TKCGFAGETGPRCIIPSVIKRAGMPKPVVVQYNINTEELYSL KEFIHILYFRHLLVNPDRRVVIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALLTLGINSAMVLDGYSRESLVLPYEGIP VLNCWALPLGGKALHKELETQLLEQCTVDSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRLKIAAKFNIDGNNERPSPFP NVDYPLDGEKILHILGSIKSDSVVEILFEQDNEEQSVATLILDSL IQCFIDTRKQLAENLVVIGGTSMLPGFLHRLLEIRYLVEKPKY KKALGTKTFRITHTPPAKANCVAWLGGAFI GALQDILGSRVSKE YYNQTGRI PDWCSLNNPPEMMFDVGKTQPLMKRAFSTEK |
| 5516 | 3 | 735 | NSREPPQAGPGSPRKSPTASSFLFPWRPLASSFWMGAGGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLTALLGGPTWAG KMYGPGGGKYPSTTEDYDHEITGLRVSVGLLVKSVQVKLGDSW DKLGLGAGGNTQEVTLQPGYEITKVFAVQAFLRGMVMTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYANSVPGR |
| 5517 | 246 | 499 | SEIYVAMRTDSSKMTDVEGSGVANFASSARAGRNRNALPDIOSSAA TDGTSDLPLKLEALS VKEDAKEKDEKTTQDQLEKPNQEEK |
| 5518 | 3 | 1375 | DAWADAVVRAWDLNMDFFCLWLGLLLPLVAALDFNYHROEGMEA FLKTV AQNYSVTHLSIGKSVKGRNLWLVVGRFPKEHRIGIP EFKYVANMHGDETGRELLHLIDYLVTS DKGKDEITNLINSTR IHIMPSMNPDGFEAVKKPCDYYSIGRENYQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETVLSANLHGALVASYPFDNGVQA TGALYSRSLTPDDDV FQYLAHTYASRNPNMKKGDECKNMNFNP GVTNGYSWYPLQGGMQDYNIIWAQCFEITLELSCCKYPREKLP SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVI VEVDQRK |

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|------------|--|--|---|
| | | | HICPYRTNKYGEYLLLLPGSYIINVTPGHDPHITKVIPEKS QNFSAKKDILLFPQGLDSIPVSNPSCPMIPLYRNLPDHSAAAT KPSSLFLFLVSLHHIFFK |
| 5519 | 87 | 477 | IKSKLNQQVEVQSEWRLEAKGPTMGKESGWDSGRAAAVAVVG GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGVA AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS |
| 5520 | 117 | 943 | PTEGRQKVLKFTTVPRSALAMTKTSTCIYHFLVLSWYTFLLNYII SQEGKDEVKPKILANGARWKYMTLLNLLQTIFVGVTCDDVLK RTKGGKDIKPLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLPHSVPSKKTGL TLLAAASIAIYISRLWLYFETGTWVVPVFAKLSLLGLAAFFSL S YVFIASIIYLLGEKLNHWKWSVQILQRWRLESVGICFQWPDWKS PAKHQLVKNI |
| 5521 | 546 | 911 | KILNMQKSCENEKGKPNMPKAEEDRPLEDVPQEAEGNPQPSEE GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER LREEIRRVNKNFVMMHWKQRHSRSRPPVPCFRP |
| 5522 | 1224 | 637 | GSRPLGQRSREKMMVFGYGLIWKVDFFPYQDKLVGYITNYSRRF WQGSTDHRGVPGKPGRVTLVEDPAGCVWGVAYRLPVGKEEVK AYLDFREKGGYRTTTFIFYPKDPPTKPFVLLYIGTCNDPDLG PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEADEHL FALEKLVKERLEGGKQNLNCI |
| 5523 | 3 | 1280 | SKGKKRMGSSMSAATARRPVFDDKEDVNFDFHQLRAIGKGSFG KVICVQKRDETKMYAMKMNKQCCIERDEVNRFRELEILQIEI HVFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVQFSEDTV RLYICEMALADYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI ATIIKDGERTALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSQYVPTWSKEM VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSSEKRVEPG FVPNKGRLHCDPTFELEEMILESRLHKKKKRLAKNKSNDNRD SSQSENDYLQDCLDAIQDFVIFNREKLKRSQDLPREPLPAPES RDAAEPEVDEAERSALPMCGPICPSAGSG |
| 5524 | 85 | 2318 | RERERDHRPGESSQGGAGGCFPSPTMELRCGGLLFSSRFDSG NLAHVEKVESLSSDGEVGGGASALTSGIASSPDYEFNVWTRPD CAETEFENGNSWFYFVSVRGGMPGKLIKINIMNMNKSKLYSQG MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA TTFFAFCYPFSYSDCQELLNQDQRFPENHPHTSSPLDTIYYHR ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF RFAGKRIFFLSSRVHPGETPSSFVFNGLDFILRPDDPRAQTLR RLFFVKLIPLNPDGVVRGHYRTDSRGVNLNRQYLKPDVILHPA IYGAKAVLLYHHVSRNSQSSEHQSSCLPPDAPVSDLEKAN NLQNEAQCGHSADRHNABAWKQTEPAEQKLSNVWIMPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHAASKRGCFMYGNSFDESTOVE NMLYPKLISLNSAHDFQGCNFSKNNMYARDRRDQSGKEGSGRV AIYKASGIIHSYTLNNTYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVLFEQVGRAMAIALDMAECNPWPRIVLEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLRSARFSFTGTSAGGSSSSQNSPQMNKNSPFPFHGSRPAGL PGLGSSSTQKVTHRVLGPVRGKPVVEPLQHVFGCLGHCWGK |
| 5525 | 105 | 834 | SNTLDFERHLFIMGQISDQTLVINKLPEKVAKHVTLVRESGS LTYEBFLGRVABLNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVCTKINKSSGIVEASRIMNLYQFIQLYKIDITSQAAGVLAQ SSTSEBPDENSSSVTSQASLWMGRVKQLTDEEBCCICMDGRAD LILPCAHSFCQKCIDKNSDRHRNCPIICRLQMTGANESWVSDAP TEDDMANYILNMADEAGQPHRP |
| 5526 | 3 | 853 | RRPCNPVRAAKRTGAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDDPPSTLLKDYQNVPGIEKVDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHKRDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL YYRRAHRRFVTKKALCIRVFQETQKLKRRRALKAAAAQKQAK |

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|------------|--|--|---|
| 5527 | 3225 | 565 | RRNPDSFPAKAIPTLKDSQ LLRKYLHQNPLLLRHQPNRTCISFSATMKLKDTSRPFQSSCG KFQTKGIKVVGKWEVKIDPNMFADGQMDLVCFEELTDYQLVS PAKNPSSLSFSKEAPKKAQAVSEEEEEEGKSSSPKKIKLKKS KNVATEGTSTQKEFEVKDPELEAQGDDMVCDPEAGEMTSENLV QTAPKKKKKNGKKGLEPSQSTAARKVPKAKTWIPEVHDQKADVS AWKDLFVPRPVLRLSFLGFSAPTPIQALTLAPAIRDKLDILGA AETGSGKTLAFAIPMIHVLQWQKRNAPPSPNTEAPPGETRTE AGAETRSPGKAESDALPDDTVIESEALPSDIAAEARAKTGGT VSDQALLFGDDDAGEGSSSLIREKPVFKQNEEENLDKEQTGN LKQELDDKSATCKAYPKRPLGLVLTPTRELAVQVKQHIDAVAR FTGIKTAILVGGMSTQKQQRMLNRRPEIVATPQRLWELIKEKH YHLRNLRLRCLVDEADRMVEKGHFAELSQLLEMLNDSQYNPK RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDDLMMQKIGM RGKPKVIDLTRNEATVETLTETKIH CETDEKDFLYYYFLMQYFG RSLVFANSISCIKRLSGLLKVLDDIMPLTLHACHMHQKQLRLNLEQ PARLEDCVLLATDVAARGLDIPKVQVHIHYQVPTSEIYVHRSG RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE EDMYKGGKADQGEERRQKQMKVLKELRHLLSQPLFTESQKTK YPTQSGKPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQBPQ QPSTSAN |
| 5528 | 3 | 895 | GFFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSFE YVRDEADDTCLAHCVVVRDLGRNFHRAEKHNFAKPNDSRAL QLMTKCAQTVMEELDIVIAYQSDSEYSFVFKRKTNWFKRRASK FMTHVASQFASSVVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQ LKDYLSWRQADCHINNLNTVFVWALIQSGSLTPVQAQGRQLQGL AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL PTMEGKKMAVTRTRTKPCPSHLPRAPCLRWL |
| 5529 | 48 | 640 | TFRLVSAHLKTRKLINPEAAERRWRDWSRQGWLSVKMQRVSG LSWTLRSVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE KPNTLEELEVVSSESCVEVQEIINEEYLVIIIRPTPTVPHCSLATL IGLCRLVKLQRCPLFPKHKLEIYISEGTHSTBEDINKQINDKERV AAAMENPNLREIVEQCYLEPD |
| 5530 | 4541 | 2606 | AQIVHAISYCHKLHVGRDLKPENVVFFKQGLVKLTDGFGFSNK FQPGKLLTSCGSLAYSAPAILLGDDEYDAPAVDIWSLGVILFML VCGQPPFQEANDSETLTMIMCKYTPVSHVSKECKDLITRMLQR DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEHN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLATPLSH ATVPQSPARAADSVLNGHRSGKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSRKSAFVLNQIFEEGESDDEFDMDENLPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRDSSEGGPPGSEGGGGQSKPSNASGGVDKASPSENNAG GGSPSSGGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISS GNAGQVPAVGGIKFFSDHMDTTTELEIRIKSNLKNVQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI |
| 5531 | 24 | 515 | GSQPRAPRPRDSMERPEPELIRQSWRAVRSRPLEHGTVLFLARLF ALEPDLLPLFQYNCQFSSPEDCLSSPEFLDHIRKVMVLDAVAV TNVEDLSSLEEYLASLGRKHRAVGVLSSFTVGESLLYMLEK LGAFTPATRAAWSQLYGAVVQAMSRGWDGE |
| 5532 | 3395 | 1402 | SDWMVVGKRMIIEDETFCGEELHLSVLQCKSVFVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLRKKKWHAKGFGMTLK GPNDFKLEDYFASSELFEPPYGGGIDGDDITRPENISAFRN FVLNTRDKGVHFLMADGGFSVEGQENLQELSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFVGLVYLLYCCFRRVCLFKPITS RPANSERYVCKGLKVGIDVDRDYLFVAVNIKLNQLRNTSDVNL |

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|------------|--|--|---|
| | | | VVPLEVIRKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTLSEPRQAEIRKECLRLWGIPTQARVAPSSSDPKSKFFELIQGTEDI DIFSYKPTLLTSKLTLEKIRPVFDYRCMVSGSEQFLIGLGSQIYTWDGRQSDRWIKLDLKTLPDRTLLSVEIVHELKGEKGAQRKISAIHILDVVLNGTIDVREQHFNQRIQLAEKFVKAVSKPSRPDMNPIRVKEVYRLEEMEXIFVRLEMKIIKGSSTGPKLSYTGRRDRHFVPMGLYIVRTVNEPWTMGFSKSPKKKFYNNKTKDSTFDLPADSIAFFHICYGRPLPWEWGDGIRVHDSQKPPQDQDKLSKEDVLSPIQMHRA |
| 5533 | 94 | 789 | MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVPTVFENYTACLETEEQRVLSLWDTSGSPYYDNVRPLCYSDSDAVLLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTDLSLTMELSHQKQAPISYEQGCIAKQLGPEIYLEGSAFTSEKSIHSIFRTASMLCLNPKSPPLPKSPVRSLSKRLHLPSRELISPTFKKEKAKXCSIM |
| 5534 | 3 | 605 | LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAKTGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIKATIESPSKDDDTVWLTYYVWVYALFGLAEFFSDLLLSWFFYYVVGKCAFLLCMAPRPWNGALMLYQVRVPLFLRHGAVDRIMNDLSGRALDAAAGITRNVKPSQTPQPKDK |
| 5535 | 1029 | 332 | KSFMDSEARLCSLVLSLSDTQDETKQSDSENECLKIDCLQESQELNLQKLKNSERILTEAKQKMRLETVNIMKEDLIKELIKTGNDAKSVSKQYTLKVTKLEHDAQAKVELTETQKQLQELNKLSDVAMKVKLQKEFRKKVDAAKLRVQLQKKQDQSKLASLSIQNEKRANELEQSVDHMKYQKIQLQRKLQEBENEKRLQDLAVIKRDQKQIKVILSYIPAKYNMCK |
| 5536 | 942 | 282 | AAATAASLSPRGCRRLRTPSSDVSFSRAPPPSAAPLPTGRAQMSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVETRAPDAVYTELQPTSPTPTWPADETPOFQTQTQQLBGTGDLVTDPTPHKSTKAAHPTDDTTLSERFSPSTDVQTDPTLTKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFTIGIIILTSKGCRQLSRLCRNHCR |
| 5537 | 3 | 2391 | RARVSSPQLRVFRSGRPRLRLVLRINRTSVALRLAGTGRFVAKTPGHFGSWEMGLLTFRDVAVEFSLSEWEHLEPAQKNLYQDVMLENYRNLVSLGLVVS KPDLLTFLEQRKEPNVVKSEETVAIQPDVFSHYNKDLLTEHCTEASFQKVISRRHGSCLLENLHLRKRWRKECEGHNGCYDEKTFKYDQFDESSVESLFHQQLSSCAKSYNFDQYRKVFTHSSLLNQEEIDIWGHKHIYDKTSVLFQVSTLNSYRNVFIEKNVHCNNSEKTLNQSSSPKNHOENYFLEKQYKCKEFEEVFLQSMHGQEKQEQSYKCNKCVVECTQSLKHIHQHTIHIRENSYSYNKYDKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNSHLHTQHQIIPTEEKPYKWKCEGKVFNLCNSLYLTKQQQIDTGENLYKCKAKCSKSFTRSSNLIVHQRHTGEKPYKCEGKAFRCSSYLTKHRIHTGEKPYKCEGKAFNRSSCLTQHQTHTGEKLYCKVCSKSYARSNLIHQHVHTGEKPYKCEGKVFSRSSCLTQHRKIHTGENLYKCKVCAKFTCFSNLIVHERIHTGEKPYKCEGKAFPYSSHLIRHRIHTGEKPYKCKAKCSKSFSDSSGLTVHRRHTGEKPYTCKECGKAFSYSSDVIQHRRHTGQRPYKCEGKAFNYSYLTTHQRSHTGERPYKCEEGKAFNRSYLTTHRRHTGERPYKCEGKAFNYSYLTTHRRSHSGERPYKCEGKAFNRSYLTIAHQRSHTREKL |
| 5538 | 926 | 161 | HSMMKIPWGSIPVLMLLLLGLIDISQAQLSCTGPPAIPGIPGIPGTPGPDGPGTGPGLKGEKGLPGLAGDHGEFGEKGDGPIPGNPGKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTI RFDHVI TNMNNYEP RSGKFTCKVPGLYFTYHASRGNLCVNLMRGERAQAQVVTFCDYAYNTFQVTTGGMVLKLEQGENVFLQATDKNSLLGMEGANSIFSGLLPDMEA |
| 5539 | 38 | 1258 | HRGPGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVDGPAAALASFETVFAVPGPYGPHRPQPLPPGLDSDGLKREKDEIYGHPLFPLALVFEKCELATCSPRDGAGAGLTGTPPGGDVCSSDSPFNEDIAAFKQVRSEPLFPSSNPELDNLVIAIQVLRFHLL |

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|------------|--|--|--|
| | | | ELEKVDLDCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM RAWLFQHLSPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV QPMIDQSNRTGQGAASFPEGQPIGGYTETQPHVAVRPPGSVGMS LNLEGEWHYL |
| 5540 | 148 | 1440 | PPLGAGAGVHARSHPARRLPITTAGVGGRAPDILPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL |
| 5541 | 148 | 1440 | PPLGAGAGVHARSHPARRLPITTAGVGGRAPDILPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL |
| 5542 | 148 | 1440 | PPLGAGAGVHARSHPARRLPITTAGVGGRAPDILPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL |
| 5543 | 2405 | 665 | RWVREQPWPLRTSEAVKTPALRPFPGRGVSPFPKPDWGKSPAP KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRVPPKPTRVHG SSASRDRLARTMIVADSECRABLKDYLRFAPGGVGDGSGGEEQ RESRRRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV DNLAVVMGLHPDYFTSFWRLLHYLLHTDGPLASSWRHYIAIMAA ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKRLKLEINK LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSL SFVFGGILPEGDADGSPAPQAPTTPSEQSSPPSRDPLNNSGGF ESARDVEALMERMOQLQESLLRDEGTSQEEMESRFELEKSESLL VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ DYTWEDHGYSLIQRLYPEGGQLLDEKFOAAYSLTYNTIAMHSGV DTSVLRRAIWNYYHCVPFIRYDDYDGEVNLLEARNLKVYIKTV ACYPEKTTREMYNLFWRHFRHSEKVVHVNLLLEARMQAALLYAL RAITRYMT |
| 5544 | 1895 | 514 | LGGLLRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD PEGRROEPLRRRASSASVPVAGASAEGTRRDLGSYSGPTSVSR QRVESLRKKRPLPPWFGLDIGGTLVKLVYFEPKDIATAEEEEEV ESLKSIRKYLTSNVAYGSTGIRDVHLELKDILCGRKGNLHFIR PPTHDMPAFIQMRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD LQCLKLDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCKQ LPFDLKNPYPLLNVIGSGVSLAVYSKDNKRVGTGSLGGGT FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVVDIYGGDYERFG LPGWAVASSFGNMMSKEKREAVSKEDLARATLITNNIGSIAR MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKQLKALF SEHEGYFGAVGALLELLKIP |

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|------------|--|--|---|
| 5545 | 802 | 131 | GAMWSAGRGGGAAPVLLGLLLALLVPGGGAAKTGAEIVTCGSVL KLLNTHHRVRLHSHDIKYSGSGQQSVTVGVEASDDANSYWRIRG GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFSPPLSNNQEV SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFOHVGTSVFLSVT GEQYGSPIRGQHEVHGMP SANTHTWKAMEGIFIKPSVEPSAGH DEL |
| 5546 | 1592 | 146 | FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT RGCTGRNIRQLSLDVRVMEPLTASRLQVRKKNLSLKDCAVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTFFQVKKYSLVDRDVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMAFMFQNLFPPI NVHKVNLNTIKRCLLDYNDPSQELDFRHSYIKVVPVGASRGMK KLLQEKFPNMSRLQDISSELLATGAGLSESEAEPDGDHNTITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEELQAILAEAKEKKRLRLKAQRQAQQANVQRKQEQREAH RKKSLEGMKKARVGGSDDEASGIPSRITASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLPFAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGPRGKRA |
| 5547 | 1592 | 146 | FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT RGCTGRNIRQLSLDVRVMEPLTASRLQVRKKNLSLKDCAVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTFFQVKKYSLVDRDVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMAFMFQNLFPPI NVHKVNLNTIKRCLLDYNDPSQELDFRHSYIKVVPVGASRGMK KLLQEKFPNMSRLQDISSELLATGAGLSESEAEPDGDHNTITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEELQAILAEAKEKKRLRLKAQRQAQQANVQRKQEQREAH RKKSLEGMKKARVGGSDDEASGIPSRITASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLPFAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGPRGKRA |
| 5548 | 1 | 2153 | DQTGFPETIAFTFPRSTMEPLCPILLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLLAWLLPLLLLLLLVLLLAAYFFRF RKQRKAVVSTSDKKMPNGILEEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADCKQFREEFNSLPSGHIQGT FELANKEEN REKNRYPNILPNHRSVILSLQDGI PCSDYINASYIDGYKEKNK FIAAQGPQKETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIKFCIQPQLPDGCKAPR LVSQHLFTSWPDFGVPTPIGMLKFLKVKTLNPNVHAGPIVVHC SAGVGRGTGTFIVIDAMMMHAEQKVDVFEFVSIRNRQRPQMVG TDMQYTFIYQALLEYYLYGDTLVDVSSLEKHLQTMHGTTTFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMRGQYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBEREQDKCYQVWPTGVSHTGEITIEI KNDTLSEAISIRDVLTLNQPARQEEQVRVVRQPHFGWPEIG IPAEKG MIDLIAAVQKQQQTGNHPITVHCSAGAGRTGTPIAL SNILERVKAEGLLDVPQAVKSLRLQRPMMVQTLQEQYEFCKYVQ DFIDIFSDYANFK |
| 5549 | 915 | 256 | FEATGGKRLAFKMAGTARHDEMAIQAKKLTATDPIERLRLO CLARGSAGIKGLGRVFRIMDDNNRTLDKFEMKGLNDYAVVME KEEVEELFORFDKGNGTIDFNEFLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWESEQVFRKFLD NFDSPYDKDGLVTPEEFMNYAGVSASIDTDVYFIIMMRTAWKL |
| 5550 | 2364 | 1210 | RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGT SLIAFTTMALLTIMEFSVYQDTWMKYEYVDKDFSSKLRLINIDI TVAMKCQYVGADVLDAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPALINPLDGTAKIAIDHNQMFFYFITVVP KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEHMPFFQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRGSGYKPVNSVPFEDGHTDNHLPLENNTH |
| 5551 | 211 | 1700 | MQRDHTMDYKESCPVSIPSSDEHREKKRFTVYKVLVSUGRSE |

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|------------|--|--|--|
| | | | WVFVRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE DERSSQKLHSTSQNINLGPSPGNPHAKPTDFDFLKVIGKGSFGKV LLAKRKLKGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKQVKH PFLVGLHYSFQTTEKLYFVLDVFNNGELFFHLQRRERSFPEHRAR FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDGFLC KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY EMLYGLPPFFYCRDVAEMYDNI LHKPLSLRPGVSLTAWISILELL EKDRQNRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNPV AGPDDIRNFDATFTEETVPYSVCVSSDYSIVNASVLEADDAFVG FSYAPPSDEFL |
| 5552 | 2748 | 930 | LGPAAGAAMGKKKKHKAWEHRSSYEDYADKPLEKPLKLVLKVGG SEVTELSGSGHDSSYYDDRSHERERHKEKKKKKKKSEKEHL DDEERRKRKEKKRKRERHCDTEGEADDFDPGKKVEVEPPDR PVRACRTQPAENESTPIQQLLEHFLRQLQKQDPHGFFAFPVTD IAPGYSMI IKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA MTYNRPDVTYKLAKKILHAGFKMMSQAALLGNEDTAVEEPVP EVVPVQVETAKKSKKPSREVISCMFEPGNACSLTDSABEHVL ALVEHADEARDIRNRLPFGGKMGYLLKRNQDGSLLYSVVNTAEP DADEEETHPVDLSSLSKLLPGFTTLGFKDERRNKVTLSSATT ALSMQNNSVFGDLKSDMELLYSAYGDETVQCALSLEQEFVKDA GSYSKKVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSKSYPDVSDISMLSSLGKVKKELDPDS HLNLDETTLLQLDLHEAQAERGSGSRPSSNLSLSNASERDQHHL GSPSRLSVGEQPDVTHDPYEFQSPEPAASAKT |
| 5553 | 74 | 1095 | LGREAVYLVSRMDGPVAEHAKEPFHVVTPLLESWALSQVAGMP VFLKCEENVQPSGSFKIRGIGHFCQEMAKKGRHLVCSGGNAGI AAAYAAARKLGIPATIVLPSTSLQVVRQLQGEAEVQLTGKQVWD EANLRAQELAKRDGWNVPFDPHPLIWKGHASLVQELKAVLRT PGALVLAAGGGGLLAGVAGLEVWQHVPITAMETHGAHCFA AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAIYSGLLRRLQAEGCL PPSLTSVVIVCGGNNINSRELQALKTHLGQV |
| 5554 | 166 | 2318 | CSGRTGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLPVLPWAVQAVEHEEVAQRVILHRGRGVAAMQSRQ WVRDSCKRLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLQ VHTFEIFQKELNESENSVFQAVYGLQALQGDYKDVVNMKESS QRLEALREAAIKEETEMELLAAEKHQVEALKNMQHQNQSLSM DEILEDVRKAADRLBEEIEEHAFDDNKSVKGVNFEAVLRVEEEE ANSKQNI TKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLFESPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSTPLVSRFLM GSARGDKEGDIIDYSTVLLGMLVTQDVQLGLFMAVMPPLIAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCVIRKYLIGPYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPFVAYEL TVLVFLTLVVVMKFLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSFVLGSRARRAGVISREVYLLILSVTTLSLLAPVLWRAAI TRCVP RPERRSSL |
| 5555 | 212 | 1425 | LSLRTRETTPAPPRCEAASQGRVGRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDK KAYRKLALQLHEDRNPDDPAQAEKFDLGAAYEVLSDEKRRQY DTYGEGLKDGHQSSHGDI FSHFFGDPGFMGGTFRQQDRNIPR GSDIIVDLLEVLYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCECPNVKLVNEERTLEVEIEPGVRD GMEYPPFGEPEHVDGEPDGLFRKIVVKHPI FERRGDDLYTNV TISLVESELVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKSGSLIITFDVDFPKEQLTEAREGIIKQLLKQGSVQK VYNGLQGY |
| 5556 | 5835 | 3346 | RTRGMSKNCVPMEEFEYLLRMFGTFFYLLQKITKDNNAHTVKSR |

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|------------|--|--|--|
| | | | LEELDES YIEKFTDFLRLEFVS VHLRRIESYSQFPVVEFTLLLFK YTFHQPTHEGYFSCLDIWTFLDYLTSKIKSRLGDKBAVLNRYE DALVLLLTVELNRIQFRYNQAQLEELDDDETLDDDDQQTWQRYLR QSLEVVAKVMELLPTAFSTLFPVLQDNLEVYLGQQFIVTSGS GHLNITAENDCRRLHCSLRDLSSLLQAVGRLA EYFIGDVFAAR FNDALTVVERLVKVTLYGSOIKLYNIETAVPSVLKPDLDIVHAQ SLAALQAYSHWLAQYCEVHRQNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRTDASA LRLVDKAQVLCRALSNI LLLPWPNLPENEQQWPVRSINHASLI SALSRYRNLKPSAVAPQRKMPDDTKLIHQTL SVLEDIVENI SGESTKSRQICYQSLQESVQVSLALPFAFIHQSDVTDEMLSFFL TLFRGLRVQMGVPFTEQIIQTFLNMFTRQLAESILHEGSTGCR VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIAERPS PDVKAELFELLFRTLHNNWRYFFKSTVLASVQRGIAEEQOMENEP QFSAIMQAFQGSFLQPDHILFKQNLFYLET LNTKQKLYHKKIFR TAMLFQFVNVLQVLVHKS HDLLQEEIGIATYNMASVDFDGFFA AFLPEFLTSCDGV DANQKSVLGRNFKMDRVRRERGRAKRAEWA RKP GTC AARRGHI EASGRGLCPPCSLAAAHEMPADLVL |
| 5557 | 1712 | 491 | VILGAGLRDKDMWIPVVG LPRRLRLSALAGAGRF CILGSEAA TR KHLPARNHCGLS DSSPQLWPEPDFRNP PRKASKASLD FKRYVTD RRLAETLAQIYLGKPSRPPHLLLECNP GP GILTOALL EAGAKVV ALES DKTFI PHLES LGKNLDGKLRVHCDFFKLD PRSGGVI KFP AMSSRGLFKNLGIEAVPWTAD I PLKVVGMFP SRGEKRALWK LAY DLYSCTS IYKFGRIE VNMFEIGEKEFQKLMADPGNPDLYHVL SVI WQLACEIKVLHMEPWSSFDIYTRKGP LENPKRRELLDQLQOKLY LIQMI PRQNLF TKNLTPMNYN IFFHLLKHC FGRRSATVIDHLRS LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKD CAY KWLYDE TLEDR |
| 5558 | 1509 | 96 | RAGCTHPQVPADLGAPAEPRRPQKTCVCLLPQPGGQRGPTTMI TGVFSMRLWTPVGVLTS LAYCLHQRVALAE LQ EADGQCPVDRS LLKLMVQVVFRRHGARS PLKPLPLEEQV EWN PQLEVPPTQTFD YVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA LGERLRKNYVEDIPFLSPTFN PQEVFIRSTNIFRNLESTRCLLA GLFQCQKEGPII IHTDEADSEVLYPNYQSCWSLRQRTGRGRQTA SLQPGISED LKKVKDRMGIDSSDKVDFFILLDNVAEEQAHN LPS CPMLKR FARMIEQRAVDTS LYILPKEDRESLQMAVGPFLLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLIMLTGIFDHKNWP FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCP LDMF LNAMSVYTLSPEKYHALCSQTQVMEVGNEE |
| 5559 | 150 | 1983 | PLAATAHFAKMSRVAKYRRQVSEDPDIDSLETLSP EEMEELEK ELDVVDPDGSGVPVGLRQRNQTEKQSTGVYNREAMLNFC EKETK LMQREMSMDESKQVETKTD AKNGEERGRDASKKALGPRRDS DLG KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA VDKKEAGKDGGRGEERAVATKKEEKKGS DRNTGLSRDKDKKREE MKEVAKKEDDEKVGGERRNTDTRKEGEKMKRAGGNTDMKKEDEK VKRG TGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG PTKPSEGP AKVEEAAAPSIFDEPLERVKNNDPEMTEVNVNNSDC ITNEILVRFT EALFNTVVKLFALANTRADDHVAFAIAMLKAN KITISLNLDSNHITGKGILAI FRALLQNNTLTELRFHNQRHICG GKTEMEIAKLLKENTLLKLGVH FELAGPRMTVTNLLSRNMDKQ ROKRLQEQRQAQEAKEKKDLLEV PKAGAVAKGSPKPSPPSPK PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNLSLPATQRKM GDKVLP AQEKNSRDQLLAI RSSNLKQLKKVEVPKLLQ |
| 5560 | 9 | 921 | SSVVEFSALSVSMACLSPSQLQKFPQDGFVLVLEGFLSAEECVAM QQRIGEIVAE MDPVPLHCRTEFSTQEEQLRAQGSTDYFLSSGDK IRFFFEKGVFDEKGNFLVP EKSINKIGHALHAHD PVFKSI THS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVS PHODASFLYT EPLGRVLGVVIAVEDATLENGCLWFIPGSHTS GVSRRMVRAPVG SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEV VHKSKQNL SDRSRQAYTFHLEASGTTWSPENWLOPTAELFPFQLYT |
| 5561 | 2175 | 1775 | CYFIFQFSSPYGLHHPQTAPALFNPGLYFPFVMSPGQPPQ |

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|------------|--|--|---|
| | | | QLLAPTYFSAPGVMNFGNPSYPYAPGALFPFPPPHLYPNTQAPS QVYGGVTYYNPAQQQVQPKPSPPRTPQPVTIKPPPEVVSRS S |
| 5562 | 342 | 1385 | SSGKNDMAAAGAAGLVRLKAGVLSQADYLNVLQVCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDLRLKEKMMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNI IRNTLYKAYLESFYKCTLLGGTTADAMCPILFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF |
| 5563 | 342 | 1385 | SSGKNDMAAAGAAGLVRLKAGVLSQADYLNVLQVCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDLRLKEKMMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNI IRNTLYKAYLESFYKCTLLGGTTADAMCPILFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF |
| 5564 | 3 | 914 | RVRDKRAVWVTARGRRRCGDSMSGGMAQVGAWRGALGLALLL LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPTKFCQRTSGLC VPLTWRCRDLDCSDGSDEECRIEPCQKQGCPPPPGLPCPCT GVSDCSGGTDDKLRNCSRLACLAGELRCTLSDDCIPLTWRCDG PDCPDSSDELGCGTNEILPEGDATMGPPVTLESVTSLRNATTM GPPVTLESVPSVGNATSSSAGDQSGSPAYGVIAAAVLSASLV TATLALLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP |
| 5565 | 993 | 138 | RWNPNPARAGSISRQAPGSVSAMVTAAVFFGCAFIAGPA LALVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVID NKDGPTQKYLIFGAFVSUYIQEMFRFAYYKLLKASEGLKSIN PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLPGPTVGIH GDSPPQFFLYSAFMTLVIILHVFVGIVFPGCEKKKWGILLIVL LTHLLVSAQTFISSYGINLASAFIILVLMGTWAFLAAGSCRS LKLCLLCQDKNFLLYNQSR |
| 5566 | 2043 | 1232 | SHIQHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT KNVKEYVRMMYIVFALYTVIETVADQTVAFWPLYELKIAFV IWLSPYTKGASLIYRKFLHPLLSKEREIDYIVQAKERGYET MVNFRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTITQI DEPVGQRPYQPLPEAKKSKPAPSESAGYIPLKDGDEKTDEEA EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVK RPQVYF |
| 5567 | 1554 | 233 | EFLSGVSPDLANEDGLTALHQCIDDREMVOQLLEAGANINA CDSECWTPHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSLQ AGADLHAPLDHGATLLHVAANGFSEAAALLLEHRASLSAKDQD GWEPLHAAAYGQVPLVELLVAHGADLNKSLMDETPLDVCDE EVRAKLLELKHKHDALLRAQSRQSLRLRRRTSSAGSRGVVRRV SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDRQTGAELR PPPPEEDNPEVVRPHNGRVGSPVRHLYSKRLDRSVSYQLSPLD STTHTLVHDKAHTLADLKRQRAAKLQRPPEGPESPEETAEP GLPGDVTVPQDCGFRAGGDPPLKLTAPAVEAPVERRPCCLLM |
| 5568 | 1731 | 587 | AEDRQFASRRGAGTTAAMAASGPGCRSWCLCEPVPSATFTALL SLLVSGPRLFLLQQPLAPSGLTALKSEALRNWQVRLVITYIFVYE NPISLLCGAIIWRFAGNFERTVGTVRHCFTVIFAIFSAIIFL SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG MVVPSVLVPWLLLGASWLIPTQSLSNVCGLSIGLAYGLTYCYS IDLSEVALKLDQTFPFSLMRRI SVFKYVSGSSAERRAAQSRKL NPVPGSYPTQSCHPHLSHPVSQTQHASGQKLASWSPCTPGHM PTLPYQPASGLCYQNHFGPNPTSSSVYPASAGTSLGIQPPTP VNSPGTVYSGALGTPGAAGSKESSRVPM |
| 5569 | 2 | 835 | QTPCPLAWERGSREDSIVPGQKFPPTCSSFSGMDVGPSSLPHLG |

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|------------|--|--|---|
| | | | LKLLLLLLLLPLRGQANTGCYGIPIGMPGLPGAPGKDGVDGLPGP KGEPGIPAIPIGIRGPKGQKGEPLPGHPGKNGPMGPMPGVPV PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL TNPOGDYDTSTGKFTCKVPGLYFVYHASHTANLCVLLYRSGVK VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG SDSVFSGFLLFPD |
| 5570 | 264 | 946 | RDRDRGGVATSTEEPAPRAPQSRGPGPVSTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVC LVINQWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEYKQKIKRYIQKYATEEALKEQEECTGDSSESSMSDFSED EAQDMEL |
| 5571 | 264 | 946 | RDRDRGGVATSTEEPAPRAPQSRGPGPVSTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVC LVINQWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEYKQKIKRYIQKYATEEALKEQEECTGDSSESSMSDFSED EAQDMEL |
| 5572 | 2802 | 2085 | RTDYRTGIPGRRFVMAAGDGVKLTGSGSESSNDGGSESPG DAGAAAEAGGWAALALLTGGEMLLNVALVALVLLGAYRLWV RWGRRGLGAGAGAGEESPATSLPRMKRDFSLEQLRQYDGS RNP RILLAVNGKVPDVTGSKFYGPAGPYGIFAGRDA SRGLATFCLD KDALRDEYDDLSDLNQVME SVREWEMQFKEKYDVGRLPKPGE EPSEYTTDEEDTKDHNKQD |
| 5573 | 2562 | 219 | VPARTPNAEDQGPAAATATPCQSGGRERAGEAAEDGVKMAAF SEMGVMPETIAQAVEEMDMLLPDIAESIPILIGGGDVLMAAET GSGKTGAFSIPVQIVYETLKDQEGKKGKTTIKTGASVLNKKQ MNPYDRGSFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE VSHDQGLCRVWSTMQASLDLGTDFKFGFGGTGKKSHNKQFD NYGEEFTMHDITGICYLDIDKGHVKFSKNGKDLGLAFETPPHMK N QALFPACVLKNAELKFNFGEEEFKPPKDFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELAETLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTS DGKR LQVIVCSATLHSDVKKLSEKIMHPTWVDLKGEDSV PDTVHHV VVPVNPKTDRWLWERLGKSHIRTDVHAKDNTRPGANS PEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQGGG PDKKGHFSCVCLHGDRKPKHERKQNLERFKKGDVRF LICTDVAAR GIDIHGVPIVINVTLPDEKQNYVHRIGRVGR AERMGLAISLVA TEKEKVYHVCSSRGKGCYNTRLKEDGGCTI WYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYQKRAAGG GSYKGHVDIL APTVQELAALKEAQTSLHLGYPNLQLPRTF |
| 5574 | 1731 | 952 | NEGLEVFEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGLTVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAMMTSSAIISSLACIISVVG M RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWN LHGLIRD FYSPLVPDSMKFEIGEALYLGIISSLSFIAGIILCF SCSCQRN RSNYYDAYQAQPLATRSSPRPGOPPKVSEFNSYSLTGYV |
| 5575 | 456 | 766 | LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTAKADSPRTAL LCSAWLLTASFSAQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP |
| 5576 | 249 | 2146 | RSWGAFWFWRMLRRRRHMPRLAMVGCAFVLFLFLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAP EA QQTLPFSINQSLCPGFYTPAELKPFWRPPQDPNAPGADGKAFQK SKWTPLETQKEEGYKHKCFNAFASDRISLQSLGPDTRPPECV DQKFRRCPPPLATTSVIIVFHNEAWSTLLRTVYSLHTTPAILLK EIIILVDASTEEHLKEKLEQYVKQLQVVRVVRQEKGLITARL LGASVAQAEVLTFDLAHCECFHGWLEPLLARIAEDKTVVVSPDI VTIDLNTFEFAKPVQGRVHSRGNFDWSLTFGWETLPPHEKQRR KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEINGGENVEM |

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|------------|--|--|--|
| | | | SFRVWQCGGQLEIIPC SVVGHVFRTKSPHTFPKGTSVIARNQVR LAEVWMDSYKKIFYRRNLQAQMAQEKSPGDISERLQRLREQLHC HNFSWYLNHVYPPEMFVDPDLTPTFYGAIKNLGTNQCLDVGNNRG GKPLIMYSCHGLGNGYFEYTTQDRDLRHNI AKQLCLHVSKGALG LGSCHTFGKNSQVPKDEWELEAQDQLIRNSGSGTCLTSQDKKPA MAPCNPSDPHQLWLFV |
| 5577 | 3 | 1275 | RNSDCSCGRISVHCLPWVLFILDLKVESSMFCPLKLI LLLPVLLD YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTL SPGEHAKDEYVLYYYNSLSPVIGRFQNRVHLMGDILCNDGSLLL QDVQEADQGTYYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL RM SVEYSQSWGHFQNRVNLVGDIFRNDGSI MLQGVRESDDGNYTCS IHLGNLVFKKTIIVLHVSPEEPRTLVT PAALRPLVLGGNQLV IIV GIVCATILLLPVLLIIVKKT CGNKSSVNSTVLVKN TKTNPEIK EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV WPSLRSDRNSLEKKSGGGMPTKQAF |
| 5578 | 3 | 783 | AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD WFGDFSSFRALLEPELRPEDRI LVLGCGNSALS YELFLGGFPNV TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLD FPSASFVVL EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI SMTSAAPHFRTRHYAQAYYGWSLRHATYSGGFHFLYLMHKGK LSVAQLALGAQILSPRPPTSPCFLQDSHEDFLSAIQL |
| 5579 | 3 | 1540 | RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLSRVFPQNL REDRVLSQLDKSDDLTCQSRLMLQVGLIYPASPGCYHLLPYTV RAMEKLVVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK ELLRLRDRRHGKEYCLGPTHEEAITALIASQKLSYKQLPFLLYQ VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANMETLDSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSI FNAQFTNVCGKPTLAEMGCYGLGVTRI LAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHI TEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYFPV I IAGKRALEDPAHF EVNCQNTGEVAFLLTKDGMDDLTPVQTV |
| 5580 | 1681 | 450 | ADAGTRCIPGFVVP SGAGYSAPAQRGRSSGRMRAAAAPGLTAP WRLQCCLEAGELGMVPAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSAVNSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHSDSDQLCWHPSNPDLFTV ASGDKTIRIWDVVRTKCIATVNTKGENINICWSPDGQTI AVGNK DDVVTPIDAKTHRSKAEQKFVEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVSINAHPSNCI C I KFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFDIA EVETGDKLWEVQCESPTFTVANHPRPLAFACDDKDKGYDSSR EAGTVKLFGLPND |
| 5581 | 54 | 947 | GGGSGPRAPSATLLDTGESVA AVASGEDKGI AASAAAAAVFACS CSPDPQSSTMNVPVSPVQPGAPYGNPKNMAYTGYP TAYPAAABA YNPSLYPTNSPSYAPFQFLHSAYATLLMKQAWPQNSSSCGTGEG TFHLPVDTGTENRTYOASSA AFRYTAGTPYKVPPTQSN TAPPY SPSPNPYQTAMYP IRSAYPQQLNYAQGAYYTPVYAAQPHVIH TTVPQNSIPSAIYPAPVAAPRTNGVAMGMVAGTMTAMSAGTLL TTPQHTAIGAHVSMPTYRAQGT PAYSYPVPHW |
| 5582 | 5775 | 2739 | ITNNNNV I I PLVIAVHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLKL VQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYASDQVALPRELLCKLHVNRACCYFTMGly EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKGLRVRKAYKRPQLETFSLLSNG TAAGVADQGTSNGLSIDDIEDCYVDPGRSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSSTD SLDDFSDGDFGPELDTLLDSL VQGLSGSGVPSQLIPVFPGGTPLLPPVVGSI PVSSPLPP ASFGLVMDPSKLAASVLDALDPPGPTLDPDLDPYSETRLDAL |

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|------------|--|--|--|
| | | | DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQQKPPSPPEPCMPN TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK RDILLGRRLRSSEDTWKIRIRPRTKTSFVGSYYLCKDMINKQDC KYGDNCTFAYHQEEIDVWTEERKGTLNRLDLDPLGGVKRGSIT IAKLLKEHQGIPTFLCEICFDSKPRIISKGTKDSFVCSNLAAL HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFQDVCHEVRYGCL REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYQQMEAH AGKASSMGAPRTHGPSTFDLQMKFVCGQWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSRPLPSIRNFPQQYD LCIHAQNGRKQYVGNCSFAHSPEERDMWTFMKNKILDMQQTY DMWLKKNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL CGKNSNGKKQWQHQQHSEKHEKVFSTSDSASGWAFFPMGEFR LCDRLQKQKACPDGDKCRCAHQEEELNEWLDRREVLLKQKLAKAR KDMLLCPRDDDFGKYNFLQEDGDLGATPEAPAAAATATTGE |
| 5583 | 3 | 1265 | SSGCRQGRPRGRSDRPPRRRHKMKVETRYDYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICKECGVGGKKGVSVEKCP CKGRGMHIHQIGPMVQIQITVCI ECKGQGERINPKDRCEC SGAKVIREKKIIEVHVKEGMDGQKILFHGEGDQEPLEPGDVI IVLDQKDHVSFQRRGHDLIMMKIQLSEALCGFKTKITKLDNRI LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPEQN WRQHREAYEDEDGPQAGVQCQTA |
| 5584 | 3 | 1265 | SSGCRQGRPRGRSDRPPRRRHKMKVETRYDYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICKECGVGGKKGVSVEKCP CKGRGMHIHQIGPMVQIQITVCI ECKGQGERINPKDRCEC SGAKVIREKKIIEVHVKEGMDGQKILFHGEGDQEPLEPGDVI IVLDQKDHVSFQRRGHDLIMMKIQLSEALCGFKTKITKLDNRI LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPEQN WRQHREAYEDEDGPQAGVQCQTA |
| 5585 | 2619 | 915 | LPAGTPESSLHEALDQCMTALDFTLNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEV CYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLQSSQYCKGENHPHFEGG VKLGVGAFNLTL SMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFLVLTGNVNIIEAEKLLKPYLNR YPKGAIPLFLAGRIEVIKGNIDAAIRRFEECEAQQHWKQFHHM CYWELMWCFTYKQWMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGGLKLIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNKYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAENFRS ISANKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLES AKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL |
| 5586 | 2619 | 915 | LPAGTPESSLHEALDQCMTALDFTLNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEV CYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLQSSQYCKGENHPHFEGG VKLGVGAFNLTL SMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFLVLTGNVNIIEAEKLLKPYLNR YPKGAIPLFLAGRIEVIKGNIDAAIRRFEECEAQQHWKQFHHM CYWELMWCFTYKQWMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGGLKLIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNKYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAENFRS ISANKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLES AKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL |
| 5587 | 1768 | 148 | SSAVPDGAVGRPVAVAVGGPPHSCRCRCPCLMAAIGVHLGCTSA |

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|------------|--|--|---|
| | | | CVAVYKDGGRAGVVANDAGDRVTPAVVAYSENEETVGLAAKQSRIRNISNTVMVKQKILGRSSSDPQAQKYIAESKCLVIEKNGKLRYEIDTGEETKFNPEDEVARLIFSKMKETAHSLVGLSDANDVVITVPFDGGEKQKNALGEAARAAGFNVRLRIHEPSAALLAYGIGQDSPTGKSNILVFKLGGTSLSLVMEVNSGIYRVLSNTDDNIGGAHFTE TLAQYLASEFQSRFKHDRVGNARAMMKLTNSAEVAKHSLSTLGSANCFLDSLYEGQDFDCNVSRRARFELLCSPFNKCEAIRGLLDQNGFTADDINKVVLCGGSSRI PKLQQLIKDLFPVAVELLNSIPPDEVIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGASRFTVLFPSGTPLPARRQHTLQAPGSISSVCLLEYESDGKNSAK EETKFAQVVLQDLDDKKENGLRDILAVLTMKRDGSLHVTCTDQET GKCEAISIEIAS |
| 5588 | 3 | 589 | TPPPPEQAMVAATVAAAWLLWAAACAQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQHYRALQQLQORDLGPHEFNVLAFCPCNQFGQEPDSNKEIESFARTYSVSFPMFSKIAVTGTGAHPAFKYLAQTSKGEPNTWFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL |
| 5589 | 1884 | 553 | LRQAWHEGGIGQTDKERGAALPGEEDPTGRSLGRASWESGSPRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPASGLNRRSSGLWLGPDRCRPRSRCSRVMENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWKKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRLSLVSFVVRIVPSPDWFGVDSLDLDCGDRWREQAALDLYPYDAGTDSGFTFSSPNFATIPQDVTVEITSSSPSPHANSFYYPRLKALPPIARVTLRLRLQSPRAFIPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPANNGSPCELEEEABCVPDNCV |
| 5590 | 72 | 896 | LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRSGDFDDPNLEDAVKETSSVQKQPDHITTTTTNRP GTTRAPAKPPGSGLDLADALDDQDDGRRKPGIGGRERWNHVTITTKRPVTTTRAPANTLGNDFDLADALDDRNRDDGRRKPIAGGGGFSDDKLEDIVGGGEYKPKDKGKGDGRYSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISYQQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAEPPPPPEPARI |
| 5591 | 68 | 1494 | AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPALLPGEEMAALRVTRNSKINAENKAKINMAGAKRVPTAPATSKPGLRPRTALGDIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPVKEEKLSP EPI LVD TAS PPMETSGCAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYLRQLEEBQAVRPKYLLGREVTGNMRAILIDWLQVQMKFRLLQETMYMTVSTIDRFMCNNCVPKMLQLVGVTAMFLASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGLRPLPLHFLRRASKIGEVDVEQHTLAKYLMELTMDYDMVHFPPSQIAAGAFCLALKILDNGEWTPTLQHLYLSYTESLLPVMQHLAKNAAMVNQGLTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV |
| 5592 | 242 | 924 | YGESKDNQKDLLSALVLTVNCLPTPIMAKSAEVKLAIFGRAGVGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILDITAGQEDTIQREGHMRWGEFVLVYDITDRGSFEEVLPKLNILDEIKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECSECTGEGNITEIFYELCREVRRRRMVQGKTRRRSSSTTHVKQAINKMLTKISS |
| 5593 | 3 | 1113 | HASGGRAANMAAERGAGQQSQEMMEVDRVESEESGDEEGKKHSSGIVADLSEQLKDGEERGEEDPEEEHLPVDMETINLDRDAEDVDLNNHYRIGKIEGFVLKKVKTCLRQNLICKIENLEELQSLRBLDLYDNQIKKIENLEALTELEILDISPNNLRNIEGVDKLTRLKLFLVNNKISKIENLSNLHQLMLELGSNRIRAIENIDTTLNLESFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLRELYLSHNGIEVIEGLENNNKLTMLDIASNRICKIENISHLTELQEFWMNDNLLESWSDLDLKGARSLETVYLERNLQKDPQYRRKV |

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|------------|--|--|--|
| 5594 | 3 | 1113 | MLALPSVRQIDATFVRF HASGGRAANMAAERGAGQQSQSEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGEERGEEDPEEEHELPMETINLDRDAE DVDLNHYRIGKIEGFVLLKKVTKLCLRQNLKICLENLEELQSLR ELDLYDNQIKKIKENLEALTELEILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIKENLNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLMSQSNRLTKIEGLQNLVNL ELYLSHNGIEVIEGLENNKLTMLDIASNRKIKENISHLTELO EFWMNDNLLESWSDLDELKGARSLETVYLERNPLOKDPQYRRKV MLALPSVRQIDATFVRF |
| 5595 | 3 | 1476 | ARWNRWVQVPAPPGPGCGTNASGERQRLPRAWRPVGRTLGSE PIALAWSPLLYLFPILPSPWAVSQPTPTLGTMFADLDYDIEDK LGIPTVPQKVTTLQKDAQNLIGISIGGGAQYCPCLYIVQVFNPT AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTHY NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC NDGLVKRLEELERTAEYKGMTEHTKNLLRAFYELSQTHRAFGD VFSVIGVREBPQAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT DLNTYLNKAIPTDRLTIKKYLDVKFEYLSYCLVKEMDDEEYSC IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKME LDQKHVQDIVFQLQRLVSTMSKYNDYAVLRDADVFPIEVDLA HTTLAYGLNQEEFTDGEDEDEDEDETAAGEPSRDRGAAGPLDKG GSWCDS |
| 5596 | 698 | 219 | GAVLAPSSLPAAELAAQGESQSLDLSNTRPTSEVYKISFIFP NGDKVDGDCRTTSSGIYERNIGIHTTPNGIVYTGSKDDKMG FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFENRV KGEGETHIQGTMRMDVTFHFTSCST |
| 5597 | 3 | 731 | ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP VFVIVGFVTLIIFKRELHTISFLGGLALNEGWNLIKNVIEPR PCGGPHTAVGTYKGMPSHSSQFMWFFSVYSFLFLYLRMHQTNA RFLDLLWRHVLSLGGLAVAPLVSYSRVLLYHTWSQVLYGGIAG GLMAIAWFIPTQEVLTPLFPRIAAPVSEFFLIRDTSLIPNVLW FEYTVTRAERNRQRKLGTQLQ |
| 5598 | 326 | 2440 | GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSVPVPHPPAPSPCCSGQTMKMLSKLILLALVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG EMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNTECGKLEEL IKCALCSPHSQSLFHSPEVLERDLVLPCLCKDYCKEFTYTCR GHIPGFLQTTADEFCFYARKDGGLCFPDFPRKQVRGPASNYLD QMEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGDERGGL SLAFHPNYKNGKLYVSYTTNQRWAI GPHDHI LR VVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDM ITLDDMEEMDGLSDFTGSLRLDLDVDTMCNVPYSIPRSNPHFNS TNQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGDYSESPSLLEFKPFSSNGPLVGGFVYRGCQSRL YGSYVFGDRNGNFTLQQSPVTKQWQKPLCLGTSGSGCRGYFSG HILGFEDELGEVYIILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG |
| 5599 | 326 | 2440 | GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSVPVPHPPAPSPCCSGQTMKMLSKLILLALVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG EMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNTECGKLEEL IKCALCSPHSQSLFHSPEVLERDLVLPCLCKDYCKEFTYTCR GHIPGFLQTTADEFCFYARKDGGLCFPDFPRKQVRGPASNYLD QMEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGDERGGL SLAFHPNYKNGKLYVSYTTNQRWAI GPHDHI LR VVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDM ITLDDMEEMDGLSDFTGSLRLDLDVDTMCNVPYSIPRSNPHFNS TNQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS |

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|------------|--|--|---|
| | | | SARILQIIKGDYSESEPSLLEFKPFSNGPLVGGFVYRGCSERL YGSYVFGDRNGNFTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDBLGEVYILSSSKSMTQTHNGKLYKIVDPKRLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG |
| 5600 | 1977 | 1244 | SLRVLSGHLMQTRDLVQDPKSPKFIIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELVAQKPEKLLERCKYWPACNGDECAVHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCCPTHVSRRIPLVSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRDC TFYHPTINVPPRHALKWIRPQTSE |
| 5601 | 1977 | 1244 | SLRVLSGHLMQTRDLVQDPKSPKFIIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELVAQKPEKLLERCKYWPACNGDECAVHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCCPTHVSRRIPLVSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRDC TFYHPTINVPPRHALKWIRPQTSE |
| 5602 | 246 | 766 | YHTSCTVWR TAKEALENTEVPVGLMVYNNNEVVGKGRNEVNQTK NATRAEMVAIDQVLDWCQSGKSPSEVFETHVLYVTVEPCIMC AAALRLMKIPLVYGCQNERFGGCGSVLNIAADLPNTGRPFQC IPGYRAEEAVEMLKTFYKQENPNAPKS KVRKKECQQILNMF |
| 5603 | 1 | 565 | FRGRTPISGGERGCAQYFIPATPARSGENRTMPGAGDGGKAPAR WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS CFGFEDLHFRWYNNSSDAFKILIEGTVKNEKSDPKVTLKDDRI TLVGSTKEKRNINISIVLRDLEFSDTKGYTCHVKNPKENNLQHHA TIFLQVDDRMRQ |
| 5604 | 1 | 1506 | EDIFPAQLLKLQRHERVWQEPVVRDHRVSGSGAGGVAGREWT DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSGFGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFTLELQPSLIVVRRRLAEKRIQVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDLFLPEGVNKEKITPLTLKEAYVQKMKVCNDSDRWSLI SLSNNSGKNVELKPVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTEFHPITIGESVYGDQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHVGLLEDKRYEYMLTLHGTVNVESTVCLMGHERRQTNL ITMLAIRVLADQNVIPNVANVTCTCYQPAPYVADANFSNYIAQV QPVFTCQQQTYSTWLPNC |
| 5605 | 35 | 1821 | SQRSCEPSPSSPAPPWARSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFO KALRSLLRRYPLPLRSKGKAKILQHFQDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNNGHFLTKELLQRCQAQKSPRVAP GSARPWPALRSLLRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKPEEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGF VWVAQETNPRDPANPGLVLDHIVERKRLDDLCSSIIDGRFREQ KFRKRCGLERRVYLVEEHGSHVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLRLYQGHRTLRSRPWGTTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFAQLMQVRG VSGEKAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGLT |
| 5606 | 3 | 1099 | GRSRCFPGFARGGTMSPRSCLSRLRLLVFAVFSAAAANWLYLAK LSSVGSISEETCEKLGKLIQRQVQMKRNLVMSVRRGAQLA IEECQYQFRRNRWNCSTLDSLFPVFGKVVTQGTREAAFYAISA GVFAVTRACSSGELEKCGCDRTVHGVSPPGFQWSGCSDNIAYG VAFSQSFVDVRRSKGASSSRALMNLHNEAGRKAILTHMRVEC KCHGVSGSCEVKTCSRVPVPPFRQVGHALKKEKFDGATEVEPRRV SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR TCNKTSKAIDGCELLCCGRGFHTAQVELAERCCKFHWCCFVKC RQCQLVELHTCR |

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|------------|--|--|---|
| 5607 | 521 | 141 | PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHORV QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEELEVRFNAP FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK |
| 5608 | 2 | 983 | WFQSPLRQADPGPRHTLFMDFVAGAIGGVCGDAVGYPDVTVKV RIQTEPKYTGIIWCVRDYHRRVWGFYRGLLPVCTVSLVSE VFGTYRHCLAHICRLRFGNPDAPKTKADITLSCASGLVRVFLT SPTEVAKVRLQTQTQAQKQRRRLSASGPLAVPPMCPVPACPEP KYRGPLHCLATVAREBGLGGLYKGSALVLRDGHSEFATYFLSYA VLCWLSLSPAGHSRPDPVPGVLVAGGCAGVLAWAVATPMDVIKSR QADGGQRRYRGLLHCVITVREEGPRVLFKGLVLNCCRAFPVN MVFVAYEAVLRRLARGLLT |
| 5609 | 1628 | 304 | AKGVWVLPSPPPRPGRGALVSGSLRRGRSGTSWRPRRMNHKSK KRIREAKRSARPELKDSDWTRHNYYESFSLSPAADVADNVERAD ALQLSVEEFVERVERPYKPVLLNAQEGWSAQEKWTLERLKRKY RNQFKCGEDNDGYSVMKMKYIIEYMESTRDDSPLYIFDSSYG EHPKRRKLLLEDYKVPKFDDDLFQYAGEKRRPPYRWVMPGPRS GTGIHIDPLGTSANALVQGHKRWCLFPTSTPRELIKVTRDEGG NQDEAITWFNVIYPRTPQPTWPEFKPLEILQKGETVVFVPGG WWHVVLNLDTTIAITQNFASSTNFPVWHKTVGRPKLSRKWYR ILKQEHPELAVLADSVLDQESTGIASDSSSSSSSSSSSSSDSD SECESGSEGDGTVHRRKRRCTSMVGNDDTTSQDDCVSKERSSS R |
| 5610 | 54 | 1196 | LERTPASADMAWTKYQLFLAGLMLVTGNTLSAKWADNFMAEG CGGSKEHSFQHPFLQAVGMFLGEFSCLAAPYLLRCRAGQSDSS VDPOQPFNPLFLPALCDMTGTSMLYVALNMTSASSFQMLRGA VIFTGLFSVAFGLRRVLVSQWLGLIATLGLVVGADLLSKH DSQHLSEVITGDLIIIMAIQVILEEFVYKHNHPLRA VGTEGLFGFVILSLLVPMYIIPAGSFSGNFRGTLEDALDAFCQ VGQPLIAVALLGNISSIAFFNFAGISVTKELSATRMVLDLSLR TVVIWALSALGWAFHALQILGFLILLIGTALYNGLHRLPLGR LSRGRPLAESEQRLLGGTRTPINDAS |
| 5611 | 2 | 577 | FVLNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE KLTAPEKYMFPDLNNEGEIDLMSLKRMEKLGVPKTHLEMKKM ISEVTGGVSDTISYRDFVNMLGKRSVAVLKLMMFEGKANESSP KPVGPPPERDIASLP |
| 5612 | 1 | 721 | ASRDGYMDATIAPHRIPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQKRTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREBALRIQTLGITPRHIVLSAPDVL IERNLGRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLEYHRNIVRVIPSYPKILKVISADQPCVDVYQALTYVQS NHRTNAPFTPRVLLGVPVGS |
| 5613 | 115 | 1279 | RGVDPALRRAEKMLPLSTKDEYKPEKFNLFKGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFPDST AILAGLAASVISKWRDNDAFSYGYVRAEVLGAFVNGLFILPTAF FIFSEGVERALAPPDVHHERLLVLSILGFVNNLIGIFVFKHGGH GSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMQNFGLMIADPICSILIAILIVSVIPLLRRESVGIIMQR TPPLENSLPQCYQORVQQLQGVYSIQEQHFWTLCSDVYVGTILKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM |
| 5614 | 3 | 1268 | LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGGQETQNER APWGARQRLGVMAELQQLQEFPIPTGREALRGNSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRLMD LQGAALRQVEARVSTLGQMVNMHEKVARREIGTLATVQRLPPG QKVIAPENLPLTPYCRRLNFGCLDDIGHGIKDLSTQLSRTGT LSRKSIPAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS SLASAGSAEGVGGAFTPKGQAAPPAPPLPSSLDPPPPPAAVEVF QRPPTLEELSPPPDEELPLPLDLPPPPPLDGDDELGLPPPPPGF GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY |

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|------------|--|--|---|
| 5615 | 9 | 1558 | SDGWCEGVSEGTGFFPGNYVEPSC ALGRRRPGDPREMEAAATPAAAGAAARREELDMVMRPLINEQNF DGTSDDEHEQEELLPVQKHVQLDDQEGISFVQTLMHLLKGNIGTG LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR FKKSTLGYSDTVSFAMEVSPWSCLOKQAAWGRSVVDFFLVITQL GFCSVYIVFLAENVKQVHEGFLESKVFISSNSTSSNPCERRSDV LRIYMLCFLPFIIILLVFIRELKNLFVLSFLANVSMVSLVLIYQ YVVRNMPDPHNLPIVAGWKYPLFFGTAVFAFEGIGVVLPLENQ MKESKRFPQALNIGMGIVTTLVTLATLGYMCFHDEIKGSITLN LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT KWKQICEPGIRSFVLSITCAGAILIPRLDIVISFVGAUSSSTA LILPLPLEILTFSKEHYNIWMVLKNISIAFTGVVGPLLGTIYITV EEIIYPTPKVAGTPQSPFLNLNSTCLTSGLK |
| 5616 | 1 | 719 | DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTSSRTTHFE LKHLSGDLRLDNMLRGTEIGVLAKAFIDQGLIPDDVMTRLAL HELKNLTQYSWLLDGFRTLPQAEALDRAYQIDTVINLNVFV IKRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDD KPETVIKRLKAYEDQTKPVLEYQKKGVLFTFSGTETNKIWPVY YAFLOTKVPQRSQKASVTP |
| 5617 | 176 | 765 | PWRGRGSRPRGAGAMAEQVNRSAGLAPDCEASATAETTVSSVG TCEAAGKSPKDYDSTCVFCRIAGRQDPGTLLHCENEDLCF KDIPKPAATHHYLVVPPKKHIGNCRILRKDQVELVENMVTGKTL ERNNFTDFTNVRMGPHMPPFCSISHLHLHLVAPVDQIGFLSKLV YRVNSYWFITADHLIRKLRT |
| 5618 | 3 | 1692 | YLYNINLKSENKLSGKEDLWEKLQYLWKSTLNLPLEDLRVPDES LFLNSGGDSLKSIIRLLSEIEKLVGTSVPGLEIILSSSILEIYN HILQTVVDEDDVTFRKSCATKRKLSNINQBEASGTSIHQKAIMT FTCHNEINAFVVLRSQSILSLNSTRLTKLGHCSACPSDSVS QTNIQNLKGLNSPVLIGKSKDPSVAKVSEEGKPAIGTQKMEHL VWRSDTGKCVASPLVVIPTFDKSSSTVYIGSHSRMKAVDFY SGKVKWEQILGDRIESSACVSKGNFIIVGCGYGLVYVLKNSNG EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQAYALDIYRKKC VWKSCKGTVFSSPCLNLI PHHLYFATLGGLLAVNPATGNVIW KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS GPIFSSPCTSPSEQKIFFGSHDCFYCCNMKGHLQWKFTTSRV YATPFAFHNYNGSNEMLLAAASTDGKVNILESQSGQLQSVYELP GEVFPSPVLESMLIIGCRDNYVYCLDLLGNGQK |
| 5619 | 2160 | 1477 | DSPVLPTSGNVISTAQPAQFWSAVEAALRSLGSPGAGRGCCPCP AQSLHSHQLAANDPLKPSLRSYPHLLQHPQLRSLTASSGHLGR RSCPPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL LWGTGKRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPPLGP TVGLRPGLLGERQRGALRAGDPQCQCLPATVREDLGVPSPWAA ECSFPATP |
| 5620 | 930 | 182 | PLPPTLAMFLTRSEYDRGVNTFSPEGRFLQVEYAIEAIKLGST AIGIQTSEGVCCLAVEKRITSPLEPSSIEKIVEIDAHIGCAMSG LIADAKTLIDKARVETQNHWFYNETMTVESVTQAVSNLALQFG EEDADPGAMSRPFGVALLPGGVDEKGPQLFHMDPSGTFVQCDAR AIGSASEGAQSSSQEVYHKSMTLKRAIKSSLIILKQVMEEKLNA TNIELATVQPGQNFHMFTEKEELEEVIKDI |
| 5621 | 3 | 819 | VVEFVEYTATDANVKNESLSSVQQLGKIMTVRYGKFLSLKLDGA ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNVAGHDWVSSLF MIMLGDKETFPQLHQFSRLLTSALFLWLPRLHISSYLPNDTVES GIHPVYFCSTHYIEMLLKAEPLVFSFAHMSGFAPSQICLQWIT QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQDDILO HTQTQDLQVFLKEALHGFVSDYFEYMEILEQNYRTVLLRDMR NIRLQST |
| 5622 | 1122 | 456 | AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY PGTFYFQFKNLWEANDRNETWLCFTVEGIRKRSVVSXKTVGFRN QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA GEVAEFLARHSNVNLTIFTARLYYFYQYFCYQEGRLSLSQEVAV |

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|------------|--|--|---|
| | | | EIMDYEDFKYCWENFVYNDNEFFKPKWGLKTNFRLKRRRLRESLQ |
| 5623 | 3 | 954 | FLPFFIRAPKISRNGQWLFTFTTFFPPFANKALPGWEGIVPACFW RKKILTPTSTGTMELLQVTILFLLPSICSSNSTGVLEAANNLSLV TTTKPSITPTNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST ATFLTSDKDEGLKATTTDVRKNDISIISNVTVTSVTLFNAVSTLQS SKPKTETQSSIKTTEIPGSVLQPDASPKGTGLTSIPVTIPENT SQSQVIGTEGGKNASTSATSRSYSSIIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPDQSDKESVKLLTVKTISHESGEH SAQGKTKN |
| 5624 | 159 | 898 | PGVAAAAGALPQYHGAPALVSCRRELSLSAGSLQLERKRDRFT SSGSRKLYFDTHALVCLLEDNGFATQQAEEIIVSALVKILEANMD IVYKDMVTMKGQIEITFQQVMSQIANVKKDMIILEKSEFSALRAE NEKIKLELHQLKQQVMDEVIKVRTDTKLDNFLEKSRVKELYSLN EKKLLELRTEIVALHAQODRALTQDRKIETEVAGLKTMLSHK LDNKKYLAGSIPTCLTVALGFYRLWI |
| 5625 | 1 | 1180 | TIPSSAAAQCRAGPPAGALEALS PGARAHAEERRGEMRATPLAAP AGSLSRKKRLELDNDLTERPVQKRARGPQPRLPCLPLSP TAPDRATAVATASRLGPVYLLPEEGGRAYALHCPTGTETTCR VYPVQEAALAVLEPYARLP PHKHVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRHRIPPEAAVLFRQMATALAHCHQHGLVLRDLKL CRFVFADRERKKLVLENLEDS CVLTGPDSDLWDKHACPAYVGP ILSSRASYSKGAADVWSLGVLF TMLAGHYPFQDSEPVLLFGKI RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRLQ DPMPLAPTRSHLWEEAAQVVPDGLGLDEAREEGDREVLYG |
| 5626 | 3123 | 2011 | PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNP AISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWVERLTQKEKRPLFLAPDFDRWLDES DAEMELRAK EERLNKLRLESEGSPETLTNLKGYLFMYNLVQFLGFSWIFVN LTVRFCLGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAUVFVFWLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSSFFLQIYILIMIFLGLYINF RHLYKQRRRRYGQKKKKIH |
| 5627 | 3123 | 2011 | PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNP AISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWVERLTQKEKRPLFLAPDFDRWLDES DAEMELRAK EERLNKLRLESEGSPETLTNLKGYLFMYNLVQFLGFSWIFVN LTVRFCLGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAUVFVFWLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSSFFLQIYILIMIFLGLYINF RHLYKQRRRRYGQKKKKIH |
| 5628 | 75 | 1455 | VAGAMASKCLKAGFSSGSLKS PGGASGGSTRVSAMYS SSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPMCPDYQSYFRTEELQKKTLCSKAENARLVVEI DNAKLAADDFTKYETEVSRLQLVESDINGLRRILDDLTLCCKSD LEAQVESLKEELLCLKKNHEEEVNSLRQQLGDRNLNVEVDAAPPV DLNRVLEBEMRCQYETLVENNRDAEDWLDTSQEELNQVVSSE QLQSCQAEI IELRRTVNALEIELQAQHSMDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNEQYQVLLDVRARLEC EINTYRGLLESEDSKLP CNPCAPDYS PSKSLCPLPAASC GPSPA ARTNCSARPICVPCPGGRF |
| 5629 | 2287 | 938 | GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPALPRGRPGTEGSTLSAPAVLVAVAVVVVVSAVANAMA NYIHVPPGSPPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGI TNKLGICYGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHCAPQLYCTFNNGLCYEFIQGEALDPKHVCN PATFRLIARQLAKITHAHNGWIPKSNLWLMKGKYFSLIPTGF |

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|------------|--|--|---|
| | | | <p>ADEDINKRFLSDIPSSQILQEEMTWKKEILSNLGSPPVVLCHNDL</p> <p>LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNFEAGVSDV</p> <p>DYSLYPPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV</p> <p>NQFALASHFFWGLWALIQAKYSTIEFDLGLYAIVRFNQYFKMKP</p> <p>EVTALKVPE</p> |
| 5630 | 1194 | 278 | <p>GFWAIAQTCAHHLPPGSPWLPVSPWRLPEMSSFGYRRTLTVALF</p> <p>TLICCPGSDEKVFVHVVRPKKLAVEPKGSLEVNCSTTCNQPEVG</p> <p>GLETSLODKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM</p> <p>NSNVSVYQPPRQVILTLOPTLVAVGKSFTIECRVPTVEPLDSL</p> <p>LFLFRGNETLHYETFGKAAPAPQEAATFNSTADREDGHRNFSC</p> <p>LAVLDLMSRGGNI FHKHSAPKMLEIYEPVSDSQMVIIIVTVSVL</p> <p>LSLFTSVLLCFIPGQHLRQQRMGTYGVRAAWRLPQAFRP</p> |
| 5631 | 1053 | 290 | <p>SRVDDFVRPEPSRAEPSSRSGRRFPARRAATMSVFGKLFAGGGK</p> <p>AGKGGPTPQEAIQRLRDEEMLSKKQEFLEKKIEQELTAACKHG</p> <p>TKNRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN</p> <p>TEVLKNMGYAAKAMKAADNMDIDKVDLMQDIADQQLAEIEIS</p> <p>TAISKPVGGEFDELMAELEBELEQEELEDKNLEISGPETVP</p> <p>LENVPSIALPSKPAKKKEEDDDMKELNWAWSM</p> |
| 5632 | 3 | 952 | <p>VVLGWSPPRRLWWSLGAAPVAVFVSGLARSLSHVETRRPHRA</p> <p>SVRVARGRLGVMAQPPQLLPVGSRRMQPPGPPPAYAPTNGD</p> <p>FTFVSSADAEDLSGSIASPDVKLNLGDFIKESTATFLRQRGY</p> <p>GWLLEVEDDDPEDNKPLEELDIDLDIYKIRCVLMMPMSLGF</p> <p>NRQVVRDNDPFWGPLAVLVFFSMISLYGQFRVSVIITWIFGS</p> <p>LTIFLLARVLGGEVAYGOVLGVIGYSLPLIVIAVPLLVGSFE</p> <p>VVSTLIKLPGVFAAAYSAASLLVGEEBFKTKKPLLIYPIFLLYIY</p> <p>FLSLYTGTV</p> |
| 5633 | 771 | 460 | <p>QCSKTMVGRPFYRSSEFMEQLLSSHLHQVPPFCCFTVVCLCN</p> <p>CLFENSVSXLYMLCFNFFMSIPFYSLSTIKLNLIIYLWGLSYQSL</p> <p>LLLLLSGHRPWGSSMV</p> |
| 5634 | 1446 | 855 | <p>PRATGRIRSRRAASRPRAGAGASGAEPSSRGRSRLSGRRAPAM</p> <p>ARNTLSSRFRVDIDEFDENKFDVDEQBEAAAAAEPGDPDPSEVD</p> <p>GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK</p> <p>SSEIEQAVQSLDRNGVDLLMKYIYKGFEXPTENSSAVLLQWHEK</p> <p>ALAVGGLSGSIIRVLTARKTV</p> |
| 5635 | 3 | 943 | <p>DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL</p> <p>RSLFHFPFVTRSGAPRAVLVGSSWPAMVAPAVKVARGWSSGLAL</p> <p>GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE</p> <p>EKYVRELKKTQLIKAAAPAGKTSSVFEDPVISKFTNMMIGGNKV</p> <p>LARSLMIQTLAVKRRKQFEKYHAASAEQATIERNPYTI FHOAL</p> <p>KNCEPMIGLVPIILKGRFYQVPVPLPDRRRRFLAMKWMITECRD</p> <p>KKHQRTLMPKLSHKLLEAFHNQGPVIRKXHDHLMKMAEANRALA</p> <p>HYRWW</p> |
| 5636 | 2253 | 1143 | <p>LEDTCIQHPPEAKKLYLYHRKLEVERNGIPRLPKDVFMDTHQG</p> <p>LTDVRAKVTGFSQGVVDSVKGGFSSFSQATHSAGAVVSKPREI</p> <p>ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK</p> <p>YGSEEDCSSATSGSVGANSTGGIAGVASSSKTNTLDMQSSGFD</p> <p>ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR</p> <p>CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI</p> <p>QEALEACQTRISKMELQQQQQVQVQLEGLNATARNLLGKLINI</p> <p>LLAVMAVLLVFVSTVANCVVPLMKTRNRTFTSLFLVVFIAFLWK</p> <p>HWDALFSYVERFFSSPR</p> |
| 5637 | 948 | 2532 | <p>MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHPLPLPPPHLH</p> <p>HHHPQHHLHPGSAAAVHPVOQHTSSAAAAAAMNLNPG</p> <p>QQQPYFSPAPGQAPGPAAPAAQVQAAAAATVKAHHHQHSHHP</p> <p>QQQLDIEPDRPIGYGAFGVVSVTDPRDGKRVALKKMPNVFQNL</p> <p>VSCKRVFRELKMLCFKHNDVLSALDILQPPHIDYFEBIYVUTE</p> <p>LMQSDLHKIIVSQPLSSDHVKVFLYQILRGLKYLHSAGILHRD</p> <p>IKPGNLLVNSNCVLKICDFGLARVEELDESRLMTQEVVTVQYYRA</p> <p>PEILMGSRRHYSNAIDIWSVGCIFAELLGRRILFQAQSQPIQQDL</p> <p>ITDLLGTFSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA</p> |

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|------------|--|--|---|
| | | | THEAVHLLCRMLVFDPPYKRISAKDALAHFYLDEGRRLRYHTCMCK CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSSEMPSPPLVWE |
| 5638 | 125 | 1155 | DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLGRHLAKIYAMHWGTD SRLLVASQDGKLIWDSY TTNKVHAIPLRSSWVMTCAVAPSGNYVACGGLDNICSIYNLKTR EGNVRSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTFITGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFGTGHESDINAICFFPNNGAFATGSDDATCRLFDLRADQEL MTYSHDNIIICGITSVSFSKSGRLLLAGYDDFN CNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN |
| 5639 | 125 | 1155 | DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLGRHLAKIYAMHWGTD SRLLVASQDGKLIWDSY TTNKVHAIPLRSSWVMTCAVAPSGNYVACGGLDNICSIYNLKTR EGNVRSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTFITGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFGTGHESDINAICFFPNNGAFATGSDDATCRLFDLRADQEL MTYSHDNIIICGITSVSFSKSGRLLLAGYDDFN CNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN |
| 5640 | 280 | 1092 | QQGNKKTMLSHNTMMKQKQKQATAIMKEVHGNDVGM DLGKKVS IPRDI MLLEELSHLSNRGARLFKMRQRRSDKYTFENFYQSRQAI NHSIAMQNGKVDGSNLEGGSSQAPLTPPNTPDPRSPNPDNIAP GYSGLPEKIEPPEKFNTTAVPKYYQSPWEQAI SNDP ELL EALYPK LFKPEGKAE L PDYRSFN RVATPF GGF EKASRMVKFKVPDFELL LTDPRFMSFVNPLSGRRSFNRIPKGWISENIPIVITTEPTDDTT VESEDL |
| 5641 | 27 | 332 | CRHNCNGDVKLLSNQMDKLF AFHLFTFHGLLHFLDGSIQKLIQA EII LSDNSSILVLENNFLFKVKSQFIHLIAKKFYISITIVSAS NGESFVLSMIVTG |
| 5642 | 199 | 1247 | ITPCRMDFLVFLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQ IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY TWEVFGYCOELELSLHYLLPYLLGVNLFFFTLTCTGNPGIIT KANELLFLHVYEFDEVMEPKNVRCSTCDLRKPARSKHCSVCNWC VHRFDHHCWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF LVHLVMSDLYQETYIDDLGHLHVM DTVFLIQYLF LTFPRIVFM LGFVVVLSFLGGYLLFVLYLAATNQTTNEWYRGDWA WCRCPL VAVPPSAEPQVHRNIHSHGLRSNLQEI FLPAFPCHERKKQB |
| 5643 | 1 | 847 | PSGGVRD VETRGPGRSRAARGPRVVMHRRGVGAGAIKKKLA EAK YKERTVLAE DQLA QMSKQLDMFKNLEEFASKHKQEIRKNPEF RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYFELGVQIIIEVC LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAENGYVTVS EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPA LF TDLYSQEITABEAREALP |
| 5644 | 83 | 1138 | PRRMGSWVQLITSVGVQONHPGWTVAGQFQEKRFTEEVIEYFQ KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE IEKVHRGCVIANVSGSTGILSVIGVMLAPFTAGLSL SITAAGV GLGIASATAGIASSIVENTYTRS AELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVETLRTRGAPTRIVRKVARNLGKATSGVLVVL DVVNL VQDSL DLHKGEKSES AELLRQWAQELEENLNELTHIQSLKAG |
| 5645 | 537 | 799 | VQSVRDLKRLSPTDPPGDSGNRDVTRDPVTGPNLSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQIRARRGLPRLAVSD |
| 5646 | 3745 | 3328 | AEQVGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTADP AGKPAPCRVTLTLRLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ |
| 5647 | 288 | 800 | GVIMATSELSCEVSENCERREAFWAEWKDLTLSTRPEEGCSLH EEDTQRHETYHQGCQCVLVQRS PWLMRMGILGRGLQEYQLPY |

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|------------|--|--|---|
| 5648 | 7 | 1518 | <p>QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALLETALGGQCVD RQEVAEITKQLPPVVPVSKPGALRRSLSRMSQEAQRG</p> <p>VLSELGCRHEALREVGAEWPPPTCSNICSGLQQAGNTDWSLTM APQSLPSSRMAPLGMILLGLLMAACFTFCLSHQNLKEFALTNPEK SSTKETRKETKAEELDAEVLEVFHPHTEWQALQPGQAVPAGS HVRNLNLTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYVYHQMNAQD LLSFGGLQVVINGLNSTEPLVKEYAAAFVLGAFFSNPKVQVEAI BGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYACRQFLK LGGLQVLRRLVQEKGEVLAVRVVTLVLDLVTEKMFEEEEAELT QEMSPEKLLQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV LQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELLGSVNSLLKELR</p> |
| 5649 | 1172 | 3006 | <p>MLQEQDLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGS IPTSLTDLASLASAPPLSGRSTPKLTSRAAQDLDR MGVMTLPDDLKRRKLLSPVSRREENREDKATIKCETSPSSPR TLRLEKLGHFALSQEEGKSALEDQGSNPSSSSSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLLQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTAQEKDRRLKKKHQLLEDARRKGMPPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDEIQRIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEMETLETSTK TDSEEGSWAQTAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGINCLKRLNYDRKE LEKRREESQHEIKDVLVWNTDQVHVHVQSIGLRDYAGNLHESGV HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNLLALG TDRKLDGDDKVFRRAPSWRKFRPREHHGRGGMLSASAEITLPA GFRVSTLGTLPQPPAPPKKIMPEAHSHYLYGHMLSAFRD</p> |
| 5650 | 1172 | 3006 | <p>MLQEQDLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGS IPTSLTDLASLASAPPLSGRSTPKLTSRAAQDLDR MGVMTLPDDLKRRKLLSPVSRREENREDKATIKCETSPSSPR TLRLEKLGHFALSQEEGKSALEDQGSNPSSSSSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLLQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTAQEKDRRLKKKHQLLEDARRKGMPPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDEIQRIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEMETLETSTK TDSEEGSWAQTAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGINCLKRLNYDRKE LEKRREESQHEIKDVLVWNTDQVHVHVQSIGLRDYAGNLHESGV HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNLLALG TDRKLDGDDKVFRRAPSWRKFRPREHHGRGGMLSASAEITLPA GFRVSTLGTLPQPPAPPKKIMPEAHSHYLYGHMLSAFRD</p> |
| 5651 | 646 | 1869 | <p>ARQGQRQPPWG*EARAKGPASESRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAAPAPAHPEHPAPAGSASASQ QTPGWFGSCCLAQGWQAEPLGAPGAEDG\VPVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLOAPPRAWASPAAGPGLSSSDYCGGLGA GWRAGISPPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTI PASA CMPSPPVEGSLGLSRKGGHGLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS</p> |
| 5652 | 735 | 343 | <p>HHKKYQHIHQKSFSCFEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRITGEKPLQCEICGFTCRQKASLNLW HQRKHAETVAALRFPCFECGRFEKPDVAAHRSKSHPALLLA</p> |
| 5653 | 66 | 1401 | <p>RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRRRRSLKEATEPQLAMAEFVTLKDVGMDFTL GDWQLGLEQGDTFWDALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ GWLLELQFRRLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMO</p> |

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|------------|--|--|---|
| | | | ES*IKERTQSCVHRFRHGRFRHG\DNVSEKTLTPAKSKEYRGEFF SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK PTVHQECEQGFDKASHSGYPKTHGTGYKFFVCNEYGTPFSQSTY LWHQKTHAGEKPKSQSDSHPPSHDTQSGEHQKTHDTSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKQATFNLKHLIQHQK THAANV |
| 5654 | 3 | 598 | TLPLFPGRFRGWRRCGAAVARNSTGGNVSNQRRDSVRMSAL NWKPFVYVGLASITABCGTFPIDLTKTRFQIQGGTNDKFKKEII YRGMHLALVRIGREGLKALYSG*VGLHAFCHCSLFHMGIDFR PRLHRSQVKSRLCV*KEQIA**/MFSLLISTLISKYIYAADV EKLFFYYIQVQTDNNKKICLFKNI |
| 5655 | 2 | 867 | RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP PLSYPSVFFPAVARVLPQRSQDYRAAGMPQLSGGGGGGGGDP ATDEMI PFKDEGDPQ\REKIFAEIVNPEEGDLADIKSSLVNES EII PASNGHEVARQAQTSQEPYHDKAREHPDDGKHDPDGLYNKG PSYSSYSGYIMPMNMNDPYMNGSLSPPIRRTSNKVPVQPSH AVHPLTPLITYSDEHFSGSHPSHIPSDVNSKQMSRHPAPDI PTFYPLSPGGGGQITPPLGWQQQP |
| 5656 | 228 | 1066 | PRRVPLPEFASGPGAFFHSGRLQRLTKDSAGCFSQCRSRAM LVLRSGLTALASRTLAPQVCSSFATGPRQYDGTFFYERTYYLK PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETETIYLIP WSKLQKPPKEGVYELAVFQMKPGGPAWGDAPERAINAHVNLGY TKVVGVFHTEYGEINRVHVLWWNESADSRAAVRHKSHEDPISWG GVRESVNYL\VSQQNM |
| 5657 | 105 | 1052 | GQRLQSPRVQMPVQPPSKDTEEMEAEAGDSAAEMNGEEEESEER SGSQTESEEEEESEMDDEDYERRRSECVSEMLDLEKQFSELKEKL FRERLSQLRLLEEVEGAERAPETEPLGGQLRSLKIRIQVAGIY KGFCLDVIRNKYECQLQAKQHLESEKLLLYDTLQGELOERIQR LEEDRQSLDLSSEWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYLMQEIDILEDWTAIKKARAASVPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRLRVCPARLLWCCWALPLHL ALVWTPPL |
| 5658 | 2346 | 3541 | TERRVYNPWPEPDP\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLALLKCTDTLQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLSPATVKEE RTMLEDIWVTLSELNVTFSEFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPRLREGGASLRHTALFTKVLENVEGLPS PGSQAEDLQODINAQSLKQVQYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCLRMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQVMCGTGMQRSTLSVLEQAAILARSHGLLPKC IMQATDIMRKQGPVEILAKNLRVKDQMPQGAFLYRLCQPKMN GDL |
| 5659 | 2 | 696 | WKRSGEVSPKGEKGAWRGNSGRPKIIGRAAEANEDRTLGRLLP GNERSQPRSPRLRLAPQLKAEAAADKGLAPVPPFSSGHSGPC\ EREGEQGRGRGRSRGAHLELKPSGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPVWMEQRKEL FRRLQKWELNTYL |
| 5660 | 229 | 853 | PVTMMAFSELPMLLINLIVSLLGFBVATVTLIPAFRGHFTIARL CGQDLNKTSRQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICMIPLGFADDVINLRWRHKLPL TAASLPLLMVYFTNFGNTIIVPKPFRPILGLHLDLGR*SYHCC PYGTYFREPFVLHILLQVFLFCLCVFPDPFW |
| 5661 | 2 | 473 | LNLYPSPCGGIPKLPGLPREAAALGASFLAEAPLPVTVRSGGL AGMAVTCDPKAFSLICFVTLVFLQLPLASICQN*GTDSCASRGK ADFDTGPHAPILAMAGGHVELQCQLFPNISAEDEMELRWYRCQP SLAVHMHGMDMDGEQKWYRGRT |
| 5662 | 2 | 1318 | LRKEGRCRGRSGNRGVAAAPAEGLGGRGMLGVRCLLRSVRCSSA PFFKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF |

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|------------|--|--|---|
| | | | LHVNDGSSLESQVVDASGLDSRELTFGSSVEVQGLIKSPSKR QNVELKAEKIKVIGNCDKDFPIKYKERHPLEYLRQYPHFRCT NVLGSILRIRSEATAAHSFFKDSGFVHIHTPIITSNDSEGAGE LFOLEPSGKLVPEENFFNVPALFTVSGQLHLEVMSGAPTQVFT FGPTFRAENSQSRRHLAEFVMIABEISFVDSLQDLMOVIEELFK ATMMVLKSCPEDVELCHKFIAPGQKDRLLHMLKNNFLIISYTE AVEILKQASQNFTEFEWGADLRTEHEKYLKHCNIPVVFVINY PLTLKPFYMRDNEGDFQLEGSVA*HSLGLMILLSIVVIGQP |
| 5663 | 119 | 698 | PADIGRSTAKTPGPPRSLEMDPRYGMCPKLGASGCPGAERSLL VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQKKEPWNKRHEMVAKPPVICSHFP QDLWAEQDIKDSFQEAAILKKYKYGHANFQIQGCKSVDECKVH KEHDNKLNQCLIPKTKK |
| 5664 | 118 | 572 | SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG GPPPGWDAAPPERGCEIFIGKLPDLFEDELIPCEKIGKIYEM RMMMDFNNGNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLGV CASVDNCRFLVGGIPKTKK |
| 5665 | 347 | 702 | VVQHLITLLHCERTSPAMITSELVQLQDSTNETTAHSDAGSELE ETEVKGKRRKRGPRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR ANGHPPQNGEGEPVTLFEVVKLGKSAMQRC |
| 5666 | 213 | 540 | VSCLPSTCKMITLNNQDPVPFNSSHPDEYKIAALVPYSCIFII GLFVNITALWVFSCTTKRRTTVIYMMNVALVDLIFIMTLFRM FYYAKDEWPFGEYFCQILGA |
| 5667 | 1 | 695 | HPLPSASISGLPSVSLGVSALCVRSALLEAVVPMPLKRRRARVGSF SGDAASSTPPSTRPFGVAIYLVPRMGRSRRRAFLTGLARSKGFR VLDACSSEATHVMEETSAAEAVSWQERRMAAAPPCTPPALLD ISWLTESLGAQVPVVECRHRLEVAGPSKGPLSPAWMPAYACOR PTFPLTHNTGLSEALEILAEAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ |
| 5668 | 691 | 894 | CSFLFCIPDLFLQFLGRKEEEAVLVGGEWSPSLDGLDPQADPQ VLVRTAIRCAQAQTGIDLSGCTKW |
| 5669 | 407 | 1 | DSGAPEGLSFLMSTQEGLSMHAHPQAYTFPIYLHARKRRGEIGD ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFPK ARGAPTKEYSGSPIGSPTTTPPTRPSPFNLPAPHLASMLQKL NSQ |
| 5670 | 3 | 373 | SSECLTMWIFLLPLLLILCTVSVASYELAQSSSVSVSPQTAI ITCSGDVLAKKYARWFOQKPGQAPVLVIYKDTBRPSGIPERFSG STSGTIVTLTISGAQVEDRADYFCYSATDNFLWVF |
| 5671 | 280 | 524 | KFPFKKTPPHLGMSAITLWQFLQLLLDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKNTNMNYDKLSRALRLLFMT |
| 5672 | 2 | 557 | FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPKADITGS SDPYCIVKVDNEPIIRTATVWKTLCFPWGEYQVHLPPTFHAVA FYVMDEDALSRDDVIGKVLTRDTIASHPKGKFLPSHTGLPSP WPPSHSETSPSGSVWSPAQKPFLLSPEAGATPCTPGLCSAACS QAWLLPLP |
| 5673 | 327 | 696 | ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV KLSSQTLIAGDDEKNQRTITVNPAMHGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVVLAAACSPYFCAMFTGDMS |
| 5674 | 17 | 984 | GGSGMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKG EAKNSITDSQMDDEVVYITIDIQYIPCYQLFSFYNSSGEVNEQA LKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEHFNSQ DLVFLLLTPSIITESCSTHRLHSYKPKGLFHRVPLVVANLG MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFEEEDGSLKEVHKIN EMYASLQEEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID MFLKVAVTTTISM |
| 5675 | 80 | 753 | EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRPPG KSGVPVPSAPGSDGKWEERPGMFSLMACCGWFKRWREPVRKVT LLMVGLDNAGKTATAKGIQGBYPEDVAPTGVGSKINLRQKFEV TIFDLGGGIRIRGIWKNYAESYGVIFVVDSSDEERMEETKEAM |

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|------------|--|--|---|
| | | | SEMLRHPRISGKPIVLANKQDKGALGEADVIECLSLKLVNE HKCL |
| 5676 | 2 | 930 | FVSSPPRRPVQPARPGGFLSGRRSLCQVASTPAHVGVMRSPV RDLARNDEESTDRTPLLPGAPRAEAPVCCSARYNLAILAFFG FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACFEHSAPIKVH HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM LLGFGILGTAVLTFTPTAADLGVGPLIVLRALEGLGEGVTFPA MHAMWSSWAPPLERSKLLSISYAGQLGTVISLPLSGIICYMN WTVYVFFFGTIGIFWLLWIWLVSDTPQKHKRISHYEKEYILSS L |
| 5677 | 1 | 1028 | PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA VTAETHPLPLAPLAVCQSVKSPAACQVRPRPRAPALPAALGGP GRSLPGLTAATMSSFSESALEKKLSELSNSQSVQTLNLWLIHH RKHAGPIVSVHRELKAKSNRKLTFYLANDVIQNSKRKGPEF TREFESVLDAFSHVAREADEGCKPLERLLNIWQERSVYGGEF IQQLKLSMEDSKSPPKATEEKKSLKRTFQIQEEDDDYPGSY SPQDPSAGPLLTELIKALQDLENAASGDATVRQKIASLPQEVQ DVSLEKITDKEAERLSKTVDACLNRNGPGTS |
| 5678 | 3 | 593 | SSSPSSSTPSLPLPFYLLGQLRLQLLWGTALHSGAGEAAPCPG GSGRTAAPRTRADPAAQSLMIMNMKNFKRRFSLVPRTEIEB SLAEFTFQFNQLHNRNENLQGLPLGRDPPQECSTFSPDTSGER PQQLSPGVQFORRQNRFRSMEVASGALPRQVAGCTHKGVHR AALQPDFDVSKRLSLPMDI |
| 5679 | 2 | 623 | LNSRVDDFVAVPGAIMDEYVGSAAEWGDEADGGQQEDDSGEGE DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVQL LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLIKH FDPKADSIFTEEGETPAWLEQMIATTTWRDLFYKLAAHPDCL MNLFTVKVGRVLELRRKVFMMNVYFWLLVCFL |
| 5680 | 258 | 592 | RRITSTSEKLQNRNHSHTPLESLIHPQPSYKGFIMFGKKKKIE ISGPSNFEHRVHTGFDPPQEQKFTGLPQQWHSLLADTANRPKMV DPSCITPIQLAPMKTIVRGNKPC |
| 5681 | 45 | 869 | LLCAKTLGVRTKESQAEGYNRSINNQAEDPRFCPSFCWMRSA RQTRPQRLRKEAAREPPTPGSCPGGTGMDGKKCSVMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP PASCVFSQVMNMAFLALVAVLRFTQLKPKVLNPNWLNISGLVA LCLASFGMTLLGNFQLTNDDEIHNVTSLTSGFGLTLCWIQAAL TLKVNINKEGRRVGIPRVLSASITLCVGPLLHPHGPKHPHVC S QGPVGPCHVL |
| 5682 | 39 | 622 | PSRSLGLTMRKWRHREVNLPVETQQDAVCPAIPSPGLSAQTGL QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLVPLLLPGSYGL PFYNGFYYSNSANDQNLNGHGXDLLNGVKLVVETPEETLFTYQ GASVILPCRYREPALVSPRRVRVWKKLSENGAPKDVLAIG LRHRSFGDYQGRVHLRQD |
| 5683 | 89 | 778 | GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRADMORA HYKTDWHRYNLRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFAYENHLKSRHVELEKAVQAVNRKVEMM NEKNLEKGLGVDSDKDAMNAIQAIKAQPSMSFKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAQKLAHSEDD SEDEEHDLC |
| 5684 | 195 | 677 | TWCFRGLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTRHDSSTVEVQDDHIKGPLKVGAI VEKNDLGAY QEAVINKLTDASWYTVVFDGDEKTLRRSSLCKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE |
| 5685 | 779 | 1262 | LLLOQPVVHCFLFPFPRFSHMIIPGPPGPHTTGIPHAIVTPQ VQEQHPHTSDLMHVKPKQEQKEQEPKRPHIKKPLNAFMLYK EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS |
| 5686 | 128 | 1181 | CTWWQVNTITLTDINDNHPTWKDAPYYINLVEMTPPDSVTTTVA VDPDLGENTLVYSIQPPNKFYSLNSTTGKIRTTAMLDRNPDP PHEAELMRKIVVSVTDCGRPLKATSSATVFVNLLDLNDNDPTF |

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|------------|--|--|---|
| | | | QNLFFVAEVLLEGIPAGVSTYQVVAIDLDEGLNGLVSYRMPVGMF RMDFLINSSSGVVVTTTELDREERIAEYQLRVVASDAGTPTKSST STLTIHVLDVNDETPTFFPAVYNVSSEDVPR\GSGWSG*AARN NDVGLNAELSYFITGGNVGDKFSGYRDAVVRTTVGLDRETTAA YMLILEAIDNGPVGKRHTGTATVFTVTLVDVNDKRPILQSSYV |
| 5687 | 17 | 917 | AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA QGDDGAAAVGHVLPVAVGPPVRVNPGLQTPVPRPELLPGP\SSS LHSDSSYPDAGLSDDDEPPDASLPDPPLTVP/ADA/PMPT SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPTSEPAAPSP LPHLTGGPGMYSSEAKLPNSFSCGLAGTGAGI*GTASAHGTG PPVLPHVCTPSLANPQP\AVGPEASSLPGLVSGIGMSA/SAPIS SSPFAIGSCWLRLGIPPPGSGFLCPGRAPGPVPIITHGQEGQGP VLDI |
| 5688 | 1 | 420 | LTKWDLFGNCRYRLKGTIEHGAMPEQGVVWYS/CLYDSRKLFF *SHMIIRSL*KVIDSLGQLPLRELL*LNVIDRCIILAYV LRVEKTFAITYLKNFTVKVDFSLGELPLISMAAILKLWIMKID DGYIPAVE |
| 5689 | 1504 | 3 | HELSGKHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGEIPAL IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPQPCGPRSTSRG GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEAGAH GSTARKPAPATPGTRHPTMETREVAQGWPAQPRSQFWDQHPHS PGEHRPSG\SLPACPPRAWPKAGAVASATGTG\POLPGSRGKQ KLPRTRPPLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\ PQTPGGRGSLEWGLPLYLGPVHDVK*RSDDL*PP*GGGGGGH GAPSTPGPGGEAW*LPQQTSRPKPGQAY*GE\GSPGLQCPCSK EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF GQELKGPLDAGRLWPGAPSASSHR*GG*ERARAGAGHRGST*A SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGLPNR/P GSPPPA*ASAGRKGTVSTLGGGLL |
| 5690 | 1424 | 58 | PSPFAGVCAAPAPLPLALARRDRRCPSPGAEAPWQTGGPAID GAWRTSVSALRRGATG/APCSPGAEAPWQTGGPAIDG\DGELP *VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAGAGQGRQDDPEP DGLRHRQHGAASHARHLRQLRPGHHQNRHVRDPQAPPGGPAP GHAAALPERTRGVAEPFAWAHAGSDAWRAGR*SQRT*ERARPRH PTFGGRAGS\GQPGYQPPNPHPGSPSPAAP\GPRGA*GNPQLE KAPRSRDNPSQGLRTRIRRPETPDGCPSPAGSASASTFRCTS SLSLLP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP* GNFVR*LLLMP/GVA*RHGTSPLGLPSLGNGGQWDSGNLFGTP KG*SHPAFTKST*SMEAESYWNHPR\DRGRQGVRLNCLRVGE SEMWPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTFPFPAG PEGDPGLNSPGLLP |
| 5691 | 107 | 550 | ISNDPSPGYNIEQMAKRGKKLVLPYTVKGMDFSGILSFIED VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG GVGVYVLESVPLSYS |
| 5692 | 1193 | 548 | TQAWTRAEKDRKGSVRALRLHLRGPPT*RGSHPL/QSVPCIQK PSIFSSYP/ILPQSGGEPGPVGEQQPVRRPEQPSGPGASRMPL TSRSVPPGRGALPPDSLSLTKGLPRPSTAGHRVRESGHKVPVSQ RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS VPGLASTQQTLPADSGPGTGGDRATRAGLPGVETMGNGVD |
| 5693 | 1258 | 1330 | ALTVPVVRKGTWVAQPHGCSNLVSRARLDLSSRPSQNTPEQAP *QAGPPSSLRPP\SRRR*APEWPKRATGSRRCGLSAPPWPWPA RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS PEAIVWRSSRFPLWFLRCCFWVSGFKDNPVLRFF |
| 5694 | 3 | 1338 | GSKEPARSLHRRGSGHKSSAGKWSVTLSAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSLSLNPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRRRPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHAQSA KVAGKPEGKATDKGLAVKNTGLQRSSSDAGRDLSDAKKPPSG IARPSTSGSFGYKKPPATGTATVMQTGGSATLSKIQSSGIPV |

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|------------|--|--|---|
| | | | KPVNGRKTSLDVNSNAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI |
| 5695 | 3 | 1338 | GSKEPARSLHRRGSGHKSSAGKWSVTLLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGLAVKNTGLQRSSSDAGRDLSDAKKPPSG IARPSTSGSGYKPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVNSNAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI |
| 5696 | 3 | 1338 | GSKEPARSLHRRGSGHKSSAGKWSVTLLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGLAVKNTGLQRSSSDAGRDLSDAKKPPSG IARPSTSGSGYKPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVNSNAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI |
| 5697 | 1147 | 47 | PSEALSPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPA QGPATVQSVDFVPDDRDLRSFLEDDTPARDEKKVGAQAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGFVPSQDITL SSEEAEVAAPT KGPAPAPQCCEPETKWSIPASKPRRGTAFT RTAAPPPWGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLS FVMDDP DFESEGSTQRRADDFPVRDDPSDVTDE DEGPAPPPPPKLPPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKKEEKEAAKKSKHKKSKDKEEGKEERR RRQRRPPRSRRTAA |
| 5698 | 2 | 666 | GAEEAAEPOEDLPPLSQSSRFFQEQQKMNKSLGPVSKDVAVDFT QEEWQQLDPEQKITYRDVLENYSNLVSVGYHIIKPDVISKLEQ GEEFPIVEGEFLQSYDVEWQTDLLIERIQEENKPSRQT VFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMAKDECSGCGKSLHLIKLBKTHPGDQAYE FNQ |
| 5699 | 2 | 1448 | RVRQPPGLWVRRTPVAMQCPAGLSRVPGVAG/DFSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKELA RPS/GRTNAPPQGGKPKAGKAAPGPAAGRAMR\PGHGPLLAS DSQRSSSKSGSWETPVWPS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPFGALRSRTEFAGWVPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQKPGCRPPCALPKPAGPERSA* GGS LGCR/SMLPASSGPPFAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGLPGPGW*TLDELPA HPAHPFGSAPPWALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG |
| 5700 | 923 | 597 | NGHKGVWEINIIY*RRSNHKNKSSESHLNQDHSFPPTPNARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRITICQEFSSCLQCAAYLD E*CSIASSLIKAILRVSVLSE |
| 5701 | 59 | 410 | IFEKICSDTQEFISPEINPOICSWLIFDKGAK/NHATGKDSLFP KNSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL LEENTGENLHDTGLGNVFLDMTPKTQPTKQK |

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|------------|--|--|---|
| 5702 | 3 | 1517 | ETFDVPSQCGIPSDSPHPVITPSRAESSASSDGHVPVITPSRAESSASSDGHVPVITPSRAESSASSDGLHPVITPSRAESSASSDGHVPVITPSRAESSASSDGHVPVITPSRAESSASSDGLHPVITPSRAESSASSDGHVPVITPSWSPGSDVTLAEALVITVNIEVINCSITEIETTTSSIPGASDITDIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAEITLSTAGTTESAAPHATVGTPLPTNSATREVTAPGATTLGALVTVSRNPLEETSALSIVETPSYVKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAAKNFTPSETLIMDI TTGKPFPTSRDPLSPVPTTTNSSRGTNSTLAKITTSAKTMTKP PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAK GCCP*PGPPPTDCSCVTVLRGTKQKVMKGSMSKPLTPDVATGPS LTSTGVYVWGGASVPVPRGVLGLTLAHVLCFSKEKT |
| 5703 | 14 | 1117 | HHKDSRSQGLPRTOECARPELRPLLCPRALWVTRLSYRCPWQA PKAGIGTKAKPSSESHLKLHPGWPSLDRQGEPTLGTGTGHCSDS RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS ALPTGPRCW*APRGRTRQPCGWPRLSPPHATADWGPCLSPSR GSWETAPGS*WCPWL*AAWWTGWRTASGASAGLGRAADRPASAWA RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSAPAGGDQC ACGRGPGSC*HPPFPWPVSPSSFPVPCPSGR*HLRGPLLSAARPA AGWPRHSPHDTQTPEP |
| 5704 | 23 | 562 | GDYFDSFVWDDISQAAKDLVTRLMEVEQDQRTAEBAISHEWI SGNAASDKNIKDGVCQAI EKNFARAKWKA VRVTTLMKRLRAPE QSSTAAQASASATDTATPGAAGGATAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP |
| 5705 | 23 | 562 | GDYFDSFVWDDISQAAKDLVTRLMEVEQDQRTAEBAISHEWI SGNAASDKNIKDGVCQAI EKNFARAKWKA VRVTTLMKRLRAPE QSSTAAQASASATDTATPGAAGGATAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP |
| 5706 | 1161 | 610 | QLGRFXAQDTVAIRKVKVFCTGAMRHVVILFTHKED*GGQALD DYVANTDNCSLKDLVRECERRYCAFNWNGSVVEEQRQQQAEALLAV IERLGREREGSFHNDLFLDAQLLQRTGAGACQEDYRQYQAKVE WQVEKHKQELRENESENWAYKALLRVKHLMLLHYEIFVLLLCISI LFFIIFLF |
| 5707 | 28 | 609 | GSPAPTGPFRRRPGRGTSPGTRHHQGRAEPEPDAPERAPLRR* MFAIQPLAEGGQFLGDPPLGQCPELQPDNSNFMASAKDANE NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA EIPGAEPKMGAGTVCSPLEDNGYASSSLSIDSRSSSPPEPACG TPRGPGPPDPLLPSSVAQA |
| 5708 | 44 | 1925 | SFSWEETISPCFPKMAEPWNLSFVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPAKPKP PRCPTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAALHRRAGAGSLCLSASLLPPSFSLGAPGAPSP LRVSPASGGPRKEGRQSGG*AGGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSAGMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRRGP*AGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRVCTCTGLPCPGIPLSGASPGSGSETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGRTRPWAGPTRCTSTAPSRAPVSRCPPPPPPP PPRPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPPEPPPPPPARRP |
| 5709 | 2 | 2031 | ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELETSWG LHQIVVRNAGAVVMRAGMGGCRCWGVMAFPAPR/NALSFLVNDCS LIHNNVCMMAAVFVDRAGENKLGGLDYMYSAGNGGGPPRKGIPE |

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|------------|--|--|--|
| | | | LEQYDPPPELADSSGRVREKRSADMWRLGCLIEWFNGPLPRAA ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFI SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFEDFCRHK VLPQLLTAFEFGNAGAVVLTPLFKVKGKFLSAEYQQKIIPVVV MFSSTDDRAMRIRLLQQMEQFIQYLDEPTVTNTQIFPHVHGLD NPAIREQTVKSMILLAPKLNANLNVELMKHFARLQAKDEQGPI RCNTTVCGLKIGSYLSASTRHRVLTSAFSRATRDPPAFSPRVAG LGFAATHNLYSMNDCAQKILPVLVCLGLTVDPBKSVRDQAFKAIRS FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAASWAGWAVTG VSSLTSKLIRSHPTTAPTETNIPQRPTEPGVPAPAPTVPVATPT TSGHWETQEEDKDTAEDSSSTADRWDEDDWGSLEQEAESVLAQD DWSTGGQVSRASQVS\TPTTNPNNPQSPTGAAGK\RGLLGTGLA GAKLPGATS*RYTAGQRV |
| 5710 | 1 | 562 | IPGSTISCEVELMARMAKTIDSFTQNTRLVVIDGLDACEQDK VLQMLDTRVRLFSKGPFIASFSDPHIIKAINQNLNSVPSGFK \LNGHDMYRNIVHLPVFLNSRGL/RQ/LOENFS*LQQQMETFHA QILQGYRKMLTETEEFHRFALGR*QNLVARQPSIDG*DAIGFELYV CIAIQFNTNKDDAT |
| 5711 | 1526 | 1130 | RRHPFQWTTVTQEAFFSHHDVAFSTSPVLFYFDSAQPFIVKSESS SQIAKAVLSQQRPSTLFECAFHFFS*SLQRHTINLDQGI*LLM LSEBRQHLFESS/IWTTPHNLK*/FEIHEHLSGHEGHWTLLFFLL QIL |
| 5712 | 3 | 1391 | GRKLFQSLDISERLKLTLTDCVDDTLVLAEHBGCLDIKELP ETVIDLNLKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPPTKPA SLFSSSLRCADLTLPEDISQLCKDINNLYLAERSIEEVYVLWC AGGDLEKELVNKEIIRSKPPICTLPNFLPEDGESFGQGRDRSS/ TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN NELSAAATLPLIIREKDTYQLNRIILFDRLLKAYPYKKNQIWIK EARVDIPPLMRGLTWAALLGVEGAIAHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRVLKAWVVSHPDLVYWGGLD SLCAPFLYLNNFNEALVYACMSAFIPKYLYNFFLKDNNSHVIQEY LTVFSQMIAPHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFLP HKIFHLW\DTLLLGEFLFPILYWE |
| 5713 | 634 | 284 | PVCAPVVDWRVPLPREDOEGQQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWVPLGTSSATSP *RAVLTSPCSHLGSADAASSHWLGCVSFH |
| 5714 | 212 | 613 | WGLGLGPTMSSSLGGGSDAGGSSSSSTNGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERNRKSGIISEPLNKSLLRRSRPLS HYSSFGSSGSGGSGGSMMGESADKATAAAAAASLLANGHDLAAA MA |
| 5715 | 131 | 1979 | ESASQQRKSKCLILTLKLELSGSAPKKTSSARPGSSLWLPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK/ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSPMVNN DSTCHEHHEGILAAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFFAAHGGPVNTPHGGEKFTFMS QIRRKETKPL*RTKTPAG\NNYQNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCLSLAGGQ*PPGL YPKTPKQRRWRRLP/LGPGSQ*GSRQSTC*EV\GALGEPVRIPL L*PDLSCILSNGSKHRRREGLSFPRSLGPGRRGPAQLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVSGSHVALQAGHDSTQDVGRF VWRWIPLE*LGLSRETGOATRRLVWISPGRAAAACVACAQALE EGPLRLPQGDRGAQPCSHCPGRAAGQBPBGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWAAMLLLLRHGSHSEL TDLTAQTSQH |
| 5716 | 1711 | 1370 | RVFSLCEGPGHCYQGAVEREACAAASPLDSAAEFHRLCEHTD *LPK*GPGYIQHFHCDNLCILYNISFNLSYSF*GVARYAC* RCPLVL*SGFFTTIIVGGYSCCMPLKT |
| 5717 | 44 | 1489 | LPTEALRESEWVSEYKCGKPRGLVPEGESTSLPSSVDTEDSLD BGPAGLVLESDDLGLDLEFEFEFEFEFEEDGNSDQMGFERDSE |

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|------------|--|--|--|
| | | | GDSLGRPGLPYGLSDDES GGGRLSAESEVEEPARGPGEARGE RPGPACQLCGGPTGEGPCGAGGPGGGLLPRLLYSCRLCTFV SHYSSHLKRHMQTHSGEKPFRCGRCPYASQVLNLRHTRTHTG EKPYPCHPCPFACSSGLNLRHQRTHAGPPTPPCPTCGFRCTP RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPVGGASFLPDCG Q\CGVKGASAGLDQNHQS/SLPFWTCRGCGQEELEEGESRLG AAMCGRCMRGEAGGASGGPQGPSDKGFACSLCPFATHYPNHLA RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGKPYKCP CPYACGNLANLKRHGRHSGDKPFRCSLCNYSNQSMMNLRHM |
| 5718 | 120 | 284 | VAHALSLPAESYGNVDSMTHPQLPPTQLAWDLCTCLPLSYNFT S**STADPLHL |
| 5719 | 48 | 428 | ELNNGPFPQMLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL LSQYNNVNAVTLDHVTPLEHACLDGHVACARTLLEAGANVNAIT IDGVTPLFNACSQGPSCAELLLEYGAKAQP\ESCLPSP |
| 5720 | 1 | 1051 | LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK \RCT\YYE\TCGGTYGLQMWVSVSQDVAQKVVAL\RKKQQ\LAI GPCK\SLPN\SPSH\SAVSAASIPARAPINQGE/SGGSAFSD Y\SSSVPTSPISQRELRIETIAASSTPTPIRKQSKRRSNIFTS RKGADP\DREKKAAGCKVDSIGSGRAIPKQGIILKRSKSLNK EWKKYVTLCDNGLLTYHPSLHDYMQNIHGEIDLRLTTVKVPG KRLPRATPATPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS LHSEPLSSAWAGPRPEGLHQRSCSVSSADQWSEATSLPFGM QHPASG |
| 5721 | 97 | 492 | RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA VFYAIAGGLFLERAYYYFAAHHTGITDTRVGIILSRGTAASI SFMFSYILLTMCNRLITFLRETFLNRYVPPDAAVDFHRLIASTA |
| 5722 | 88 | 1043 | VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGGQGRGAERERAAQARRGRPPGPEPDQSCG GRPRRAAAPGRAPADPPAPRPAPADVRFPADAPAPAPAPA PPPPPHLGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI |
| 5723 | 88 | 1043 | VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGGQGRGAERERAAQARRGRPPGPEPDQSCG GRPRRAAAPGRAPADPPAPRPAPADVRFPADAPAPAPAPA PPPPPHLGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI |
| 5724 | 3 | 1841 | FTNEAPPAPLPDASAPLSPHRRAKSLDRRSTEPSVTPDLLNFK KGWLTQYEDGQWKXHFALADQSLRYRDSVABEADLDGBID LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRTBKQAEELGEP DPEQKRSRARE\RRREGRSKTFDWAERFPIQQAQAQERVGGVGP ADTH\DPWRPEABHGELEERARRRERERRKRFGLMDATDGPTE DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWQHVVETPLREEK QVPIAPVHLSSEDGGDRSLSTHETLSLEKELEQSQKEASDLLEQ NRLQDQLRVALGREQSAREGYVLQATCERGFAMEETHQKKIE DLQRQHORELEKLRKEDRLAEETAATISAIEMKNHAHREEME RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSQYQS QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE ITRLRLTLLTGDDGGEATGSPLAGGKDAYELEVPSSGARPCLTQLC TQEPQGSAAWPLSYRVVGGTDLRQESQGPGRSKSPGEGEEQ |
| 5725 | 3 | 1049 | VNGHSEETSQSPNRTPEPHSDCSVDLGISKSTEDLSQKSGPVG SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG KNIVRSKAATLLYDQPLQVFTGSSSSSDLSGTAKIFKFDNNHN PE/GAKYNKRPHKWAHNLHLYMVLHSIIISNTVAV\RSQRHFVA |

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|------------|--|--|--|
| | | | LQTKSPNRPCCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFNSHN NVRANTAYHLHQLRGLPARHGEMWAISPNDRLIPAVTRSTIQRQS SVSSASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG SQRPLSARTYSIDGNASRPQARSINEIPERTMSVSDFNYSR TSP |
| 5726 | 2 | 486 | SRSLSMWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG QSGPGSGEGPPLSSPSQPLPADLPGLATLPDVGLELEVRPLAVT GLIFHLGQARTPPYLQVTEKQVLLRADDG |
| 5727 | 21 | 221 | RPILILKETRRLPWATGYAEVINAGKSTHNEQASCEVLTVKKK AGAVTSTPNRNSKRRSSLPNGE |
| 5728 | 2 | 877 | GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDPFAVE GR/PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ GGPAGAGGDAG/LPGRCPSPAPWRAGSRPAASCPDWIPGPQGLWL HRNPTS/GPPSQIGEGAEQGDGVDAPQIQCKN/GAEDPPAED EPPQVPEAGEEDAVPABEGPGGT PETQADQVRERPEAHLAEGGA KGSRRRLADPQDLFAGQMSLAPFPFPVAVIRSNK |
| 5729 | 1 | 1525 | AGGAREVLTLLQGHFAGFVGAHWNQDAAALGRATDSKEPPGEL CPDVLYRTGRTLHGQETYPRLILMDLKGSLSSKEEGGLYRDK QLDAAIAWQGLKLTTHKEELYPKNPYLQDFLSAEGLSSDGVWRV KSI PNGKSSPLPTATTPKPLIPTASIRVNSDFLRVHLHPRSI CMIQKYNHDGEAGRLAEPGQGESVLKEPKYQEELEDRLHFYVEE CDYLQGFQILCDLHDGFSGVGAKEALLQDEYSGRGIITWGLLP GPYHRGEAQRNIRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS/YRLCSSPVS MVHL/ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLQFGGAT PWTPLSACGEPGSGTRCFAQSVVLRGIDRACHTSQLTPTGTPPPSA LHACTTGEEILAQYLQQQPGVMSSSHLLLTPCRVPAPPYPHLFS SCSPPGMVLGDSPKGAIVESVPVFG |
| 5730 | 1258 | 1713 | KKFQAPARETCVEQCTVYPMERLLANQQVFHISCFRCSYCNK LSLGTYSALHGRYICKPHFNQLFKSKGNYDEGFGRPHKDLWAT KIETEGFWERPRNFENQGRPLKSPGGEDCPC*GGCPCGSNY*AQ GSSSREKGGQASWNPKLRA |
| 5731 | 122 | 443 | RSHRGELIPKDCYMRKPPRRPKRRQG/CALPQGCCLTFKDVAI EFSLEENKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRQEWFFLRVY |
| 5732 | 226 | 772 | PPSRSCQSPRRKSRRAHVTVTLVCGFTSFSFSLFLYLCGCCLRF PERTCSQLQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLEQGRGKDQPGRLKKVQGIWYLDENLA QVSTNLLDFEVTALHTVYBETCREAQELSFPVVGSQLVGLVPLK ALLDAA |
| 5733 | 1 | 460 | PALQEVNANALAWGQYENDARTLFEPTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\BFIGKMDEVLSRDPM |
| 5734 | 3 | 968 | RCNSPESLTSLLVLLTTANNLFVLI PAYSKNRAYAIFPIVFTVI GSLFLMNLITAIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEAGFAPQAVGVKPNLLQVLQVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSFPLQSAQFLFG HYFYDYLGNLIALANLVSCVFLVLADVLPAERDDFILGILNC VFIVYLLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL/VCTDCHTQAGGRWW/RLLSLWDMTRMLNLIVFRFLRIIP SMKPMVAVVASTVLGL |
| 5735 | 2 | 540 | FFTPCVARAFNFPDQATVKKAAYS LPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLQ YPVFPWVLTNYESEELD LTLPGNFRDLSKPIGALNP KRAVFYAE RYETWBDDQSPPHYNYHSTATSLSWLVIRVISIFIELACLWY LKILT |
| 5736 | 1 | 382 | GTRPSTKSGYSPQQVAVIHCKGHQKENTAVAHNSQKADSAQV |

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|------------|--|--|---|
| | | | TARLSVTPPNLLPTVSFPQDLDPNPVYSTTEKLASDLRANKN QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR |
| 5737 | 290 | 1041 | KACLHLLSSFLTNSFLNPLLPDSLYSVEARSQRANLGPCCRKR LQTLMLRLAAGFYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG* RTADGSCGRGPDGAHHPGPKSSSWRASRLPLGLGGSHHLDAYVG RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V ETRPLTDGRR*PGVRPVGWTPAHAGTTLRPRGAVEPSVSACGKW APSPTSQGCCEGRCDAPVKHRAWRTPLCSQ |
| 5738 | 8 | 460 | DTLSLNLCTLPETLPMTPSF*LSFL*FPGLARAKSIPKTYTSEV VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT ATQPAAPLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI FRILSEEAWALCAVETHR |
| 5739 | 1 | 1222 | SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV SAEVDGVPVGYLSSPQSITDTCLYIFTSGTGLPKAARISHLKI LQCCGFYQLCGVHQEDVIYALPLHYMSGSLIGVCMGIGATV VLKSKFSAGQFWECCQHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRFPGLQVLETYGLTEGNVATINY TGQRGAVGRASWLYKHIFPFSILIRYDVTGEPIRDPOGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPPELAQGLKLDVFRPGDVFFN TRDLLVCDDQGLRFRHRTGDPFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV |
| 5740 | 265 | 231 | PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPLCLGMLMA LQSELHLKYDEETQSVWSGSACGGYP |
| 5741 | 1 | 650 | PRKTMRRGVMLTLLQQSAMTLPWLWIGKPGDRPPLCGAIPASGD YVARPGDKVAARVKAVDGDEQWILAEEVVSYSYSHATNKYEVDIDE EGKERHTLSRRRVIPLPQWKANPBTDPALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLFEEDTSYADGYSPPINVAQRYV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPLKKK |
| 5742 | 2 | 362 | TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTETVQDLDLAG TYVNIIPDRSGDVTLVIGAVRGHVEIVRALLQKYADIDIRGQDNK TALYWAWEKGNATMVRDILQCNPDEICTKDG |
| 5743 | 2 | 415 | GKTPEGIDAIEEIEIDLEETEREISPOENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPOE |
| 5744 | 3 | 703 | TRRTTTTSPTTTQMTTTPAALPTTVVTTTPTDITGTFLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVNDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEPISQLLMIAP SLGFVLFAFVAFLLRGKLMETCYCSQKHTRLDYIGDSKNVLDV QHGREDEDGLFTL |
| 5745 | 1400 | 599 | GKSRFVNLMKHSKKTYSDFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPSCNIPQT VENRLPQWLPAHDSRLRLDSLSCQFTRDCFSEKPVPLNFNQOE YICSGHGEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEERSKHKKKSCEEIDLKHKSIQRKKTEVEIETVHVSTE KLKNRKEKSRDVVSKEERKRTKKKKEQGQERTEEEMLDQSI LGF |
| 5746 | 3 | 821 | SFASGRLTPSSPAFDGELDLQRYSNPGFAVSAWSLGMGAVSWSES RAGERRFPCVCGKFRFNSILALHLRTHQPERPRSPAARLLE LEERALLREARLGRARSSGGMQATPATEGLARPOAPSSSAFRCP YCKGKFR TSAERERHLHLRHPWKGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPPQPPQPPQPEPRSVPPQPEPEPQPER EATPTPAPAAPEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHA SFDHACPV |
| 5747 | 2 | 1328 | DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PPRGKGYSSNYRRSPERPTGDLRERIKNRQDQVDTEPQKRNTE ESSSPVRKESSRGRHREKEDIKITKERTPESEENVEWETNRDD |

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|------------|--|--|---|
| | | | SDNGDINYDYVHLSLEMKRQKIQRELMKLEQENMEKREETIIK KEVSPVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS AVSSPLDQQRNSKTNQSKKKGPRTSPPPPIPEDIALGKKYKE KYKVKDRIEKTDRGKDRGRDFERQREKRDKPRSTSPAGQHHS ISSRHSSSSSQSGSSIQRHSPSPRRKRTFSPSYQRTLTPLRRS ASPYPHSLSSPQRKQSPPRHSPMREKGRDHRTSQSHDRRH ERREDTRGKRDEKDSREEREYEQDQSSSRDHRDDREPRDGRDR RE |
| 5748 | 934 | 473 | SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSSLKHLVKWAI PAEG KKNENLQNLGCGAGVISKTLTYPLDLFKKRLQVGGFEHARAA FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLKKAALSTGFM FFSYEFFCNVFFHMCNRTASQR |
| 5749 | 552 | 1 | GFPVDPVRVGSSTLSLAERP KGMIRSGSFRDPTDDVHGSVLSLAS SASTYSSAEERMQSEQIRKLRRLESSQEKVATLTSQLSANAN LVAAPFQSLVNMTSRLRLHAEAEKDTELLDLRETIDFLKKN SEAQAVIQGALNASETPKELRIKQNSSDSISSLSITSHSSI GSSKDADA |
| 5750 | 22 | 866 | IFISICLWNAHLCFLLLPKDCIDQVMKLNLFVDDSGRYLAIQF HLEWAYVFLYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTF QENYVAQLILDVRREGDVLNCEFTPAFTPQEHILTNNLELNDT ILNDIKLADCEQFQMPDLCAEETIILGICTNFQKNNPVHTL VELLAFTSCLLSQPKFWAIQTSALILRTKLEKSTRRVERAMRQ TQALADQPEDKTTSLERLKI FYCCQVPPHWAIRQLASLLFEL GCTSSALQIFEXLEMME |
| 5751 | 3 | 751 | SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA FAAGETPLVLRSSAHWWLAARARSGETGYVPPAYLRLQGLEQ DVLQAI DRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS RRGPSASSVAVMTSSTSDHLDAAAARQPNVCRAGFERQHSLS SSEHLGADGGLFQIPLPSSQIPQPRRAAPTTPPPPVKRRDREA LMASGSGGHNTMPSSGNSVSSGSSVSSCI |
| 5752 | 3 | 471 | GPVCGVGLSVAWAGPWRGPVHVSVGGGGRALHGAELPCLSGAAT VEREMELRHKNEMLRVETBARARAKAERENADI IREQIRLKASE HRQTVLESIRTAGTLFGEGFRFVTDKVTATVNI FIKQGWQV AERQHVGSWSVSRSCPCRLCTAL |
| 5753 | 34 | 483 | DDXAI PGGVQAFPGAVRNITYTPTGHRIRKLDQIQSGGNYVAG GQEAFFKKNLYLDIGEI KKRPMEEVNTVVKPIHSRINVSARFRK PLQEPCTIFLIANGDLINPASRLIPKRLNQWDHVLQMVTEKI TLRSGAVHRLYTLLEGRLV |
| 5754 | 14 | 331 | TLVHVVEPAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW WPTPATPSPLTAPFSME |
| 5755 | 3 | 888 | LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI WMEKRHRGPGGLAPGQLYTPARCWRKRRRLHPPDPKLRLLLEIK PEVELPLKKGFTSESTLEALLRGEGVEKKVDAREEESI QEI Q RVLENDENVEEGNEEDLEEDI PKRKNRTRGRARGSAGRRRRD AASQEDHDKPYVCDICGKRYKNRPGLSYHYATHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDTGTVIPNNYCDPCLGGSNMNKK GRPEELVSCADCGRSAHLGGEGRKEKEAAA |
| 5756 | 3 | 621 | SSKLQALFAHPLYNVPEEPPLIGAEDSLLASQEBALRYRRKVAR WNRHRKMYREQMNTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFYFIDFQRHNAEI AAFHLDRILDFFRRVPPTVGRIVNVTKEL |
| 5757 | 3 | 473 | YKDALLPDNHRQVVFENGTLKLTVDQKGMDEGEYLCVLTQPO LSISQSVHVAVKVPPLIQFEPFPASIGQLLYIPCVVSSGDMPI RITWRKDGQVVISGSGVTIESKEFMSSLISSVSLKHNGNYTCI ASNAATVSRERQLIVRVPPRFV |
| 5758 | 1 | 474 | FRGAGAERGEHREGGAAGMGFEKVHVRVFFNYVPSGIRCV YNNQSNRLAVSRDTGTVEIYNLSANYFQEKFFPGHESRATEALC WAEQQLRFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP |

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|------------|--|--|---|
| | | | SGSQLLVGCEDGSKVLFQITPDKIPV |
| 5759 | 2 | 1240 | GNAAFAGQGVVYETFFHMSDLPSYTTNGTVHVVNNQIGFTTDP MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAEWRNTF NKDVGADLVYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA DKLIAEGTVTLQEFEEIAYDRICEEAYGRSKDKILHIKHWL DSPWPGFFNVGDGPKSMTCPATGIPEDMLTHIGSVASSVPLEDF KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVR NGQDVERGTFSHRHVLDHQEVDRTTCVPMNHLWPDQAPYTCN SSLSEYGVLFELGYAMASPNALVLEAOFQGFHNTAQCIIDQF ISTGQAKWVRHNGIVLLPHGMEGMGPEHSSARPERFLQMSNDD SDAYPAFTKDFEVSQ |
| 5760 | 1 | 1221 | VRDITSDLSLSWTVPFEGQDFHFLVQFKNGDGQPKAVRVPGHED GVTISGLEPDHXYKMNLYGFHGGQVRGVPVSAVGLTAPGKDEEMA PASTEPTTPEPPIKRLEELTVTDATPDSLSLSWTVPFEGQDFH LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNXYKMNLYGFHGG QVRGVPVSAIGVTAEEETPTPTPEPSMEAPEPPPEPLLGELTVTG SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPVVRVGGEESEVT VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGTAPQEDVDETPSP TEPGTEAPEPPPEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR RLGPVSAIGVT |
| 5761 | 3 | 1275 | SCDMAEAAALVWIRGFGFGCKAVRCASGRCTVRDFIHRHCQDN VPVENFFVKCNGALINTSDTVQHGAIVSLEPRLCGGKGGFGSML RALGAQIEKTTNREACRDLSGRRRLRDVNEKAMAEWVKQAEARE AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK GMQAASSKMVSAEISENRKRQWPTKSQTDREGASAGKRRCFWLG EGLETAEGSNSSESDDDSEEAPSTSGMGFHPKIGSNGVMAAK FPSGSQARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETETQEKKAESKEPIREEPTGAGLNKDKETEERT DGERVAEVAPEERENVAVAKLQESQFGNAVIDKETIDLLAFTSV AELELLGLEKLEKLMALGLKCGGTLQ |
| 5762 | 2 | 344 | GSTGQTPLHSQGGGGGGSGGRRRTPRGMPKEKYEPDPDRMYTI MSSEBAANGKKSHWAELEISGKVRSLASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR |
| 5763 | 3 | 429 | LDKDTGLIMLIARLDYELIQRTLTIIARDGGGEETTGRVRINV LDVNDNVPTFQKDAYVGALENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN |
| 5764 | 19 | 441 | VCARACGEMRQLLRPIDRQRYDENEDLSVVEITVSVRGFSLEEK LRSQLYQGDFFVHAMEGKDFNYEYVQREALRVPLIFREKDGGLIK MPDPDFTVRDVKLLVGSRRRLVDVMDVNTQKGTMSMSQFVRYE TPEAQDKL |
| 5765 | 3 | 825 | QKILRLNNSHQPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETS KSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSTSTSTS AATAGAGSCGSKSEKPGKSQSSRGAKRDKDAGKSRKDKHDLQ GHQNGSGSQAPSGGHLYGFGAKSNGGASPFHCGGTGSGSVAAA GEVKSAPDSGLMGNSMLVKKEEEEEESHRIKKLKTKEVDPLF TVPAPPPHV |
| 5766 | 1608 | 663 | SGLFSVDPASSQAMELSDVTLEIGVGNEMVAVGVVLLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTLPHPSGNDKAEAGEGRDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSSESTCLPSPGLITVRLKPLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFFVLLGVVWYFRINRYQFFATPATVSLVGTVVFFSFLV FGMYGR |
| 5767 | 2 | 892 | NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRKMKANIKLVG SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS LTEVKEVEEERDPQSFEFEIEEEEMLSVIPSRRRENEPLDFP |

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|------------|--|--|---|
| | | | HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLEKRRLDIEABR LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKRLQIV NSEKPSLRNELGQGEKSMQPDIEKLEKLERERLQLEKDRLO FLKFESEKLEKLERLQVEKDRRLRIQKEGHLQ |
| 5768 | 3 | 476 | SSRSRLSVSVSPPPGIVELGPPFAWEFCRSLGSVTSQRAGPA AMVAKDYPFYLTVKRANCSLELPPASGPAKDAEPPSNKRVKPL SRVTSANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP WSRNAAPSSTKRRDSKLSWSETFDVC |
| 5769 | 38 | 667 | TKTKKGVEKATDQSVKFAEHCPQLQYVGMGCSVTSKGVHIL TKLRNLSSLDLRHITELNETAMEIVKRCNLSLNLCLNWIIN DRCVEVLAKEGQNLKELYLVSKITDYALIAIGRYSMTIETVDV GWCKEITDQATLIAQSSKSLRYLGLMRCDKNEVTVQVLVQY PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS |
| 5770 | 1 | 484 | DSRRYDVKTRKWSFLLLEHSLIAKVRCLPQVQLDPLPTTLTA FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAVNF AKGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVPSSVRFT WEQAFRLRWLPSLSPDCINVVTGKDRLLTA |
| 5771 | 168 | 741 | GLLPSACLARSWREASEGPPSSRACSNQSQDTFEACYSGTSPS FHGSHCSGSDHSLGLEQLQDYMVTLRSKLGPLEIQFAMLLRE YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF LEGVIGREGGILTDSFGRIKRSMSSTSASAVRSYDGAQRPEAQ AFHRLADITHDIE |
| 5772 | 148 | 383 | EFNLALVSPSHPIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG ILTFSNLVTCSAIYHLPVFPEREPCGSMRDLRA |
| 5773 | 2 | 723 | PRVRSKHNFCEMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE KIPLSQEEITLQGHAFBARIYAEDPSNNFMPVAGPLVHLSTPRA DPSTRIETGVRQGEDEVSHYDPMIAKLVVMAADRQAALTCLRYS LRQYNIIVGLHTNIDFLNLSGHPEFEAGNVHTDFIPQHHKQLLL SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHQDQSPFSSSSG RRLNISYTRNMTLKDGNKSK |
| 5774 | 2 | 592 | FVEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST VTEBCVHILHGHRLNLTGQIQLNPNHLLQYSCSLDGTIKLWDYI DGILIKTFIVGCKLHALFTLAQAEDEVFVIVNKEKPDIPQLVSV KLPSKSSQEVKELSEVLDYINQSPKCIAFGNEGVIYVAAREF YLSVYFFKKETTSRVTLSSS |
| 5775 | 3 | 538 | SSGCCDPAAPSSLAEAATMPVSKCPKKSSELWKGWDRKAQRNGL RSQYVAVNGDYVGEWKDNVKGKGTQVWKKKGAIYEGDNKFGK RDGYGTLSLPDQQTGKCRVYSGWVKDKKSGYGIQFFGPKYY EGDWCGSQRSQSGWGRMYYSNGDIYEGQWENDKPNEGMRLRLSQNP RP |
| 5776 | 2 | 484 | RLPQDCVCQNLSESLGTLCPSKGLLFVPPIDIRRTVELRLGGNF IIHISRQDFANMTGLVDLTLSRNTISHIQPFSLDLESRLSLHL DSNRLPSLGEDTLRGLVNLQHLIVNNQLGGIADEAFEDFLTL EDLDLSYNNLHGPVAVGLRGDAWVQFSTS |
| 5777 | 2 | 949 | QDPEPGQDLFQPEREVDPSWGRGREPRLGKLRQNDHLSVLKQ VKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSRRPWDRSLENV YRGSEGSPTKPIINPLPKPRRTFKHAGEGDKGKPGIGFRKEKR NLPLPLSLPPPLPSSPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRDWYAQTKLGLTRTLSEENVYEDILDPMKENP YEDIELHGRCLGKKCVLNFASPTSSIPDTLTQSLSKPAFFRQ NSERRNV |
| 5778 | 1 | 1210 | QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEGGEPAGVAEPPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENQPPSKQVKPLFRHFRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSLRSASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV |

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|------------|--|--|--|
| | | | PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHNELPRCVHELEFV DYVFHGE |
| 5779 | 138 | 1671 | EAVQVLIKHSADVNRDKNWQTPHVAANKAVKCAEVIIPLLS SVNVSDRGRTALHHAALNGHVEMVNLALLAKGANINAFDKKDRR ALHWAAYMGHLDVVALINHGAEVTCDDKKGYTPLHAAASNGQI NVVKHLNLNLGVEIDEINVYNTALHIACYNQGDVAVNELIDYGA NVNQPNNGFTPLHFAAASHTGALCLELLVNNGADVNIQSKDYGK SPLHMTAVHGRFTRSQTLIQNGGEIDCVDDKNTPLHVAARYGH ELLINTLTITSGADTAKCGIHSMFPLHLAALNAHSDCCRLLSSG QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAGGNVECI KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGRALTALHYAAASMDRNTILGNAHDNSEELERARELKEK EATLCLEFLLQNDANPISIRDKEGYNSHYAAAYGHRQCLELLE RTNSGFESDSGATKSPHLAVSEMP |
| 5780 | 154 | 624 | QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDSENGEKESEPV EITSVVKGSHFPVGVVPPRAKSPTEPSESTIASYVTLRKTCKMM DLTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQACREK KKQLNVIGASDQSPSQSPNLDRNP |
| 5781 | 19 | 941 | RGSLGGHPWRPFMRASQGCPLVSVFTGPHQERAYGGRPGGAF PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAHRDGE QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEPRRPLDRSPPLQG VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHSIHTVTCSPQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR CRQALPPQG*ROQPRQRPR/PTGASRSHPAKAGCQGPPIRNY NIMD |
| 5782 | 5176 | 1237 | DRSMMSMAADSYTDSYTDITYEAYMVPPLPPEEPPTMPFLPPEE PMPTPLPPEEPPEGPALPTEQSALTAENTWPTVEVPSLPSEESV SQPEPPVVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEP PEPSITLTPVESAVVAREHEVVPBPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDMSRASGHVASEVSTSLVPAVTTPLVLA ESILEPPAMAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPPEPPVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVITEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPETIGMQUEIALHSGEEPHE EHLKGDFFESEHGINIDLNNHLLIAKEMEHTVCAAGTSPVGE IGEKILPTSETKQRTVLDTPGVSEADAGETLSSTGPFALPD ATG\TSKGIETFTASTLSLVNKYDVLSTLTQDTEHDMLISTSP SGGSEADIEGCLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVPRVSSPRTWNLPSPRAG\EGP\LLASDFGPVQNLVSSPVV \SSMP\ERASGS\SSGEGG\YEIFVKVDTHEKSKKNKNDKG EKEKKRDSSLRSRKRKSSSEHKSRKLTSSESRRARKRSKSKS HRS\QTRSRRS/RDRRRSSRSRKSRRGRSVSKEKRRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFISISRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRSRSVVRSSFSISPVLRRSRTPLRRRS RSPIRRKRSSSERGRSPKRLTDLDKAQLEIAKANAAAMCAKA GVPLPNLKPAPPPTIEEKVAKSGGATIEELTEKCKQIAQSKE DDDVIVNKPVSDEBEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPKQSQTLTKEFPVSSGSQHRKKEADSVYGEWVPEKNGEEN KDDNVFSSNLPSPEVDISTAMSERALAQKRLSENADLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQALANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGRGEGGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSNGFSAAAMKDLGKHPVSALMEICN KRRQPPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y |
| 5783 | 1693 | 698 | DSGLRVAFTMEGINSFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNI VGYRAFTEANDGSLCLAMEYGGESL NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLYLHQEKKL |

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|------------|--|--|---|
| | | | LHGDIKSSNVVVIKGFETIKICDVGVSPLDENMTVTDPEACYI GTEPWKPKAVEENGVIITDKADIFAPGLTLWEMMTLSIPHINLS NDDDEDKTFDESDFDEAYYALGTRPPINMEELDES YQKVIE LFSVCTNEDPKDRPSAAHIVEALETDV |
| 5784 | 2669 | 1388 | PRVRPRVRTDHNYYISRIYGPSSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTGEVH RMLTATQYIAPLMANFDPVSVRNSTVRYFDNGTALVVQWDHVL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVHRIQQIPNVRRRTIYEHVRELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSSWCKLQRCSSGFDHRQDW VDSGCPESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPPTSLPTEDDTKIALHLKDNASTDDSAEKKGGTL HAGLIVGILILVLIVATAILVTVMYHHPTSAAISFFIERPSR WPAMKFRRGSGHPAYAEVPEVGEKEGFIVSEQ |
| 5785 | 2669 | 1388 | PRVRPRVRTDHNYYISRIYGPSSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTGEVH RMLTATQYIAPLMANFDPVSVRNSTVRYFDNGTALVVQWDHVL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVHRIQQIPNVRRRTIYEHVRELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSSWCKLQRCSSGFDHRQDW VDSGCPESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPPTSLPTEDDTKIALHLKDNASTDDSAEKKGGTL HAGLIVGILILVLIVATAILVTVMYHHPTSAAISFFIERPSR WPAMKFRRGSGHPAYAEVPEVGEKEGFIVSEQ |
| 5786 | 2532 | 1674 | SYKLPAEERRASSCSQPPTPTRRRWPAGRTSRGHRFQM*SGTF APRPPARSTVSPASPLPKPRAGRCGRSPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK SPPLACSFQAAQKSQSLSSGRSTR*PERMSFRP/SPPGNPAIP SLAPSSRP/PKGRPQCTWI PSRWASPTAPPTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPNWNPMMAE |
| 5787 | 2 | 1460 | MASAAVSITSLADEVNCP\ICQGTLEAGSLNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCOEHGEKIYFFCEDDEMQLCVVCR EAGEHATHIMRFLDAA\APYREIHKCLKCLIKEREIEIQEIQS RENKRMQVLLTQVSTKRQVISEFAHLRKFLFEEQQSILLAQLES QDGDILRQRDEFDILLVAGEICRFSALIEELEBKNERPARELLTD IRSTLIRCETRKCRKPVAVSPQLGRIIRDFFQALPLQREMKMF LEKLCFELDYPAHISLDPQTSHPKLLSLEDHQRAQFSYKWQNS PDNPQRFDRTATCVLAHTGITGRHTVVSIDLAHGGSCITGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGVVTFNNAVTRPIYTTASFTRKVIPFFGLWG RGSSFSLS |
| 5788 | 2 | 6860 | EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGETEGDVHTSNRLHMVRLMLLERLLQLPLQRLNVGGVR AIFYMQVILMLTTDLGDEKDKGALDNLSQLIAELGMDKDV SKKNERSALNEVHLVVMRLSVFMSRTKSGSKSSICESSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEATYQLLTEMVLRPLPYQI KKITDNTSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGI FLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSAS SSPAPVAASSGQATTQSKSTKSKKKEKEKEKDGSTSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQELLDLMLWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYLES DPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQOVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDPLPIVASNLMI EFADFYENYQAS TETLQCPRCASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF |

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|------------|--|--|---|
| | | | LCNACGFCYARDFDMLYAKPCCAVDPIENEEDRKKAVSNINTL LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPODDSGTAGGIS STSASVNRYYILQLAQEYCGDCKNSFDELSKIIQKVPASRKELLE YDLQQREAATKSSRTSVQPTFTASQYRALSGLGCGHTSSSTKCYG CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRGA AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP DLASSLQYEMLLLTDSISKEDSCWELRLCALSLFLMAVNIKTP VVVENITLMCLRILOKLIKPPAPTSKKNKDVPEALTTVKPYCN EIHQAQQLWLKRDPKASYDAWKCLPIRGIDGNGKAPSKSELRH LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFPTAT QAARQAACTIVEALATIPSRKQVLDLLTSYLDLSIAGECAAE YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA TLSTDQLQQYALKSLTGLSSSFVEVESIKRHFKSRLVGTVLNGY LCLRLVVQRTKLIDETQDMLLEMLDMTTGTSETKAFMAVCI ETAKRYNLDDYRTPVFIIFERLCSIIYPEENEVTEFFVTLEKDPQ QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED DSGMELLVNNKIIISLDLPVAEYKVKVWCTTNEGEPMRIYVRMRG LLGDATTEEFIESLSTTDEEEDDEEVYKMGVMAQCGGLECMNLN RLAGIRDQKGRHLLTVLLKLFSCVKVKVNRQQLVKLEMNLTIN VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP LSEDKGNLLLTGDKDQLVMLLDQINSTFVRNPSVLQGLLRIIP YLSFGEVEKMQILVERFKPYCNFDKYDEHSGDDKVFL\DCPCK IAAGIK\NNSNGHL\KDL\ILQKGI TONALD\YMKKHIP\SA RIWDADI\WKSFCRLPALPFILRLRLGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\ENL\LESREHPDVNKKIDA\AR RETRAEEKRMAMAMRQKALGTG\MTTNEKGQVVD\TRTALLEA DWEELIEEP\GLTCCICREGYKFPQPTKVLGIYTFTRKRVLGGVW ENKPRETSRATSTVSHFNIHVYDC\HLA\AVSLARGREEWESAA LQANTKCNGLLPVWGPVHPESAFATCLARHNTYLQECTGQREP TYQLNIHDIKLLFLRFAMEQSFADTGGGGGRESNIHLIPYI IHT GLYVLNTRATRSREKNLQGFLEQPKKEKWESAFEVDGPYYFTV LALHILPPEQWRATRVEILRRLVTSQARAVAPGGATRLTDKAV KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTGEGWSSCSLAEYIR HNDMPYIEAADKALKTFQEEFMPVETPSEFLDVAGLLSEITDPE SFLKDLLNSVP |
| 5789 | 1 | 2407 | LPLHAVEKTRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ TEEEKKKEPKSKDKTEEIAEEETVFPKAKQVKKKAEPSEVDMN SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVSSKTKK VTKNEEPSEEEIDAPKPKMKKEKEMNGETREKSPKLKNGFPHP EPDCNPSEAASESNSIEIQEI PVEQKEG\AFSNFPISEETIKL LKGRGVTFLLPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\ELQDRKRGAPQVLVLAPTRELANQVSKDFSITKKL SVACFYGGTPYGGQFERMRNGIDILVGTGRIKDHQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYBQVDLIGKKTOKTAITVEHLAICH WTQRAAVIGDVIRVYSGHQGRITIFCETKKEAQELSONSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIOSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEI IKASSKDAIRLLDSVPPTAISHF QSAEKLIEKGAVEALAAALAHISGATSVQDQSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSVKVGMVFLKGLGVCF DVPTASVTEIQEKWHSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGRGQRDGNRRFRGQREGSRGPRGQRSGGKNSNRQNK GQKRSFSKAFGQ |
| 5790 | 3786 | 1585 | ARRQRDPLQALRRRNQELKQVDSLLSESQLEALEPNKRQHIY QRCIQLKQAIKENKNAQLKLSKADESAPVANYNQRKEEHTLLD KLTTQQLQGLAVTISRENITEVGAPTEEESESESDSGGEE DAEEEEEEKEENESHKWTGEEYIAVGDFTAQQVGDLTFFKKEI LLVIEKKPDGWWIAKDAKNEGLVPRTYLEPYSEEEBQGESSE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAI SEAGIFCLVN HVSFCYLIVLMNRNMTVEDTNGSETGFRAWNVQSRGRI FLVSK |

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|------------|--|--|---|
| | | | PVLQOINTVDVLTMTGAIPAGFRPSTLSQLLEEGNQFRANYFLQ PELMPSQLAFRDLMDATEGTIRSRPSRISLILTLWSCKMIPLP GMSIQVLSRHVRLCLFDGNKVLNIHTVRATWQPKPKTWTSP QVTRILPCLLDGDCFIRSNSASPDGLIFELGISYIRNSTGERG ELSCGWVFLKLFDAAGVPIPAKTYELFLNGGTPYEKIEVDPSI SRAHGSVFYQIMTMRQPLLVKLSLNRRSRNVLSLLPETLI GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLSHPMLATFPM LEQPDVMDALRSSWAGQES\TLKRSEKRPKEFLKVPFLLVYH \GCVLPL/HTPTRLPPFRWAEETETARWKVITDFLKQNGENQ GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV |
| 5791 | 3 | 1636 | LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH GN/GKQL/AMSSQGSDEQIKRENIRSLTMSGHVGFESLPDQLV NRSIQQGFPCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY IDAQFEAYLQEEELKIKRSLFTYHDSRIHVCLYFISPTGHSKLT DLTMMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSSELVSN VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGKMKVKA RQYPWGVVQVENENHCDVFKLREMLICTNMEDELREQTHTRHYEL YRRCKLEEMGFTDVGPEKPVSVQETYEAKRHEFHGERQRKEEE MKQMFVQRVKEKAILKEAERELQAKFEHLKRLHQEERMKLEEK RRLLLEEIIAFSKKKATSEIFHSQSFLATGSLNRKDKDRKNSQF FVKQKVPHEHRSSSQANFIKKKLEVCDFFAVICFITSIFGEQPO LLIFMEKYFQVQGGYISQSE |
| 5792 | 2263 | 653 | AAAAPS PAWVCGVFVYVVTWCWVMYGIIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT YVMPKPEEINLLTGESDTQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRRLRFWIHQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDPLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLLEQTSLLVLVP AGVGAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEY DTQAMKYL SYLLYPLCVGGAVYSLN IKYKSWYSLINSFVNGV YAPGFLEMLPQLFVNYKLKSAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVFLVLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD |
| 5793 | 2263 | 653 | AAAAPS PAWVCGVFVYVVTWCWVMYGIIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT YVMPKPEEINLLTGESDTQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRRLRFWIHQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDPLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLLEQTSLLVLVP AGVGAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEY DTQAMKYL SYLLYPLCVGGAVYSLN IKYKSWYSLINSFVNGV YAPGFLEMLPQLFVNYKLKSAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVFLVLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD |
| 5794 | 1 | 5016 | MGPRLSVWLLLLPAALLLHEEHSRAAKGKGCAGSGCGKDCCHGV KGQKGERGLPGLQGVIGFGPMQGPQGPQGPQKGTGEPGLPG TKGTRGPPGASGYPGNPGLPPIPGQDGPQGPPIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKDGPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGVVGPFTGPPGPPGPPGPPGKEGQM GLSFQGPQKDGKQGVSGPPGVPGQAQVQEKGFATKGEKQKQK EPGFQMPGVGEGKEPGKPGPRGKPGKDGDKGEKSGPGFPGEPG YPGLIGRQGP\QGEKGEAGPPPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGPFGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGPGYTNGIVECQPGFP GDQGGPPGIPQGPFGIGEIGEKQKGESCLICDIDYGRGPPGPGQ PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPLIGQPGAK |

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|------------|--|--|--|
| | | | <p>GEPPGEFYFDLRLKGDGDPGFFGQPGMPGRAGSPGRDGHPLPG PKGSPGSGVLKGERGPPGGVGFPGSRGDTGPPGPGYGPAGPIG DKQAGFFPGGPGSPGLPGPKGEPGKIVPLPGPPGABGLPGSPGF PGPGQDRGPPGTGPR\PG\PEKGAVG\QPGIGFPGPPGPKGV DGLPGDMGPPGTGPRPGFNGLPGNPGVQGOKEPVGVLPLGLKGL PGLPGIPGTGPEKGSIGVPVPGVGEHGAIGPPGLQGIIRGEPGPPG LPSVSGSPGVPIGPPGARGPPGGQGPGLSGPPGIKGEKGFPG FPGLDMPGPKGDKGAQGLPGITGQSGPLPLPGQQGAPGIPGFFG SKGEMGVMTGPPGPGSPGWAGPLPGEKGD\HGFFGSSGPRGD PGLKGDGKDVGLPGKPGSMDKVYMGSMKQKGDQGEKQIGPIG EKSGRGDPGTGVPVPGKDGQAGQPGPGPKGDPGISGTGAPGLP GPKGSGVMGMLPGTPGEGKGVPGIPGPGQSPGLPGDKGAKGEKQ AGPPGIGIPGLRGEKGDQGIAGFPSPGEGKEKGSIGIPGMPGS PGLKSPGSGVYPGSPGLPGEKGDGKGLPGLDGI PGVKEAGLPG TPGPTGPAGQKGEPPGSDGIPGSAGEKGEPLPGRGFPFGPAKG DKGSKEGVGFPGLAGSPGIPGSKGEGQFMGPPGQGPGLPGSP GHATEGPKGDRGPQGPGLPGLPGMPGPPGLPGIDGVKGDKNP GWPGAPGVPGKDPGFGQMPGIGGSPGITGSKGDMGPPGVPFG QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPGFYDIKGEF GLPGEPGPPGLKGLQGLPGPKGQGVTLVGI PGPPGIPGFDGA PGQKGEAGPAGPTGPRGFPGPDPGLPGSMGPPGTSPVDHGL VTRHSQTIDDPQCPGSGTKILYHGYSLLYVQGNRAHQDLGTAG SCLRKFSTMPFLFCNNVNCNFASRNDYSYWLSTPEPMPMSMAP ITGENIRPFISRCVCEAPAMVMAVHSQTIQIPCPGSGWSSLWI GYSFVMHTSAGAEGSGQALASPGSCLEEFPSAPPTECHGRGTCTN YYANAYSFWLATIERSEMFKKTPSTLKAGELRTHVSRQVCMR RT</p> |
| 5795 | 1192 | 61 | <p>STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECI RHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATPKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELIILDRH FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFPQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR</p> |
| 5796 | 2 | 1078 | <p>GRVGWELWCMYISPPKDWWDAGDPSLPIRTAMIGCSFVVRNKF FGEIGLLDPGMDVYGGENIELGIKVLCCGSMELVPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSCKCNQWYLDHVYPEMRRYNNYTVAYGE LRNNKAKDVCLDQGPENHTAILYPCHGWGPQLARYTKEGFLHL GALGTITLLPDTRCLVDNSKSRLPQLLDCDKVSSLYKRWNFIO NGAIMNKGTRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTS CPGGETARGQVLDGPPRASPG QHRDPG</p> |
| 5797 | 2 | 891 | <p>PRVRQKTLVDVTLSENSNIKDQIRNLQOTYEASMDKLEKQRQLE VAQVENQLLKMKESSQANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKMQAAEISLEEKDQRI GEL DRLIERMEKERHQLQLLLEHETEMSGELTDSKERYQQLEEAS ASLRERIRHLNDMVHCQKKVKQMVVEEIESLKKKLQKQLLILQ LLEKISFLEGNNELQSRDLTETQAKTEVETREIGVGCDDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT</p> |
| 5798 | 644 | 115 | <p>KILGSRWKSMSNOEKQPYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKLRIGEYKQIMRSRRQEMRQFTVGGQPPQIPITGTG VVYPGAIITMTTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN</p> |
| 5799 | 2679 | 1435 | <p>LLSTYIKFINLPETKATIQGVLRAGSQLRNADVELQORAVEYL TLSSVASTDVLATVLEEMPPFERESSILAKLKRKKGPGAGSAL DDGRDPSSNDINGMEPTSTVSTPSPSADLLGLRAAPPAP PASAGAGNLLVDVDFGPAAPSLGPTPEEAFSPGPDIGPPIP EADBLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTLAVQTKRVAQVDGGAQVQVQL NIECLRDFLTPLLSVRFRYGGAPQALTCLKPVTINKFFQPTM AAQDFFRWKQLSLPQCEAQKIFKANHPMDAEVTKAKLLGFGSA</p> |

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|------------|--|--|--|
| | | | LLDNVDPNPENFVGAGIIQTKALQVGCCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCCELLAQFF |
| 5800 | 2679 | 1435 | LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVLOQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPTSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAPQPSLGPPTBEAFLSPGPEDIGPPIP EADLLNKFVCKNNGVLFENQLLQIGVKSEFRONLGRMYLFYGN KTSVQFQNFSPITVVHPGDLQTLAVQTKRVAQVDGGAQVQQVL NIECLRDFTLTPPLLSVRFYGGAPQALTLKLPVTINKFFQPTM AAQDFFQRWKQLSLPQQAQKIFKANHPMDAEVTKAKLLGFGSA LLDNVDPNPENFVGAGIIQTKALQVGCCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCCELLAQFF |
| 5801 | 3 | 1413 | FPRLYHLIPDGEITSIKINRVDPSSELSIRLVGGSETPLVHIII QHIVRDGVIARDGRLLPGDIIKLVNGMDISNPHNYAVRLLRQP CQVLWLTVMREQKPRSRNNGQAPDAYRPRDDSFHVLNKSSPEE QLGIKLVKQVDEPGVFI FNVLDGGVAYRHGQLEENDRVLAINGH DLRYGSPESAHLIQASERRVHLVSRQVRQSPDIFQEAQWNS NGSWSPGPGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVA GGASHREWDLPYIVISVEPGGVI SRDGRITGDILLNVGVELT EVSRSSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH NMAPPSPDWSPSWVMWLELPRCLYNCKDIVLRRTAGSLGFCIVG GYEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG MIHACLARLLKELKGRITLTI VSWPGTFL |
| 5802 | 3 | 290 | CFSLYQIMERIMDLPTLLRHAFREMFVSGGLFWMFRIRIILCLM GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV ITQRLTR |
| 5803 | 2234 | 1299 | EAQFGTTAEIYAYREEQDFGIEIVKKAIGRQRFKVLELRTQSD GIQQAQVQILPECVLPSTMSAVQLESLNKQIFPSKPVSRQDQC SYKWWQKYQKRKFHCANLT SWPRWLYSLYDAETLMDRIKKQLE WDENLKDDSLSPNIDFSYRVAACLPIDDVLRIQLLKIGSAIQR LRCELDIMNKCTSLCKQCQETETTKNEIFSLSLCGPMAAYVN PHGYVHETLT VYKACNLNLIGRPSTEHSWFPGYANTVAQCKICA SHIGWKFTATKKDMS PQKFWGLTR SALLPTIPDTEDEISPDKVI LCL |
| 5804 | 2 | 1707 | EMEKQRQEEQRKRTTEERKRRIEQDMLEKRIQRELAKRAEQIE DINNTGTESASEGDDSLITVVPVKS YKTSKMKKNFEDLEKE RBEKERIKYEEDKRI RYEBQRP SLKEAKCLSLVMDDEIESEAK ESLSPGKLKLTFEELERQRQENRKKQAESEARKREEEKRAPEE ARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR KAESEARRRI EEEKKAFAEARRNMVDDDSPEMYKTISQEFLLTP GKLEINFEELKQKMBEEKRRTEERKHKLEMEKQEFQELRQEM GEESEENETFGLSREYEELIKLRSGSIQAKNLKSKFEKIGQLS EKRIQKKIEERARRRAIDLEIKEREAENFHEEDVDVDRPARKS EAPFTHKVMNKARFEQMAKAREEEQRRIEBQKLLRMQPEQREI DAALQKKREEEEEEGSIMGSTAEDDEEQTRSGAPWFKPLKNT SVVDSEPVRFVTKVTGEPKPEITWWFEGEILQDGEDYQYIERGE TYCLYLPETFPEDGGEYMKAVNNKGSAASTCILTIESKN |
| 5805 | 3 | 776 | YISDTLGQVYKSKIRWWIEENGNGNISVDDLIALLDLAEHASS APKESQQQSEDRYEYVKERLYPKSKRRYDTYNIAGYQGEIEVGL YTIQILQLIPFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA LKNYIPLYTLKLFSLKKSDFDFDEYFVLLKPRNNIKQNEEAKTR RKVAGYFKKYVDIFCLLEESQNTGLGSKFSEPLQVERCRRNLV ALKADKFSGLLEYLIKQSQDAISTMKCIVNEYTFLK |
| 5806 | 1257 | 877 | AVFTFHNHGRRTANLYSLHSWLGITTVFLFACQRFGLFAVFLLPW ASMWLSLLKPIHVFFGAALLSLSIASVISIGINEKLFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRF |
| 5807 | 2267 | 1302 | RFSKKTFRPMAVDIQPACGLYCGKTLFLKNGSTEIYGECCGVC PRGQRTNAQKYCQCTESPELYDWLYLGFMAMLPVLHWFIEW YSGKSSSALFQHITALFECSSMAAIIITLLVSDPVGVLVYRSCR LMLSDWYTMLYNPSPDYVTVHCTHEAVYPLYTIVFIYAFCLV |

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|------------|--|--|--|
| | | | LMMLLRPLLKVIACGLGKSDRFKSIYAALYFFPILTVLQAVGG GLLYYAFPIIILVLSLVTAVYMSASEIENCYDLLVRKKRLIVL FSHWLLHAYGIISIRVDKLEQDLPLLALVPTPALFYLFYFTAKFT EPSRILSEGANGH |
| 5808 | 2 | 433 | SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS EGRITHGFQPKSAYENNLMPTNYTTFDFKGVIDYIFYSKTHMNV LGVLPDLPQWLVENNITGCPHPHPSDHFSLLTQLELHPPPLP LVNGVHLNRR |
| 5809 | 464 | 2422 | ILVPGFQGIHPGVYCALQSQHQAEVLADIDECEVSLGRCHGG RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDTATCTEIDCGTTP EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE SPGGKITSVCTEKGTTWRESTLTCTEILTAKINDVSLFNDTCVRWQ INSRRINPKISYVISIKQRLDPMESVREETVNLTTDSRTPEVC LALYPGTNYTVNISTAPRRSMFAVIGFQTAEDLLEDGGSFNI SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN FTTREQVPVCLDLYPTDYTVNVTLLRSKPRHSVQIT IATPPA VKQTIISNIGFNETCLRWSIKTADMEEMYLFIHWQRWYQKEF AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSSELVVISL TTQITEPPLPEVEFTVHRGFLRLRLKAKEKNGPISSYQVLV LPLALQSTFSCDSEGASSFFSNASDADGYVAEELLAQDVDDAM EIPIDRLYYGEYNAPLKRGSDYCIILRITSEWNKVRHSCAV WAQVKDSSLLMLQAGVGLSLAVVILITFLSFSFAV |
| 5810 | 3 | 1641 | KVPGTHKDEHVESTLDTAISAVKVLAEFLENLQEKSLRIEAFVS EIESFFNTIENCCKNEKRLEBQNEEMMKVLAQYDEKAQSFEE VKKKKMEFLHEQMVFHLSQMDTAKDTLETIVREAEELDEAVFLT SFEEINERLLSAMESTASLEKMPAAFSLEHYDDSSARSQMLK QVAVPQPPRLEPQEPNSATSTTIAVWMSMNKEDVIDSFQVYCM EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWMAVNF TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTPEA TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLPNDNYFFYV RAINAFGTSEQSEAALISTRGTRFLLRETAHPALHISSSGTVI SFGERRRLTEIPSVLGEELPSCQGHYWETTVTDCPAYRLGICSS SAVQAGALGQGETSWYMHCSPEQRYTFFYSGIVSDVHVTERPAR VGILLDYNQRLIFINAESQELFIIRHFRNEGVHPAPALEKPG KCTLHLGIBPPDSVRHK |
| 5811 | 1918 | 851 | AAALADPLPEDKWSAEKRRLKSSSLGYEITFSLNPDPKSHDVI WDIEGAVRRYVQPFNLALGAAGNFVSQSILYYAMLGVNPRFDS ASSSYLDHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKGAPVATNAFHSRWWGIMVYNVDSKTYNASVLPV RVEVDVVRVMEVFLAQLRLFLGIAQPLPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLSLAQLLGKISNIVIKDDVASE VYKAAVAVQKSAEELASGHLASAFVASQEAFTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD |
| 5812 | 5204 | 2744 | GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGFLQSGSQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIQEQQHMLLGHSLGA YISTLDKEKLRKLTRILSDTTLWLCLRIFRYENGCAFYHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHDTKIGRLKELCEQYGIWLHVGEVNLAT LALGYVSSSVLAAKCDSTMTPGWGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVFRFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDEA EGTCLRFSPMTAAVLGTRGEDVDQLVACIESKLPVLCCTQLGR EEFKQVEATAGLLYVDDPNWSGIGVVRVYEHANDDKSSLSYPQ GENIHAGLLKLNLESDLTFKIGPEYKSMKSLCYVGMASDNVH AELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS EERLLEGVLRQIPVVGSVLWNFSPVQALQKGRTFNLTAGSLES |

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|------------|--|--|---|
| | | | TEPIYVYKAQGAGVTLPTPSGSRKQRLPGQKPFKRSLRGSDA LSETSSVSHIEDLEKVERLSSGPEQITILEASSTEGHPGAPSPQH TDQTEAFQKGVPHPEDDHSQVEGPESLR |
| 5813 | 2936 | 699 | HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG LLRLSPCVLLAGLCRGNISVERKIYIPLNKTAPCVRLNATHQI GCQSSISGDTGVIHVVEKEEDLQWVLTGDPNPPYVVLLESKHFT RDLMEKLGKRTSRIAGLAVSLTKPSPASGFSVQCPNDGFGVY SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLDENETKVI KQCYQDHNLSQNGSAPTFFPLCAMQLFSHMAWLSFSTAT\CMRRS SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLPDDRUVVA ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP AVILRRPNQSQPLPPSSLRQFLRARNISGVVLADHSGAFHNKYY QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV LGRALYELAGGTNFSDDTVQADPQTVTRLLYQ\FLIKANNISWFS ILQGRDLRSYLG*RLGFQ\YIAV\SSPTNTIYV/VLQYALANL TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP RCVRSTARLARALSAPFELSQWSSTEYSTWTESRWKDIRARIFL IASKELELITLTVGFGILIFSILVITYCINAKADVLFIAPREPGA VSY |
| 5814 | 8500 | 432 | ALKCRPRRVLAILVGEVQPDMAEEGAVAVCVVRPLNSREESL GETAQVYWKTHNNVIYPVDSKSFNFDRVLHGNETPKNVYEA\I AAPIIDSAIQGYNGTIFA\YQQT\ASGKTYTMMGSEDLGVIPQ GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM KPLIREDVNRNVVADLTEEYVYTSEMALKWITKGEKSRHYGE TKMNQSSRSHTIFRMILESREKGEPSNCEGSKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLERAQ AMEKDQLAQLLEEKDLQKVQNEKIEINLTRLVTSSSLTLQOEL KAKRRRRVTWCLGKINKMKNSNYADQFNIPNTITTKTHKLSINL LREIDESVCSSEDSVFSNTLDTLSEIENPATKLLNQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLEKNLDEFEALERKTK KDQEMQLIHEISNLKNLVKHREYVNDLENELSSKVLELREKED QIKKLQEIYDSQKLENIKMDLSYSLESTIEDPKQMKQTLFDAETV ALDAKRESAFLRSNENLEKEMKELATTYKQMENTIQLYQSOLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSBLKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVHVKESEVQGLLEEIGTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQYKVMVLEENRMNQEIIVNLSKE AQKFDSSLGALKTLSYKTQELQEKTEVQERLNEMEQLKEQLE NRDSPLOTVEREKLITELQQTLEEVKTLTQEKDDLKQLOESL QIERDQLKSDIHDVTNMNIDTQEQRLNALESKQHQETINTLKS KISEEVSRLHMEENTGETKDEFQOKMVGIDKKQDLEAKNTQT TADVKNDEIEQQRKIFSLIQEKNEQLQMMLESVIAEKEQLKTDL KENIEMTIENQEEELRLGDELKKQOETVAQEKHAIKKEGELSR TCRLAEVEEKLKEKSQQLQKQQLLNQVEEMSEMOKKINBIE NLKNELKNKELTLEHMETEERLELAQKLNENYEVKSIKERKVL KELQKSPETERDHLRGYIREIEATGLQTKELKIAHILKEHQE TIDELRRSVSEKTAQINTQDLEKSHTKLQEEIPVLHEEQELL NVKVSSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSQEQESLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLSQESDQLKENIKEIV AKHLETEELKVAHCCLEKEQERTINELRVNLSEKETEISTIQKQ LEAINDKLONKIQEIEYKEEQNLKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEEEMKRVQEA LQIERDQLKENTKEIVAKMKSQEQEYQFLKMTAVNETQEKME IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD DLRSVEETLKVERDQKLENRETITRDLRKEELKIVMHMLKEH |

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|------------|--|--|--|
| | | | QETIDKLRGIVSEKTNESNMQKDLHSNDALKAQDLKIQEELR IAHMLKEQQETIDKLRGIVSEKTDKLSNMQKDLSENSAKLQEK IQELKANEHQILITLKKDVNETQKKVSEMEQLKKQIKDQSLTSLK LEIENLNLAQKLHENLEBMSKVMKERDNLRRVEETLKLERDQLK ESLQETKARDLEIQOELKTARMLSKHEKKTVDKLRKISEKTIQ ISDIQKDLKSKDBLQKKIQELQKKELQLLRVKEDVNMSSHKKIN EMEQLKKQFEPNYLCKCEMDNFQTLKKLHESLEEIRIVAKERDE LRRIKESLKMEDQFIATLREMIARDRONHQVKPEKRLSLDGGQQ HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH RIMKKLYVLSYVTIKIEEQHCINKFEMDFIDEVBKQKELLIK IQHLQQDCDVPSERLDLKLNQNMDLHIEILKDFSESEFSPK TEFQQVLSNRKEMTQPLEEWLNTFRDIEKLKNGIQKENDRIQV NNFFPNRIIAIMNBSTEFERSATISKWEQDLKSLKEKNEKLF KNYQTLKTSLASGAQVNPTQDNKNPHVTSRATQTLTEKIRELE NSLHEAKESAMHKESKIKMQKELEVTNDIAKLQAKVHESNKC LEKTKETIQVLQDKVALGAKPYKEEIEDLKMMLGKIDLEKMKNA KEFEKEISATKATVEYQKEVIRLLRENLRSSQQAQDTSVISEHT DPQPSNKPITCGGGSGIVQNTKALILKSEHIREKEISKLKQON EQLIKQKNELLSNNQHLSENVKTKERTLKREAHKQVTCENSPK SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS LPSPHPVRYFDNSLGLCPEVQNAEVSQSP\GPWARLFQGGK DVP\ECKTQ |
| 5815 | 23 | 1460 | SELVMWTVQNRESLGLLSFPVMITMVCCAHSSTNEPSNMSYVET VDRLLKGYDIRLRPDPFGPPVDVGMRIDVASIDMVSEVNMDYTL TMYFQOSWKDKRLSYSGIPLNLTLDNRVADQLWVPDITYFLNDKK SFVHGVTVKNRMIRLHPDGTLYGLRITTTAACMDLRRYPIDDE QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY KMVSKKVEPTTGAYPRLSLSPRLKRNIGYFILTQYMPSTLITL SVVSFWINYDASAARVALGITVLTMTTISTHLRETLPKIPYVK AIDILMGCFFVFLALLEYAFVNYIFFGKGPKQKKGASKQDQSA NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSTVSDPKA TMYSDSASIQYRKPLSSRE\A*GRAPDRHGVPKGRIRRRAS\ QLKVXIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH |
| 5816 | 861 | 191 | TSSRSRAAAEGDAETPGSVERRRAGAEAGMSQAPGAQSPSP TVYHERQRLELCAVHALNNVLQQQLFSQEAADBIKRLAPDSRL NPHRSLGTGNYDVNVIMAAQGLGLAAVWDRRRPLSQLALPQ VLGLIILNLPSPVSLGLLSLPLRRRLRWPCARL/VTVSYNLDLS K\LRAPGPGGLRTE*GPFLAAALAQGLCEVLVVTKEVEKGS SWLRTD |
| 5817 | 851 | 118 | RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCP*PPSPPAAD VMSNTTVPNAPQANSDSMGVYVLGPFFLITLVGVVAVVMYVQK KKRVDRRLRHLLPMYSYDPAEELHEAEQELLSMDGDPKVQ\QAG RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLS GSPCWVLGLHPSLHPPSAASASHALTITSLPPGLLPFVGVELTA HPQALMGRGFPFGMAAAGRHLCLF |
| 5818 | 3 | 3918 | QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQKIQAAAFDKGD DRRLGKKPIFSSSQQRKQVSDSGDIKISWRGNKKKECWSYLS NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI TKELKTGGKNVSGPKPTVTKSTENGDKARLENMSPRQVVERSA TAAAAATGQKNLLNGKGVNRQEGQISGARPKVLTGNLNVQAKAK PLKKATGKDSPLSIAGPSSRSTDSSMEFSISTECLDEPKENG TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRT NGTSNKKSIHEQDTNVNNSVLKVKSGKGCSEPVQAI LKKRGTS NGCTAAQQRKTSTPSNLTKTQSGQGESPNVSVSSVSRQSDNV AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK KGETLNNKDSKQKMPGQVISTQPSQRPLKHETSTVQKSMFH DVRDNNKDSVSEQPKPKPLINLASEISDAEALQSSCRP\DPQK PLNDQEKELALECQNI SKLDKSLKHELESKQICLDKSETKFPN HKETDDCDAANICCHSVGSDNVNSKFYSTALKYMVSNPNENSL NSNPVCDLSDTSAGQIHLISDRENQVGRKDTNKQSSI KCVEDVS LCNPRTNGTLNSAQEDKSKVPVEGLTIPSKLSDSAMEDKH |

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|------------|--|--|---|
| | | | <p>ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH</p> <p>WNLSTGVLHQRESPESDTGSATTSDDDIKPRSEDYDAGGSQDDD</p> <p>GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK</p> <p>MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR</p> <p>GSVQFAQEIDQVSSADETERSEAEVNAENFSISNPAPQFQ</p> <p>GIINLAFEDATENECEFRSANKKFKRSVLLSVDECEELGSDEGE</p> <p>VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE</p> <p>CKQNKGSVCNKNESTVLDLSSIDSRKNKQSVSATEKKNTIDVL</p> <p>SSRSRQLLREDKVNNGSNVENDIQORSKFLSDSVKQSERPCHL</p> <p>DLHQREPNSDI PKNSSTKSLSDFRQVLPQEGPVKESHSTTEK</p> <p>ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPYEMDVIEAEFQ</p> <p>KVESETHVTDMDF*DDQHFAQDWTLLKQLLSEQDSNLDVTNSV</p> <p>PEDLSLAQYLINQTLLLARDSSKPGGITHIDTLNRWSELTSPLD</p> <p>SSASITMASFSSDCSPQGEWTILELETQH</p> |
| 5819 | 1 | 5557 | <p>AAAGLLGALHLVMTLVVAAARAEEAFVQSESIIEVLRFDGGGL</p> <p>LQETTLGLSSVQQKSISLYRGNCRIPEPPMLDFHEQPVGM</p> <p>KMEKYLHNPSSE*ITLVSI FATTSHFASFQNRKILPGGNT</p> <p>SFDVS/VFLARVGNVENTLFINTSNHGVFTY\QVFGVGVNPNY</p> <p>RLRPFLGARVTNSSFPIINIHNPHEPLQVVMYSSGGDLHL</p> <p>ELPTGQQGGTRKLWEIPPYETKGMVRSFSSREADNHTAFIRIK</p> <p>TNASDSTEFILPVEVEVTTAPGIYSSTEMLDGTLRTQDLPKV</p> <p>LNLHLLNSGT KDVPITSVRTPQ\NDAITVHFKPITLKAS\ESK</p> <p>YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV</p> <p>LDGYLGFDAATLPHIRDSPADPVERPIYLTNTFSFALLIHDVL</p> <p>LPBEAKIMFKVHNFSKPVLLPNESGYITLLFMPSTSSMHIDN</p> <p>NILLITNASKPHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT</p> <p>EASNILFAIINSNPIELAIKSWHIGDG\LSIELVAVDRGNRTT</p> <p>IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH</p> <p>DGAIQITTDYEILTIPVK\AVIAGVSLTCSPKHVVLPPSPFGKI</p> <p>VHQSLNIMNSFSQKVIQQIRSLSEBVRFYKRLRGNKEDLEPG</p> <p>KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM</p> <p>WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI</p> <p>TAEISWSPILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV</p> <p>VYQFIPALALYSNPSVFVDKLVSFRNLSKVAKIDLRTLEFQVFRN</p> <p>SAHPLQSSSTGFMEG\LSPHLILNLILKPEKKS VKV\FTPVHN</p> <p>RTVSSLIIVRNNTVMDAVMVQGGTTENLRVAGKLPGPGSSLR</p> <p>FKITEALLKDCDTSKLRPNFTLKRFTKVENTGQLQIHETIE</p> <p>ISGYSCEGYGFKVNCQEFTLSANASRDIIILFTPDFTASRVIR</p> <p>ELKFITTSGBEFVILNASLPYHMLATCAEALPRPNWELALYII</p> <p>ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD</p> <p>VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA</p> <p>GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA</p> <p>SSQFANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHSQHHAHS</p> <p>PLEQHPOPPPLFPVPQPQEPQPERLSAPLAHPSPHERASSARH</p> <p>SSESDSITSLIAMDKDFDHDSPALEVFTEQPPSPLPKSKGKG</p> <p>KPLQRKVKPPKKQEEKEKKGKGPQDELDKSLADDDSSSTTTE</p> <p>TSNPDTEPLLKEDTEKQKQKQAMPEKHESEMSQVKQKSKLLNI</p> <p>KKEIPTDVKPSSELEPYTPPLESKQRRNLP SKIPLPTAMTSGSK</p> <p>SRNAQKTGTSKLVNRPALAKFLPNSQELGNTSSSEGEKDS</p> <p>PPEWDSVPVHKPGSSTDLSYKLSLQTLNADIFLKQRTSPTPAS</p> <p>PSPPAAPCPFPVARGSYSSIVNSSSSSDPKIKQPNKSKHKLTKAA</p> <p>SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS</p> <p>HAPVDSGSDSSGLWSPVSNPSSPDFTPLNSFSAPGNSFNLTGE</p> <p>VFSKLGLSRSCNQASQSRWNEFNSGPSYLWESPATDPSPSWPAS</p> <p>SGSPHTATSVLGNTSGLWSTTFSSSIWSSNLSALPFTTTPAN</p> <p>TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPITGR</p> <p>RSSDPWSNSHFPHEN</p> |
| 5820 | 310 | 1270 | <p>RVLSLGPVSLGVLLCARSSMTGKRDNRAVYMNPIAMARSRGPIQ</p> <p>SSOPTIQ\VI*IDQGLPGKK*KSN*KRRKK/DSKALAEFEEMKN</p> <p>ENWKKELEKHREKLLSGSESSSKRQRKKKKKKSW*\DSSSS\</p> <p>SSSSSDSSSSSDSEDEDKKQKRRKKKKNRSHKSSSESSMSETES</p> |

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|------------|--|--|---|
| | | | DSKDSLKKKKKSKDGTETKEKDIKGLSKKKRMYSEDKPLSSESLS ESEYIEEVRAKKKSSSEEREKATEKTKKKKKKKHKKKKKKKAA SSSPDSP*H*EKSGFPYKESAMSEISTVKTTTYLLKCMNPLVF GIIPGLFSSSHSDATV |
| 5821 | 179 | 915 | KWRNQSQRWPKPGTNWMLSCSVCWRRVTWTGVSVMRKLKGHPQT PT/IKDCSIAATGKRPSARFPHQRRKKRREMDGLAEGGPQRSN TYVIKLFDRSVDLAQSENTPLYPICRAWMRNSPSVRERECSPS SPLPLPEDEEG\SEVTNSKSR*CVQACPTHTPGGQPKNACR\ SRIPSPLAALRMQGT*P*RWSPFEPEPSPSTLIYRNMQRWKRIRQ RWKEASHRNQLRYSESMKILREMYEQ |
| 5822 | 464 | 4379 | QTLKEMPIVMARDLEETASSEDEREVISQEDHPCIMWTGGCRR PVLVPHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA HGFHEVHPSSTDYNLMWTGSHLKPFLRLTLSEAQKVNHFPRSYE LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLPAEYAEFCNSYS KDRGPWIVKPVASSRGRG\YVLINPNQISLEENILVSRYINNP LLIDDFKFDVRLVYLVTSYDPLVIYLYEGLARFATVRYDQGA NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLR LKQGRDRTALMAHVEDLIKTIISAEALAIATACTFVPHRSSC FELYGFDVLIDSTLKPWLLEVNLSPLACDAPLDLKLKASMISD MFTVVGFCQDPAQRASTRPIYPTFESSRRNPFQKQRCRPLSA SDAEMKNLVGSAREKGPGLGGSVLGLSMEEIKVLRVKEENDR RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFPQDRMTADG APELKI*SLNSKAKLHAALYERKLSLEVRKRRRRSSRLRAMRP KYPVITQPAEMNVKTETSEEEEEVALDNEDEEQEASQEEESAGF LRENQAKYTPSLTALVENTPKENSMKVREWNKGGHCKKLETOE LEPKFNLMLQIQDNGNLSKMQARIAFSAYLOHVQI\RLMKDSGG QTFASAWAKEDEQMELVVRFLKRASNNLQHSRLMVLPSSRLAL LERTRILAHQLGDFIIVYNKETEQAEEKSKKKVEEEEDGVNM ENFQEFIRQASEAELEEVLTFFYTQKNKSASVFLGTHSKISKNN NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSCLKSRFTTSA EKEAKLVYSSSSSGPTATLQKIPNTHLSSVTTSDLSPPGCHHSS LSQIPSAIPSPHQPTILLNTVSASAPCLHPGAQNIPTPTGLP RCRSGSHTIGPFSFQSAAHYISQKLSRPSAKAGSCYLNKHHS GIAKTQKEGEDASLYSKRYNQSMVTAEQLRLAEKQAAQYSPSS HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH KYHPTAGSYQLQFALQQLQKLSRQLLDQSRARHQAFSGST LPNSNLWTMNGAGCRISSATASGQKPTTLPPQKVVPPSSCASL VPKPPPNHEQVLRRTSQAASKGSSAEGQLNGLQSSLNPAAFVP ITSSDTPAHTKIMNHKHTKQPVHHSWVHD |
| 5823 | 42 | 2293 | LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKFDF DLSSLSSSSANEDDEVFFGPPGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLALHIESSSRNQAAQAAKP EDPRSQGVVERFIQESKF\KINLFEKEKMKKSPTSLKRETYYS DSPLLGPPVGEPRLLASSPALSSGAQARLTRAPGPFHSAHALP RESCATAHAASQAATQRKPGTKLLPRAASVRGRGIPGAEEKPKK EIPASPSRTKIPEKESHARDVLPDKPAPGAVNPAAGSHLGQK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSSGASSA CTPQPVAKASSEFASIPAN*LPGLCPNISK\GRMGPAMLRPA L\PAGEVG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPTPE GGG\QWLNSSCAWSESSQLNKTRSIIRRDSCLSKTKVMPTFTN QFKIPKFSIGDS\PDSSSTPKLSRAQRPSCTSVGRVTVHSTFVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPTKMPRAVGS PL\CVPARRRSSSEPRKNSAMRTEPTRESNRKTDNR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVQQLIDLSSPLIQLSPADK ENVDSPLPKF |
| 5824 | 42 | 2293 | LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKFDF DLSSLSSSSANEDDEVFFGPPGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLALHIESSSRNQAAQAAKP |

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|------------|--|--|--|
| | | | EDPRSQGVVERFIQESKF\KINLFEKEKEMKKSPTSLSKRETYTLLS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP RESCATAHAASQAATQRKPGTKLLLPRAASVVRGRGIPGAEEKPKK EIPASPSRTKI PAEKESHDRDVLDPKPAAGAVNPVPAAGSHLGQK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPLGLCPNISK\GRMGFAMLRPA L\PAGFVG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIIRRRDSCLSNKTVMPTPTN QFKIPKFSIGDS\PDSTPKLSRAQRPSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPMPPTKMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDNR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGGQLIDLSSPLIQLSPADK ENVDSPLLK |
| 5825 | 2 | 4210 | FLQTESASPAPFSSGFLAAHPHSPGGLATKGRSRLSAPGMLHL SAAPPAPPPPEVTATARPCLCSVGRRGDGGKMAAGALERSFVEL SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYVESG KLFSVTRNRFIHWKTSQDTELEMEESLDINLLNNAIRLKFNCS VLPGGVYVSETQNRVILMLTNQTVHRLLLPHPSRMYRSELVVD SQMQSIFTDIGKVDFTPCNYQLIPAVPGISPNTASTAWLSSD GEALFALPCASGGIFVLKLPFYDIPGMVSVVELKQSSVMQRLLT GWMPTAIRGDQSPSDRPLSLAVHCVHEHDAFIFALCQDHKLRMWS YKEQMCLMVAADMLEYVPVKDLRLTAGTGHKLRLAYSPTMGLYL GIF\MHAFKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF ALTSTDIWALWHAENQTVVKYINFEHNVAGQWNPVFMQPLPEE EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL DLSWSELKKEVTLAVENELQGSVTEYEFSSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHNTNMVCLLKKGYLSFLIPSSLVD HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVT DMSVIMEMSCYNLQSPKAAEQILEDMITIDVENVMEDICSKLQ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLQLY GSNTAGYIVCRGVHKIASTRFLICRDLILQQLMRLGDAVIWG TGQLFQAQDQLLHRTAPLLSYLIKWSECLATDVPLDTLESEN LQHLVLELTDGALMANRFVSSPQTIVELFFQEVARKHII SHL FSQPKAPLSQTGLNWPemitaitSYLLQLLWPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL ECFQAASEVGKEEFLDRILRSEDGEIVSTPRLQYYDKVLRLLD VIGLPELVIQLATSITBASDDW\KSQATL\RTCIFKHL\DLG \HNSQAYGSL*PQIPDSSRQLDCLRQLVVLCCERSQLQDLVEFS YVNLHNEVVGIIESRARAVDLMTHNYELL YAFHIYRHNRYKAG TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIREYANI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE CSLARIRLTLAQHDPASAVAVAGSSSAEEMVTLVQAGLEDTAIS LCQTFKLPLTPVFEGLAPKCIKLQFGGEAAQAEAWLANQLS SVITTKESSATDEAWRLLSLYLERYKVQNNLYHHCVINLLSHG VPLENWLINSYKKVDAEELLRLVLYNVDLLDTPYQVIRICGC |
| 5826 | 3 | 871 | KSQLLRDHSAPPPKPTSVGAMGC*PRQ/SPKEQQRQLKKQKNR AAQSRQKHTDKADALHQHESLEKDNLALRKEIQSLQAEALW WSRTLHVHERLCPMDCASCSAPGLLCWDQAEGLLGPQGGH CRQLELFQTPGSCYPAPQLSPGPQPHDSPSLLQCPLPSLSLGP AVVAEPPVQLSPSPLLFASHTGSSSLQSSSKLSALQPSLTAQTA PPQPLELEHPTRGKLGSSFDNPSSALGLARLQSRHKKPALSAT WQGLVVDPSPHPLLAFLPSSAQVHF |
| 5827 | 194 | 2287 | GMGSENSALKSYTLREPPTLPSGLAVYPAVLQDGKFASVIFYK RENEDKVNKAAPV**HLKTLRHPCLLRLFLSCTVEADGIHLVTE RVQPLEVALETLSAEVCAGIYDILLALI FLHDRGHLTHNNVCL SSVVFSEGDHGWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP EEMSPFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS SFQOTLHSTLLNPIPKWRPALCTLLSHDFFRNDPFLVNVFLKSL TLKSEEEKTEFFKFLLDVSVCLSEELIASRLVPLLLNLQVFAEP |

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|------------|--|--|---|
| | | | VAV\KSFLPYLLGPKKDHQGETPCLLSPALFQSRVTPVLLQLF EVHEEHVRMVLSSHIEAYVGALSLEQLKKV\IL\PQVLLG\LR D\TSDSIVAITLHSLAVLVSLGPEVVVGERTKIFKRTAP\SF TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSNFSSSKK SEEPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL GLGEEFTIQVKKKPVKDPEDMDFADMIPEIKPSAAFLILPELRT EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWDNN W |
| 5828 | 2 | 257 | AREGGSLGAVAACGELS YSCDFCPARPHTSWLTRFVKMEFQAVV MAVGGSRMTDLTSSIPKPLLPGVGNKPLIWIYPLNLLERVGFEEV IVVTTTRDVQKALCAEFKMKMKPDIVCIPDDADMGATDSLRIYIP KLKTDVLVLSCDLITDVALHEVVDFRAYDASLAMLMRKGQDSI BPVPGQKGGKKAVERDQFIGVDSTGKRLLFMANEADLDEELVI GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS BL\IPYLV/RGKQFSSASSQGTREKEGEGSGKGRGLKSFRISY SFY*KEANYTGTGAPY\D\ACWI |
| 5829 | 260 | 1259 | PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS GTCIASAGSDQTVKVDVRVKNLLQHYQVHSGGVNCSIFHPSGN YLITASSDGTLLKILDLKGRLIYTLQGHGTGPVFTVSFSKGGELF ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY PRTPHPEBKVETVEDFFLHLLRLIQSLR*SICRSLPLLWISF LLILPQQQKPVVGLCQTRVKRPVDIS*TL*CHQNVCCQPRKKR QKT*VTSFVKVK/VSIPLAVTDALEHIMEQLNVLQTQVSILEQR LTLTEDKLDCLLENQQLFSVAVQQKS |
| 5830 | 4496 | 3139 | GGKMAAPEERDLTQEQTCLKLQFQDLTGIESMDQCRHTEQHNW NIEAAVQDRLENEQGVPSVFNPPSRPLQVNTADHRIYSYVVS RPPRGLLGWGYLLIMLPFRFTYTYTILDFRFAIRFIRPDPRSRV TDPVGDIVSFMHSFEKYGRAHPVFFYQGTYSQALNDAKRELRL FLVYLHGDDHQDSDEFRCNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDLL INQLTFIMDANQTYLVSERLEREERNQTVLRQQQDEAYLASLR ADQEKERKKREERERKRRKKEEVQQQLAEERRRQNLQEEKERK LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLSLTVIHDF LFSLKESP\EFQIEA\NPPRR\VLPCIPSEE\WPNPPTLQEA GLSHTVELFVQDLTDE |
| 5831 | 71 | 2897 | FCSDKCCLYLPDSINRSKCTAKPGAHSQDRHAVMDSERQVKD TDDIESPKRSIRDGSDYDCWDSERSDSLSPRRHGRDSDSFLDS FGSRSRQTPSPDVVLRGSSDGRGSDSEDLPHRKLDPVKDDMS ARRTSHGEPKSAVPFNQYLPNKSNTAYVPAPLRKKKARREBYR KSWSTATSPAGLGKALQDYGPRT\PVS\DDAESTSMFDMRCEE EAAVQPHSRARQEQQLINNQLREDDKWQDDLARWKSRRKRSVS QDLIKKEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE RELHEAYKNARSQEEAEGILQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSPQKNSQDVLKTFK VDGKVSVNGETVHREEEKEKRECPVAPAHSLTKSQMPEGVARVH GSPLELKQDNGSIEINIKKPNVFPQELAAATTEKTEPNSEQEDKN DGKSRKGNIELASSEPHFTTTVTRCSPTVAFVEFPSSQLKND VSEKDKQKKNEMSGKVELVLSQKVVKPKSPPEATLTFFFLD KMPEANQLHLPLNLSQVDSPESEKSPVTTFFKFWAWDPEEERRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEBRRY YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKSFQGDSDLLKTRSDRLEEKGSLEBEGAL AHSQNPVSKGVHEDHQLDTEAGAPHGCTNPQLAQDPSQNQQTNS PTHSSBDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSGCL PLGKGAAAMIEITLNLFIHQCFROG\ICKGQLGDAVSGTDVIR NGLLNCNDCYMRSRAGQPTTL |
| 5832 | 2454 | 829 | PGRRRFRHSGCAFOKQCTIMLHICQYFLOGECKFGTSCKRSHDFSN SENLEKLEKLGMSDDLVSRLPTIYRNAHDIKNKSSAPSRVPLPF |

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|------------|--|--|---|
| | | | VPQGTSEKRDSSGVSVPNTLSQEEGDQICLYHIRKSCSFQDKCH RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES ASTFHSCLNFMNTYGTATQARRLSTASSVTKPPHFILTTDWIW YWSDEFGSWQEGYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGVR PGSHLEVPGRKAQLRVRFQSLRSEKPLWHN*KGLFPQTQIR\AP QDVTMTQTCNTKFPKPKSIPDYWDSSALPDGPFQKITLSSSSEE YQVWNLFNRTLPPFYVQKIERVQNLALWEVYQWQKQMQKQNG GKAVDERQLFHGTSAIFVDAICQNFQDWRVCGVHGTSYKGSYF ARDAAYSHHYKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ |
| 5833 | 170 | 3289 | SILCLLSPCVVQFGKPVVSISSSRHSRSPCTKKGWEGMRKHLHT RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR GRDWNVKWEENLLHAAVAKNYTLTQTIPEFERPFKDQVCLWNMG YIWNLRANRIPQCPLNDVVALLGFPYASSGENTGIVKKFPRF RNRLEATRQRMDDYPVFTVSLWLYLLHYCKANLCGILYFVDSN EMYGTPSVFLTEEGYLHIQMHVKGEDLAVTKFIIPLEKWFRL DISFNGGQIVVTTSIGQDLKSYHNQTTISFREDPHYNDTAGYFII GGSRYVAGIEGFFGPKLYRLSLHPAQIFNPLEKQLAEQIKL YYERCAEVQEI VSVYASAAKHGGERQEACHLHNSYLDLQRRYGR PSMCRAFPWEKELKDKHPSLQALLEMDLLTVPRNQNESVSEIG GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYLAV FYETGLNVPRDQLQGMLYSLVGGQSSERLSSMNLGYKHYYQGDIN YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDIIL KVQTKEDGDVFMWLKHEATRGNAQAQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGGQGVKNRRLALELM KKAASKGLHQA VNGLGWYHFKKNYA\KAAKYWLKA\EE\MGN PDASYNLGVHLHDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL WCSLYYITGNLETFRDPEKAVVWAKHVAEKNGYLGHVIRKGLN AYLEGSWHEALLYVLAETGIEVSQTNLAHICERPDLARLYL GUNCVWRYYNFSVFQIDAPSFAYLKMGDLYYGHQNSQDLELS VQMYAQAALDGDSSQGFNLAALLIEGTIIPHHILDFLEIDSTLH SNNISILQELYERCWSHSEESFSPCSLAWLYLHLRLWGAITH SALIYFLGTFLLSILIAWTVQYFQSVASDPPRPSQASPDAT STASPAVTPAADASDQDQPTVTNNPEPRG |
| 5834 | 17 | 4020 | RFRFGGRVFPFGAFPASPSDSLQGGNSQGFPTPKPPT/ QECG SAAPGPIPGQSSS*VPLRLEIQKQKADCPLELALKPRMAAQV TLEDALSNVDLLEELPLDQPCIEPPSSLLYQPNFTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSRRAI PQVKCNEQPNRVEIYEKTVLEVLEPEVTKLMMNFYFQNAIERFC GEVRRILCHAEERRKDFVSEAYLITLKGFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMDPQSIQESQNLMSFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYENRMYLTPSEKHMILLKVMGF GLYLMGDSVSNYKLDKAKRINLSKIDKYFKQLQVVPFLFGDMQI ELARYIKTSAHYEENKSRWCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTSGRQEAQKTDAYRKLFDLALQGLQLL SQWSAHVMEVYSWKL VHPTDKYSNKDCPDASAEYERATRYNYS EEKFPALVEVIAMI KGLQVLMGRMESVFNHAIKRTVYAALQDFSQ VTLMEPLRQAIAKKKNVQSVLQAIKRTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRAVGPSTQLYMVRTMLESLIADKSGSK XTLRSSLEGPTILDEKFHRESFFYTHLINFSETLQCCDLSQL WPREFFLELTMRRIQFPIEMSPWILTDHILETKEASMMYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPFSNRYETLLKQR HVQLLGRSIDLNLRIQTVSAAMYKSLAIGRFESEDLTSIVE LDGELLEINRMTHKLLSRYLTDGFDAMFREANHNVSAPYGRITL HVFWEELNYDFLPNYCYNGSTNRVFTVLPFSQEFQRDKQPNAP QYLHGSKALNLA YSSYGYRNFGPPHFQVICRLLYGQGIADV MEELLKVVKSLLQGTILQYVKTLMVMPKICRLPRHEYGSPGIL EFFHHQLKDIVEYAEKTVCFQNLREVGNAILFCLLIEQSLSLE EVCDDLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP |

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|------------|--|--|--|
| | | | LIERLGTPQQIAIAREGDLTKERLCCGLSMFEVILTRIRSF LD DPIWRGPLPSNGVMHVECEVPHRLWSAMQVYCI PVGTHEFTV EQCFDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDKD EIIKNVPLKKMVERIRKFIQILNDEIITILDXYLKSGDGBGTPVE HVRCFPPIHQSLASS |
| 5835 | 4209 | 1904 | SGNIRMAQGS HQIDFQVLHDLRQKFPEVPEVVSRCLQNNNNL DACC AVL S Q E S T R Y L Y G E G D L N F S D D S G I S G L R N H M T S L N D L Q SQNIYHHGREGSRMNGSRITLTHSISDGQLQGGQSNSELFQQEPQ TAPAQVPQGFNVFGMSSSSGASNSAPHLGPHLGSKGTSSLSQQT PRFNPI MVTLAPNIQTGRNTP TSLHIHGVPPFVLNSPQGNSTIYI RPYITTPGGTTRQTQOHSGWVSQFNPMNPQQVYQPSQPGFWTTC PASNPLSHTSSQQPNQQGHQTS HVYMP ISSPTTSQPPTIHSSGS SQSSAHSQYNIONISTGPRKNQIEIKLEPPQNNSSKLRS SGPR TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMRSRQPKVYISA NAATGDEQVMRNQPTLFISTNSGASASRNMSQGVSMGPAFIIH HPPKSRAIGNSATSPRVVVTQPNTEYTFKITVSPNKPAPVSP GVVSPTFELTNLLNHPDHYVETENIHLTDPTLAHVDRISETR K LSMGSDDAAYTDI *RISNSWLGMVAHACNSSALGGQDGR I I *A QEFETSWGNIWRLRLYRRF *NYAGMVAHTCSPSYSD *ALLVHQ KARMERLQRELEIQKKLKLKSEVNEMENLRRRLKRSNSIS QIPSEEMQQLRSCNRQLQIDIDCLTKEIDLQFARGPHFNPSAI HNFYDNIGFVGPPVPPKPKDQRSIIKTPKTQDTEDEGAQWNCTA CTFLNHPALIRCEQCEMPHF |
| 5836 | 361 | 2303 | FHITMCGICCSVNFSAEHFSQDLKEDLLYNLQKRGPNSSKQLLK SDVNYQCLFSAHVLHLRGVLTTPQVEDERGNVFLWNGEIFSGIK VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS HYLWFGDRDFGRRSL LWHFSNLGKSPCLSSVGTQTSGLANQWE VPAS \DFSELILSLLSFPDALFYNCILGNIFLGRILLKMLIA * VKPQOTYOHLYQR *QMKPNCILKNLLFL *I *CCHKLHWRLIAVI FPMCHLQERYFKSFLMYT *KEVIQQFIDVLSVAVKKRVLC LPR DENLTANEVLKTCDRKANVAIFLFGGIDSMVIATLADRHIPLDE PIDLLNVAFIAEETMPTTFNREGNKQKNKCEIPSEEFSDVAA AADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKLRRTRICHLIRPLDVLDDSIGCAVNFASRGIGWLVAQEG VKSYSQNAKVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISRRNLGRDDRVIDGHGKEARFPFLDENVVSFLNSLPW EKANLTLPRGIGKLLRLA AVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGR LQIMSLNLSIEKETKL |
| 5837 | 4792 | 903 | NGNAVAQAPVTNCCYLATGSKDQTIIRIWCSSRGVMI LKLPFL KRRGGGIDPTVKERLWLT LHWPSNQPTQLVSSCFGELLQWDLT QSWRRKYTLFSASSEGNHSRIVFNLCPLQTEDDKQLLLSTSM D RDVKCWDIATLECSWTLPSLGGFAYS LAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFQGVKSVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKT VYTLAWGFPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPKLSGEAFDINKLIRDTNSIKY KLPVHTIISWKADGKIMALGNEDGSIEIFQ \IPNLKICTIQQH HKL VNTISWHHE \HGSPAQKLSYL \MPSGSQQCS PFTCHNLKNC P *KAAPESPSDPLQSPYRTPPQGHTAQDY PVNAWEPIH *WEG L VFCFPIDGYSFGCWD \AFPGKEAPVAIFRG \HQGRLLCVAWSPL DPDCIYSG \ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVS DQ EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKRKARSLLPLSTSLDHSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELPHQLMLWKGDLKGVLTAAERGETDNLVAMAPAA GYHVWLWAVEAFKQLCFQDQYVKAASHLLSIHKVYBAVELLS NHFFYREAIATAKARLRPEDPV LKDYLSWGTVLERDGHYAAK CYLGATCAYDAKVLA KGDASLR TAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE EKQLSEKSSSSVHTWNTGTGEPFVERVTAVWKSIFSLDTP EQY QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW |

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|------------|--|--|---|
| | | | DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD HQSPATPAFKSLEAFFLYGRLYEFWWSLSRCPNSSVWVRAGHR TLSVEPSQQLDTASTEETDPETSQPEPNRPSLDLRLTEEGERM LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS TANGPDKNRPEVEAEQPLCSSSQCKEKEKNEPLSLPELTKRLE ANQRMAKFPESIKAWFPDVLCECLVLLLIRSHFPGCLAQEMQQ QAEQLLQKYGNTKTYRRHCQTFCM |
| 5838 | 110 | 98 | KTMPHLLVTRFDVAIDFSQEEWECLDPAQRDLRYDVMLENYSNL ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFYNG LGDNMECKGNLEGQVSKSEGLYMCVKITCEKATESHSTSTFTH RII/HYQGGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH RNTFSKKPSYI*HQ\KFRLEKPYECMECGKAFGRSTDLIHQK IHTNEKPYQCNAKGAFIRGSQLTEHQRVHTGEKPYDCKKCGKA FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG EKPYECKECGKAFILGSHLTQHVRVHTGEKPYICECKGKAFILCA SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERP YKCKEKGKAFISNSNLIHQRIHTGEKPYKCKEKGKAFICGKQLS EHQRHTGEKPFECKEKGKAFIRVAYLTQHEKIHGEKHYECKEC GKTFFVRATQLTQHRIHTGEKPYKCKEKGKAF/HLWLTILSEHQ RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRHTGEKPYECKEC GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL HN*EYSSHKICMHSIALASLDFAHLQEKNPEN |
| 5839 | 1 | 2425 | GRPFPRPPRALPRPLRGRQRDGRWTVDFEECLKD\SPRFRAAL EEEGVDAEELK\DKLVKLCIA\MIDTGKAFVANKQFMNGI RD\LAQNS\NDA\VVETKFAPSFLDLQEMINFHTIL/L*PNS EIN*GHSFQNFVKEDLRKFDAKKQFENSQ*KRKKIALVKNAFV PSRPASLEL*KPPNLTATRKCFRHIADYVLOINVLSQSKRRSE ILKSMLSMFYAHLAFFHQGYDLFSELGPFYMDLGAQLDRLVGDA AKEKREMEQKHSTIQCKDFSRDDSKLYNVDAANGIVMEGLFK RASNAFKTWNRWFSIQNNQVYQKKFKDNPTVVVEDLRLCTVK HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT AYREKDDSEKLDKSSPSTGSLDSGNESKEKLLKGESALQVQ CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSIGVHFSK VRSILTLDTWPELLKLMCELGNDVINRVYEAIVEKMGIKKPPQG QRQKEAYIRAKYVERKFVDKIPL*SLSP*\BQKK\FVSKSE EKRLSISKFGP/GDQVRASQSSVRSNDSGIQSSDDGRESLPS TVSANSLYEPBGERQDSSMFLDSKHLNPGQLYRASYEKNLPKM AEALAHGADVNNWANEENKATPLIQAVALGGSLVTCEFLQNGAN VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGDP LSIAVEAANADIVTLRLRLARMNEEMRESEGLYGPQDETYQDIF RDFSQMASNNPEKLNRFQQDSQKF |
| 5840 | 698 | 3610 | KHLHLPRQHLTTLWQISSPRWRSFQRAFMSALSKTQTSAPALQ GLSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS AQPFIPKSFNYPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP SNTKGTATHTNTSPAAPPTEVTICQSEVSKPKL\ESESTS PSL \EMKIHNFLLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSSVDTMSLL SKIISPGSSPTSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE SPYKQPSDGMERPSSSLMDSSQEFYPTDSFQEDEDYRDFEYSGP PPSAMNLOKKPAKSILKSSKLSDTTEYQPIILSSYSHRAQEFV KSAFPSPVRALLDSSENCRLSSSPGLFGAFSVRGNEPGSDRSP SPKNDSTFTPDNSHNLSQSTTGHLSLPQKQYVPSPHVPHRS LFSPQNTLAAPTGHPPPTSGVEKVLASTISTSTIEFKNMLKNAS RKPSDDKHFGQAPSKGTPSDGVLSNLTPSLTATDQQQBEHY RIETRVSSSCLDLPDSTEEKGAPIETLGYSASNRMSGEP IQT VESIRVPGKNGRNGHREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGSGGLTGFTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTFFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS VDLNSNPTKEAALAAHAPPPPGHSGIPFPTPPPPPPGHESS SGGSGVPFSTFPFPPPPVDHSGVVPFAPPLAEHGVAGAVVFP KD:SSLLQGTAEHFGVLPGRDHGGPTQRDLNGPGLSRVRESL |

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|------------|--|--|---|
| | | | TLFHSLSLEHLGPPHGGGGGGSSSSSGPPLGPSHRDTISRSGIT LRSRPDPFRPREPFLSRDPFHSLSLRPRPPFARGPPFFAPKRPF PPRY |
| 5841 | 1908 | 762 | GLRLFLVLTVWPMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY TRSMKMTTSINRRSRTSTKSTRTSAREPLTATVIGLSDSPW RHCMTARSCSGEKGHWAPRQGVYLLPGRVGCSSRVSPSPFP GDGLDSGLARRGSASVALASGLVEEPLMGPFFHTPRPKAVSAK SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND QSTSDYLVVYLRLLTSGYLQRESKPFHEHIEGGRTVKEFCQ\QE \VEPMCKESDHIHIALAQGLQRVHPGWBYMGPRPRAATTNPHI FP*GLPSFKVYLLYRPG\HYDILYKIGLGSSPLGCPGCLLARA LGHCYRGFSVVVWKSIFYTPFFLSHDPFPMFY |
| 5842 | 307 | 1918 | QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVRVRKL WSSRRPRTRRNLGLTACAIYLGFLVSQVGRASLQHGQAAEKGP HRSRDTAEPSPFEIPLDGLAPPESQNGSTLQPNVYITLRSK RSKPANIRGTVKPKRRKKHAVAAPGQEAALVGPQLQPEA\EG KLML*HLGTLREQTWLRLESDEGGWCGVRE/WRAGGPDFLQPS RESNIRIYSESAPSWLSKDDIRRMRLADSAGVLRPVSSRSGA RLVLVEGGAPGAVLRCPSPCGLLKQPLDMSEVFAFLDRILGL NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSVKLTW GTYYQLLKQKQWQNGRVPKPESGCTEIIHHEWSKMALFDLLQI YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAALHI IQRK DPRHLVFDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH LRQKLLQSLFLDKGYWESQGGRGIEKLIDVIEHRAKILITYIN AHGVKVLPMNE |
| 5843 | 500 | 1453 | GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPGKWGLGAGM RGRMSQPPQLRRASQSCCHFMVKLLDDGTPIIPEGKVAHTSL DALVTFHQKQPIEPRELLTQPCRQDPAENVYEDFLYSNAVA EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQSGSHFL LPPKIPSWRDPPEETLEEQNAPRERPEGPAACKPPRHCELVVT LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSCLCGHISQKP LTAPGTQRKQKPGHGEQREVQQLH*GDPRGQELAPNGSESPIPG VQARAPGLGRA |
| 5844 | 202 | 2471 | FDSAVLSSINVMVAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI KPLPPQIPQMPPIQYQPLGQQVPHMPLAKDGLAMGKEMPHL QYGEYPHLPQYMKIEIQAPAPRMGKEAVPKKGKEIPLASLRGEQ PRGEPGRGPPGPGPLPGHGIPGIGKPGPGQYPGVKGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPFGHGLPGIGK PGCGPLPGQPGKGRGPGKPLPGPQCLRGPKGDKGPGMPGAPGV KPPPGMHGPPPGVGLPGVKGPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRMGVPGALGPRGKPGIGA PGIGGPPGEFGLPGIPGPMGPFPAIGFPGPKGEGGIVPGQSGPG PKGEPGLQGFPGKPGFLGEVPGPMRGFPPIGPKGEHGQKGV GLPGVPGLLGPKGEPGIPGDQGLQGPPIPGIGGPGSGPIGPPGI PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQQPG PGPPPGPPGPPAVMPPTPPPGGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPVVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYFYAYHVHCKGGNVVWALFKNNEPVMYTYD EYKKGFLDQASGSVALLLRPGDRVFLQMPSEQAAGLYAGQYVHS SFGYLLYPM |
| 5845 | 215 | 2061 | HASNKASLQDKMANPKETAMCLVNELARFNRVQPYKLLNER GPAHSMFVSQSLGEQTWESESSIKKAQQAVGNKALTESTLP KPI*KPPKSNVNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK FPNNRANYNFQVMYNQRYHCPKPKIFYVQLTVGNNEFFGEGKT RQAARHNAAMKALQALQNEPIERSPONGESGKMDDDKDANKS EISLVFEIALKRMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE GEGNSKKLSKKRAATTVLQELKKLPLPVVEKPK\HFFKKRPKT IVKAGPEYGGMNPI SRLAQIQAKKEKEPDYVLLSERGMPPRR EFVMQVKVGNVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ DQLEKTGENKWSGPKPGFPPEPTNNTPKGILHLSPDVYQEMEAS |

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|------------|--|--|---|
| | | | RHKVISGTTGLVLSPKDMNQPSSTSSSISPTSNSSATIARELLM NGTSSTAEAGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC DRSGKCEVCTCLTAPVQMTFHAIGSSIEASHDQV*YATAILLC YGPARKWKAIMEAMCAHAALLSLIHVLLAPSARLEKSKLFAIG N. |
| 5846 | 1126 | 456 | FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLNCSVISQDDFF KPESEIETDKNGFLQYDVLEALNMEKMSAISCMWESARHSVVS TDQESABEIPILIEGFLFNKPLDTIWNRSYFLTIPYEECKR RRSTRVQPPDSPGYFDGHVWPMYLYKRYQEMODITWEVYLDGT KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNP/CK*IRK LQGV |
| 5847 | 2769 | 505 | APEMEDLSSPDSTLLQGGHNLSSASFQESVTFKDVIVDFTOEE WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGT PWIMPSIPVGTCDWETRENSVSAPEDISEEELSPEVIVEK HKRDSWSSNLLESWEYEGSLERQQANQQLPKKIKVTEKTIPS WEKGPVNNFSGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK KEKSCCKNECGKAFSYCSALIRHQRHTHTGKPKYKCN*/CVEKAF SRSENLIHQRIHTGDKPKYKCDQCGKGFIEGSLTQHQRIHTGE KPYKDECGKAFSQRTHLVQHQRHTHTGKPYTCNECGKAFSQRG HPMEHQKIHTGKPFKDECDKTFTRSTHLLTQHQRHTHTGKPYK CNECGKAFNGPSTFIRHMIHTGKPYECNECGKAFSQHNSLTQ HQTHTGKPYDCAECGKSFSYSSSLAQHLKIHTGKPYKCN GKAFSYCSSLTQHRRHTHTGKPFCECGKAFSYLSNLNQHKOT HTQEKAYECKEKGAFIRSSSLAKHERHTHTGKPYQCHECGKTF SYGSSLIQHRKIHTGERPYKCNCEGRAFNQNIHLTQHKRIHTGA KPYECACGKAFRHCSSLAQHQRHTHTGKPYQCNCKEPTFSQSS HLTQHQRHTHTGKPYKCNCECDKAFSRSTHLLTQHQRHTHTGKPYK CNECGK\TFSQSTYLIQHQRHTHTGKPFKFCNDCGKSFYRSALN KHQRLHPGI |
| 5848 | 22 | 2961 | AAPRRLLRGGDGRTPRFPPLPALLRPGPPAEAPERRKMPAVSK GDGMRGLAVPISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIILLGHIDIFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNELIRLINNAIKNDLASRNPTFMGLALHCIAV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNLQGLQHRETNLRYLALESMTCLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIRBEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIIQVINRDDVQGYAAKTVEALQ APACHENLVKVGYYILGEFGNLIAGDPRSSPLIQFHLHLSKPHL CSVPTRALLSTYIKFVNLFPPEVKPTIQDVLRSQSRLRNADVEL QORAVEYLRLLSTVASTDILATVLEEMPPFPERESSILAKLKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTSPSADLLG LGAAPPAPAGPPSSGGSGLLVDVFSASVVAFLAPGSEDNFA RFVCKNNGVLFENQLQIGLKSEFRQNLGRMFIYVGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQVNVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFQ RWKQLSNPQEVQNI*FKAKHPMDTEVTAKIIGFGSALLEEVD NPANFVGAGIHTKTQIGCLLRLEPNLQQAQMYRLTLRTSKEAV SQRCELLSAQF |
| 5849 | 3545 | 1895 | KRREIKETVFFHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWTSEVHNW TLEDTLQWLIIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQQLQLKALDVVLPGLTRPPHNWMDPILTVSI VIGVGGCWFAITQNTSKHEHVAKMMKDLESQTAEQSLMDLQER LEKAQENNRNVAVEKQNL*RKMMDEINYAKEEACRLRELEGAE CELSRRQYAEQLEQVRMALKAEKEFELRSSWSVPDALQKWLQ LTHEVEVQYNIKRQNAEMQLAIAKDEAEKIKKRSTVFGTLHV |

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|------------|--|--|---|
| | | | AHSSSLDEVHDKILEAKKALSELTTCLRERLFRWQQIEKICGFQ IAHNSGLPSLTSSLYSDHSWVMPRVSIIPPYPIAGGVDDLDEDT PPIVSQPPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA PHAPHPSPHRPHHPQHTPHSLSPDPDILSVSSCPALYRNEE EEAIYFSAEKQWEVPDTASECDLNSSIGRKQSP/SKPRDIPN IIS/DERYQEMRCP*RIPSGGIL |
| 5850 | 3 | 1895 | KAVLNFSASGSVISLTGSNPMHDSMWHLKNGIIVYLDVPLLN LICRLKLMKTDRIVGQNSGTSMKDLLKFRQYKKWYDARVFC SGASPEEVADKVLNAIKRYQDVSETFISTRHVWPDCEQKVSA EFFIEAVIEGLASDGLFVPAKEFPKLSCGEWKSIVGATYVERA QILLERCIPADIPARLGEMITAYGENFACSKIAVRHLSGN QFIELEFHGPTGSPKDLQLMPHIFAQCIPPSCNYMILVATSG DTGSAVLNGFSRLNKNDKQRIAVVAFPENGVSDFOKAQIIGSQ RENGWAVGVESDFDQCATAIKRIFNDSDFTGFLTVEYGTILSSA NSINWGRLLPQVYHASAYLDLVSQGFISFGSPVDVCIPTNGR NIIAAVYAKMMGIPIRKFCASNQNHVWTDFTKTG\HYDLRGKE N*AQTFFTVQ*IPLNLSNLERHLHLMANKDQQLMTELFNRLES QHHPQIEKALVEKLQDFVADWCSEGECLAINSTYNTSGYILD PHTAVAKVVADRVQDKTCPVVISSTAHYSKFPAPAIMQALKIKEI NETSSSLLYLLGSYNALPPLHEALLERTKQKQEKMEYQVCAADN VLKSHVEQLVQNQFI |
| 5851 | 3120 | 1802 | RCYLQFLALLLTSTSAARAAATAAAEFPAGSFSVMTRAGDHNRO RGCCGSLADYLTSAKFLLYLGHSLSTWGDMMHFAVSVFLVELY GNSLLLTAVYGLVAGSVLVGAIIGDWVDKARLKVATQSLV QNVSVILCGIILMMVFLHKHELLTMYHGWLTSCYILITIANI ANLASTATAITIQRDWIVVAGEDRSKLANMNATIRRIDQLTNI LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQT PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH ELEHEQEPTCASQMAEPFRFTFRDGVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTEWPHQYFDGSIYNWNNGNCSPY LATSKMWFSGSDRDLRIGTAFDLFDLVDLCIHWKPPGLVRFSP |
| 5852 | 1 | 422 | KITTFPSSLCPLRQLEVRGYSQPLTDLPLISLCRSHKCRGKGW SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR SGWAQAQPTILLVPLRLKSLPSIWG/SLMGPFITSGPG/WFRQ YVFFISGRH*VLFTESDPFYVAMDGFGHGLSSHYSPPGVFYLLQ FVSEIRRVVAGKKQSVYFRRCGCCSRAPPLITGGGVGSRKQRP ESGAWALAPGLPAIHGRSWES |
| 5853 | 223 | 1346 | RLGLSRVKGHLHGPAASAWISDPETRGDPGPGWGMWRGSDLRPR PVSLTGLTLVCK*AAQGPQV\HSVKLFCGLGG\PCLL\FPIFRP LLHPRRRLHPTGRGVAVEPHALRVVHVHAGEEAGIRAAGPGH GGVEIPQG/VGSLGARRGLRPSRPSRHRNRVPAPPPGRPLATP HRRRFPPDPALTCPLGQDQGPREQQKQSGRHDITLGDWGESE SRWVRGNFRGTAAATLIGFSRNPTLNGSENWGLSVISQEEGPDT GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSONWTPCLLLLTCPRLG |
| 5854 | 86 | 938 | KGRNTAPEKKGAAALNNRENASS*NGY/SRWKQDIRRIENHIQ LKHLCAIMKRVLLERLENTKRLRELTEGRTLDPQNRITEVSAK RQIVTEYREKGRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS GAETIKDLE/ENFPKLNELDLQMEKAHRIPLKFNEKKAASRH IRVTF/LKQRRNILQASSQRKQVYTKGAKVRLTSDFPSAILNA RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQ LGKYNQELSLKILLKDLLQLTENLN |
| 5855 | 536 | 2391 | LSRYGCKAPSRISHLH\FLFLLPSLLMGYSESPPFITDSWAP FISLTHHVLSSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS NVSLHISYLAIPFLADSFLLKPV/L*PGNSAKHLSFKLSSLSMV GRAVALLHLIASGLTSIQNTASSKPPWGY\LSTQTSFISPPP LCLSRTPNPAHAMVGVQVPSLCGLIFTL/RTPCRPSILHPNY KIISTSAWKVLCFSGSPITHTSLHLTTGSSFLSFHPIPGFPAA NSALYVSSLKGGPKGNVTIPSPVTGT*QPPHRGSN/RLTVDKDN |

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|------------|--|--|--|
| | | | FFLSPKPNLSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFPQAPTIN ILPPNQTLISVEASISSSPIRNKWLHLITLLTGLGITAALGT GIAGITTSITSYQTLFTTSLNTVEDMHTSITSLQRQLDFLVGVI LQNRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD RAEL*HQVADSWWQSSLLRWIPWVAPFLGPLIFLFLMLMIGP CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH SEAPEPRP |
| 5856 | 173 | 1137 | PWLHGLGLSAVFLPYL*/YVTFHLYGGIILLLLIFISIAGILYK FQVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGI RLNLIL IRYTGDNPSYSPSTIIYFHGNAGNIGHRLPNALLMLVNLKVNLL VDYRGYKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG RSLG\GAAAIHLASDNSHRISAIMVENTFLSI PHMASTLPSFFP MRYLPLWCYKKNFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ LYELSPSRTRKRLAIFPDGTHNDTWQCCGYFTALEQFIKEVVKSH SPEEMAKTSSNVITII |
| 5857 | 1597 | 563 | KLIGKVLVLSVVADAMAFAVEPQGPALGSEPMMLGSPTSPPKPG VNAQFLPGFLMGDLAPVTPQPRSISGPSVGVMMRSPLLAGGS PPQPVVPAHKDKSGAPPVRSIYDDISSFGLGSTPLTSRRQPNIS VMQSPLVGVSTSPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ GDSLTSSEDH\LDSSWGDCIWGFLKASA\SYILL\QFAQYGGIS* NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI DKSVMESDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP LATAYKASTSDYQVISDRQTPKKDES LVSKAMEYMFGEW |
| 5858 | 355 | 1419 | PPHQAAAASXHQQQQPPPPQDSSKPVVAQGGPGAPGVGSAP PASSAPPATPPTS GAPP GSGPGPTPTPPPAVTSAPP GAPPPTP PSSGVPTTPPQAGGPPPPPAAVPGPGPGKQPGPGGPKGGKMP GGPKPGGGPGLSTPGGHKPPPHRGGGEPGRGRQHHPYHQHHQ QFPFGPGGRSEEEKISGPRRGFKANLSLLRRPGKTYTQRCRFC LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR ALA*NCPKPELG*YTP*GGRQLPSSSLFPTHACLPLSCSVIFSPF MFPQ*NCWGRKPFRRPNLGPLHKGAVCNRWDDFWEGPTGKGHCLN FAS |
| 5859 | 307 | 1503 | GGSSARPRASSRRLSRKKTINEVSKPAEVQGGYVKKETSPLLR NLMPFSIRHGPPTIPRRDIDLDDSSPNAFSTSGDGVVSRNQSF RTPIORTPHEIMRRESNRLSAPSYLARSLADVPREYSSQSFTV EVSPFAVENGDSGSRYYSNFFDQGRKRPLGDRAHEDYRYEYN HDLFQRMPPQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS VDWTMRGRKYYIDHNTNTTHWSHPLERGLPPGWERVESSEFGT YYVDHTNKKAY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT YQGMKLLFMKELEQIVKMYEAYRQALLTELENRKORQWYAQQ HGKNF |
| 5860 | 2956 | 1270 | TIRVEEFPLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLLFP LLLF SRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI SWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLPKNYSINDATI TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP NETATIIISQYKLPTRFARGRRITCVVKHPALEKDIRYSFILD QYAEVSVTGYDGNWFVGRKGVNLKCNADANPPPKSVMSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPTA*TSRD\LAEP*KIA PSPLSTL\ATIKGTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDYPYDVS KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYIEDL KMGKMFVSDHYDENEDDLVSHVDGVSISRREYV |
| 5861 | 2051 | 1305 | EVCACVQAFWLVAASGDDSGGDKCGCEVGSWVGSMRVMMARLL SEGEQGIPTACAAFAQQPAG/BPFRRLAGVGEQGPQCSWVNYRC TLEFLVSLGLTDLARGRNSASGPTAPADSKQL/ML*DVHRRVI LE*RMNSGSPARDNAPSQRFCNTLSEGLRFGISPSWREALYGC |

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|------------|--|--|--|
| 5862 | 1556 | 483 | <p>A</p> <p>PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG PRSIRCPILFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW DHLEFCDFGRKLLDHLQDKVHLFGASLGGFLAQKFAEYTHKSP RVHSLILCNSFSDTSIFNQTTWTANSFWLMPAFMLKKIVLGNFSS GPVDPMMADAIDFMVDRLESIGQSELASRLTLNCQNSYVEPHKI RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFY LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPSRLRCRKA ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPPPSGSSGS PVLTVSGK</p> |
| 5863 | 2714 | 249 | <p>FFPSRGSLLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPN VNISGGTFTLSHGWAQPSLLTYSCPQGLYPSPASRLCKSSGQWQ TFGATRSLSKAVCKPVRCAPVSPFENGITYPRLGSYPVGGNVSF ECBDGFI\LRGSPVRCRPNMGWDGETAVCDNGAGHCPNPGISL GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECCQNGVWSGTE PICRQPPYSYDFPEDVAPALGTSFSHMLGATNPTQTKESLGRKI QIQRSGLHNLNLYLLDSCQSVSSENDFLIFKESASLMVDRIFSFEI NVSVAIIITFASEP KVLMSVLNDNSRDMTEVISSLENANYKDHEN GTGTNTYAALNSVYLMNMNQMRLLGMETMAW\QEIRHAIILLT DGK\SHMGSGPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELNELGSKKDGGERHAFILQDTKALHQVFEHMLDVSKLTDIT CGVGNMSANASDQERTFWHTIKPKSQET\CRGALISDQWLT AAHCFRDGNDHSLWRVNVGDPKSGWGKEFLIEKAVISPGFDVFA KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \EANLGFLRETFCGSTCR\DHENEL/VWNKQSV\PAHF\VALN GSKLEHLTLRMGVWETSCCRGLSPKKTM\FPNT\DVRE\VVT D\QFL\CS\GPOEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR\DFHIN\LFP Q*SPWLRQHPGMS*IFLPLLANGHLSPPFACPARICRPLHLFPS EWATLRTL</p> |
| 5864 | 173 | 1013 | <p>PLISVPQSLISLPQPLLCPFGGQEPSAPSPCLYSFLWACSFTMG KLPPSIIPSSPLACVLNKLPLQLTPLDKPKCLIFFCNTAWPQY KLDNSK*PENGTFEFSILQVLDNSCHKMGKWEVDPVQAFF\S HWSLPSLCSQC/GLIPNLSSFSFPCSPG/PPQVPSP/TESFFS MDSSDLPPSPQAAPRAEPGPNSHLASAPPYPNPFITSPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQP</p> |
| 5865 | 568 | 1684 | <p>CLPGPRWEGEGWRAGHTIVGCIFFKTAIISHFGKGYMLCVMCTC LSVCVCVQVGSWICV/CVSMCAVSLCTC\ICRCISMYTRHAC ACTRV*VYMCS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVC/MCACSVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVG*ACTCVMMH/CSCTCR/C VHVCCMSMHACECLCVYLHICGAGTRRWAGSARGSRSCSRP CWAPGGLSLPGPSCPSVEQGLGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNTVSPRRGADCFEAPDVPKQPPGWGRASFEERG GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK</p> |
| 5866 | 98 | 3197 | <p>ARPEVPAPPAWLSRRGAAMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRYNTDCVQGLTHSKAQEILARDGPNA LTPPPPTPEWVKFCRLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAADVITGCFSYQEAQSSKIMESFKNMVBPQ QALVIREGEMQVNAEEVVVGDVLEIKGGDRVPADLRISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNFVEGTA RGVVVATGDRVTMGRIATLASGLEVGKTPAIEIEHFIQLITGV AVFLGVSFILSLILGYTWLEAVIFLIGIIVANVEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNR TVAHMWFNDQIHEADTTEDQSGTSFDKSSHTWALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASEALLKCIELSSGVSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGGKQPLDEEMKEAFQAYLELGGGLGERVLGFCHYYL PEEQFPKGFADCDVNFNTDNLCFVGLMSMIGPPRAAVPDAVG KCRSAGIKVIMVTGDHPITAKAIAGVGIIFEGNETVEDIARL</p> |

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|------------|--|--|--|
| | | | NIPVSVQVNPDAKACVHGTDLKDFTEQIDEILQNHTEIVFAR TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI AGSDVSKQAADMILLDDNFASIVTGVBEGRILFDNLKKSIAVTL TSNIPETITPFLFIMANIPPLPLGTITILCIDLGTDMVPAISLAY EAAESDIMKRQPRNPRTDKLVNERLISMAYGOIGMIOALGGFFS YFVILAENGFLPGNLVGI RLNWDDRTVNDLED SYGQWQTYEQRK VVEFTCHTAFFVSIVVQWADLIICKTRRNSVFQGMKNKILIF GLFEETALAAFLSYCPGMDVALRMYP LKPSWWFCAPPYSFLIFV YDEIRKLILRRNPGGWVEKETYY |
| 5867 | 3 | 1485 | LPGRRARGGGRLGWPPAQAALDGSRMGKARVPASKRAPSSPVAKP GPVKTLTRKKNKKKKR FWKSKAREVSKKPASGPGAVVRPPKAP DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQONKK ETSPQVKGEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT EHNKKGTKERTNGDIVPERGDI EHKRRKAK\GQPPHPPR/IDI WFDVDVPADIEAAIGPEAAKIARKQLGQSEGSVLSLVKEQAFG GLTRALALDCEMVGVGPKGEESMAARVSVINQYKCVYDKYVVKP TEPVTDYRTAVSGIRPENLKQGEELVVQKEVAEMLKGRILVGH ALHNDLKVFLDHPKKKIRDTQKYKPKSQVSKGRPSRLRLSEK ILGLVQQAHEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLITA PDHCSDDA*QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS BSWQRGVAWCY |
| 5868 | 2122 | 833 | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFQ IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHELKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT |
| 5869 | 2122 | 833 | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFQ IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHELKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT |
| 5870 | 2122 | 833 | LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LESRV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKHQFQ IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHELKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT |
| 5871 | 3 | 3465 | FFFCRPLRLYSKTTGDRSAMAGAGLTAEVSWKVLERRARTKS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYIRIVKSTLLLYQSPTTGLFPPTKT CGDQKAKIQDSL YCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQFQKQDPRPTTCLHSVFNVTGDELLS YEEYGHQINAVSLYLLYL VEMISSGLQIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFNGQGCWSVI FVDLDAHNRNRQTLCSL LPRBSR SHNTDAALLPCISYPAFALDDEVLF SQTLDKVVRKLKGKYGPKR FLRDGYRTSLEDPNRCYYPKAEIKLFDGIECEFFIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNPQSGQKRFPSNCGRDGKLPWGQALYIIAKLLADELISP KDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLD DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDM LAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS FEELEPPKHSKVKRQSSSTPSAPELGQQPDVNI SEWKDKPTHEIL QKLNDCSCLASQAILLGILLKREGPNFITKEGTVDHIERVYRR |

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|------------|--|--|---|
| | | | AGSQKLWSVVRRAASLLSKVVDLSLAPSTNVLVQGRQVTLGAFG HEEEVISNPLSPRVIQNIYYKCNTHDEREAVIQQELVIHIGWI ISNNPELPSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGPFYDRVWQI LERTPNGIIVAGKHLPPQPTLSDMTMYEMNFSLLVEDTLGNIDQ PQYRQIVVBLMVVSI VLERNPELEFQDKVDLDRLVKEAFNEFQ KDQSRLEIEKQDDMTSFYNTPLPGKRGTCSTYTKAVMNLLEG EVKPNNDPCLIS |
| 5872 | 68 | 665 | VQGYMYRFVIKINSYSEKTSICRHRCCPELPATQPWPTPTVFF NIAIDSESLGCT\SFKLFADKV\PKRWKNFVLLNTGEKVLGDK GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDENFI\LKH TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFQKVDGMS IVEALERSGSRNGKTSKKITAAACGQL |
| 5873 | 2240 | 506 | RRPPEGSGGGRTRARMPLPWSLALPLLWSVAGGFNAASAR HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF GECVGPKNCRCPFGYTGKTCSDVNECGMKPRPCQHRVCVNTGHS YKFCPLSGHMLMPDATCVNSRTCAMINCCQYSCEDTEEGPQCLCP SSGLRLAPNGRDLCDIDECASGKVICPNRRVCVNTFGSYCKCK IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC KQGYKGNGLRCSAIPENSVEVLRAPGTIKDIRKLLAHKNSMK KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGNSHGG\KKG NEEKMEGLEDEKREEKALD*HRRERPFGR\DVFFPKVNEAGE FGLIL\VORKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\ EDDFDW\NPADR\DNAI\GFY\MAVPGWQGHK\KDIGRLKLL PDLQPSQNFCLLDYRLAGDKVGLRVFVKNNSNALAWEKTTSE DEKWKTKGIQLYQGTDATKSIIFEAEKRGKTGEIADGVLLVS GLCPDLSLSVDD |
| 5874 | 2 | 3387 | ACPRLARRRRRVRSLRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAMEYDD VHSDGRYSLSGVAHSRDAGRESLRSDVFGSPFRSSNPSISDD SYRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDGFGSSRLIEKECLEKE\ SRDYDVHDSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTARGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI KQNTSPSDVTLGTNPGTEDIQFPQKIPGLDLKLNRLPRRMS FDIIDKSDVFSRFGIEIKWAGFHTIKDDIKFSOLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVTKNCFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLNPLDLALALETTNSLCRKSLLLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAPPNFEDSTLFGREYIDHLKAWL VSSGCPQVKKABPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSFKPAGVDISEAPQTSSPCPSADIDMDKNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDWFL\HDQNSS\AFK FY\RKKVFELCPSICTSSPHNL\HTGGGDTT\GSQSPVDLME GEAEFEDEPPPREAELESPEVMPEEEDDEDGGEAP\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGFSSSKSLKVGMIAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDPAQQL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSQWL IFVF |
| 5875 | 296 | 1848 | LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVYQVRA LEFSGSLPPHAI CLGDVDNDTLNELVVGDTSGKVSUYKNDSDRP WLTCSQGM LTCVGVGDVCNKGKLLVAVSAEGWFHLDLTPAK VLDASGHHTLIGEBQRPVFKQHI PANTKVMLISDIDGDCREL VVGYYTDRVVRFRWELGEGPEHLTGQLVSLKKWMLGQVDSLS VTGLPLGLPELMVSPGQGCAYAILLCTWKKDTGSPPAEGPTDGS /SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESGGS |

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|------------|--|--|--|
| | | | GLFALCTLDGTLKLMEEEMEEADKLLWSVQVDHQLFALEKLDVTG NGHEEVVACAWDGGQTYIIDHNRTVVRFQVDENIRAFCAAGLYACK RGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST TACCRSAWILTTSL*LVPCPTKRSTIQTSHHSVLPQASRIFFS WTCLIAEGGF*TTPLPKGVFGSHCAAAGSITKQ |
| 5876 | 1122 | 224 | HLPLGVPSKVAGAAAMEPQEERETQVAWLKKIFGDHPIQYEV NPRTEILHHLSENRNRVDRDYYLVIEDLKQKASEYESEAKYLQ DLLMESVNFSPANLSSSTGSRYLNALVDSVALETKDTSLASFIP AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV KKAELHLSTER\AKVDNRQNM\DFLKAKSEEFRTGIIAAGEQL SARGQ\DAFSVPISQLVALIRENWPRLKQQTIPLK\KKLESYLD LMP\NPSHCSK*RIEBAK\RELA\SIEABLRRVS\MMEL |
| 5877 | 2030 | 1907 | GTLGKMAAASSGGEKERLGGGLGVAGGNSTRELLSALEDLEV LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA LNQGIKHEMQVLEKEVEKRDSIQQLQKQKAEQILATAVYQ AKEKLKSIKARKGAISSEETIKYAHRIASNAVCAPLTWVPGD PRRPYPDTLEMRSGLLGQMNPSTNGVNGHLPDGDALA\RRKIAR CPCSTVS\NGSQMTCR*INIILILQKSVCEL |
| 5878 | 950 | 2113 | GLWKCMQLQCPHTRVQP*PTFRQQGPQ\VPVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITYFIDGYEPMDDVVALFGLRGIQHTP ISIKNARVSQHYKASLTATFNLFPFAKFAVVEEDLDIAVDFFS FLSQSIHLEEDDSLYCISAWNDOGYEHTAEDPALLYRVETMPG LGWVLRRLSYKEELEPKWPTPEKLWDWDMWMMRMEQRRGRECI PDVRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL KAEAYEVVHRLLEAEVLDSKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDRGNHRGLWRLFRKKNHFLVV GVPA SPYSVKKPPSVTFIFLEPPPKKEGAPGAPEQT |
| 5879 | 3 | 981 | RLTEAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRRLGFLATAWLTIFYDIAMTAGWLVL AIAMVRFYMEKGTTHRGYKSIQKTLKFFQTFALEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTV EITRYSFYTFSLDLHLPYFIKWARYNFFIILYPVGAGELLTIY AALPHVKKTGMFSIRLPNKYNVSEFYLLITMASYIPLFPQL YFHLRQRRKVLHG\G*L*KRMK*SLQTRCFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI |
| 5880 | 1138 | 1324 | SLWCLVAGGLGLGPSSQNPLQAGILARPREARGTFSALTACSA SVTSKKGKSSSGMWPSAASDRDSPVPLRPPGFVQLPSGTGWVLS *KKRGRCSS/WLSQPQHEREKEVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERS DQSEHTDGHTSVQSVIEKLEENRLLKQKVTHVEDLNKQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRNLRLQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSEADRE AQSRILEEKKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGLQCPH CLQCFSDQGEELLRHVAECCQ |
| 5881 | 26 | 441 | GGIHPSPTAPRAQHLTMDCTWRILFLVAAATGTHAQVQLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHVVRQAPGKLE*MGPPD LQDVETIYPQKFQGRVSMTEETSTETTQ\AYLELSSLRSED TAVHHCATDV |
| 5882 | 2407 | 2216 | SGCVMELYSHSLEYNPEWISVQSAVAPALNSDGL*LHSGE RTRRD*QLPEAGGPGLEPLQLGELDITSDEFILDEVG\VDLR HYSKQVELELQIEQKSIIRDYIQESENIALHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPALVTAILEAPVTEPRFLEQLQELDAKAAVREQE ARGTAACADVRGVLDRLRVKAATKIREFILQKIYSFRKPMYNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYR SYLGRMLKVQYEEVAEKDDLMGVEDTAKKGFSSKPSLRSRNTIF TLGTRGSVISPTLEAPILVPHTAQRGEQRYPFALFRSQHYAL LDNSCREYLFICEFFVVSPPAAHDLFHAVMGRTLSMTLKHLD SYLADCYDAIAVFLCIHIVLFRFNIAAKRDVPAIDRYWEQVLALLW |

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|------------|--|--|---|
| | | | PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV SINQTI PNERTMQLLQQLQVEVENFVLRAABFSSRKEQLVFLI NNYDMLGLVLM\E*ERAADDSKEVESFQQLINARTQEFIEELLS PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRPHRV\L SQQLRALPARAELINIHLMVELKKHKPNF |
| 5883 | 2 | 1374 | EFPGRRFRAVMEAGAGAGAGAAGWSCPGPGPTVTTLGSEASEG CERKKGQRWGLERRGMQAMEGEVLLPALYEEEEEEEEEEVE EEEEQVQKGGSVGSLSVNKHRLSLTETELERLAQVLQVLAEL EETRELQGHEDDSLELQGLLEDERLASAQAQAEVFTKQIQQLQG ELRSLREEISLLEHEKESELKEIEQELHLAQAEIOSLRQAADS ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME MKSSEPSGSLGLSDYSGLQEEELQELRERYHFLNBEYRALQESNS SLTGQLADLESERTQATERWLQSQTLSTMSAESQTSEMDFLEP DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEELQHHRQVSEE EQRRQLRELKCAQNEVLRFTSHS\SPSHPLPPIPPSSPCLL*A LVVISALLWCWAAETSS |
| 5884 | 4261 | 2522 | GVLARASARLRVPLTGVRAAEPEVGAEPKAVAGAAEPDEDGGR SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV FVAGDDDBQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLOF SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTIRHKVRQM HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE IPSTSDTKSDTATGGESAGHATSSQEPSCGSDQRPADLNIIRVE RLTKKLEERREEKRKEEQREIKKEIERRTKGKEMLDYKXKQEE ELTKRMLBEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE EVEAAKAAALLAKQAEMEVEKRESYARERSTVARIQFRLPDGSSF TNQFPSPDAPLEEARQFAAQTVGNITYGNFSLATMFPRREFTKEY KKLLDLELAPSASVLLP/ALFINF*AGRPTASIVHSSSGDIW TLTGTVLYPFLAIWRLISNLFSPNPPPTQTSVRVTSSSEPPNPAS SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNWTW NGNSTQOM |
| 5885 | 900 | 467 | AAGGGRSRLRSRWSPTGPSKSPSGVRCGG\RR\AWEDKDEFLDV IYWFRQIIAVVLGVWGLVPLRGFLGIAGFLINAGVLYLYFSN YLQIDEEYGGTWELTKEGFMSTFA/IVHGHLDHLLHCHPL*LM VYSSQVLPISQKGPS |
| 5886 | 86 | 1341 | PFRGRALTLLKKQPRPGVAPPSTLGTCHKSDPGRPAQAQSPSPGS GTFGLLSFRMVRTKIWTLLKKHFVGYPTNSDFELKTSSELPLKNG EVILLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVEKSNVAL PKGTVLASPGWTTTHSISDGKLEKLLTEWPDITPLSLALGTVG MPGLTAYFGLLEICGVKGGETVMVNAAGAVGSVVGQIAKLKGC KVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEBETLKKASPDGY DCYPDNVGGFEFSNTVIGQMCKFGRIAICGAISTYNRTGPLPPGP PPEIGIYQELRMEAFVYRWQGDARQKALKDOLLKWLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIYKEYIIEGFE NMPAAFMGLKGDNLGKTIVKA |
| 5887 | 1937 | 104 | APGCRGCRATRCPCRGPRWDSIGDEAARSAPAFGGAPGLLGLRE RPDRCHPGGDDRGQLHRGSPG/SPSELSRRPGPPGLPGLQGP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPCSSVDFSVFS ACSVVPVVTGDSQFCSQKAVIYSLNFTANPPQRFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSBGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDFSFLRFPSSLTSSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPSRKR KVPITVQSIYQSLNKTLLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFIEHFLQ ENTQPVPLSGNPGYVVGVLPLAAGFQPHKSGIIQTTNRYGQLT LHSTTEQDCLALEGVRTPVLFGYTMSQSGCKRLTGLALPCQLVQA KVKSLLWGGGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPPEAN SGNERTILISTAVTFVDVSAFAEAGFRAPPAINARLPFNFFFPF V |

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|------------|--|--|---|
| 5888 | 375 | 2302 | LLCRTPGVAMQRADSEQPSKRPRCDSPRTPSNTPSAEADWSFG LELHPDYKTTWGPQVCSFLRRGGPEEPVLLKNIRENEITGALLP CLDESFRFENLGVSSLGGERKKLLSYIQLRVQIHVDTKVINDPIH GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYVFPGASHNRFEH SLGVGYLAGCLVHALGEKQPELQISERDVLVCVQIAGLCHDLGHG PFSHMFDRGFIPLARPEVKWTHEQGSVMFEHLINSNGIKPVE QYGLIPEEDICFIKEQIVGPLESPEVDSLWPYKGRPENKSFLEY IVSNKRNIGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIDTMIT DAFLKADDYIEITGAGGKKYRISTAIDMEAYTKLTDNIFLEIL YSTDPKLDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LRVYCKKVDKRS LYA\ARQYFVQW\CADR\NFT\KPDGRCY*PPTP*HPQKKGW\ NDSTFSPIKIPTRLPRLPKSRV\QLFKDDPM |
| 5889 | 1831 | 731 | LPAACGRPVTAARPRQAEGRSGRPRDLDPYPPQVFPFRPRDRAI VTGGTDGIGYSTAKHLARLGMHVI IAGNNDKAKQVVSKEET LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLK FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMVMPQR KTRDGFEEHFGNLGHLTNLLDNLKESGSPGHSARVVTVS SATHYVAELNMDLQSSACYSPPHAAQSKLALVLFTHLQRL AAEGSHVTANVDPGVVNTDLYKHVFWATRLAKKLLGWLKFPK DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ LWSKSCMIGVLDVTL |
| 5890 | 1322 | 200 | FRRCWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERSQRDITLVHLFAGGCGGTGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFFECVRKVYQTDGLKGFYRGMSASYAGISETVIFVYIESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSSLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVYLLNG |
| 5891 | 1322 | 200 | FRRCWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERSQRDITLVHLFAGGCGGTGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFFECVRKVYQTDGLKGFYRGMSASYAGISETVIFVYIESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSSLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVYLLNG |
| 5892 | 1764 | 379 | VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGP DSGWMPQAAPCLSGAPHASAAADVHHGRRTAICRAGRGGFKDT TPDELLSAVMTAVLKDVNLRLPEQLGDCVGNVLQPGAGAIMARI AQFLSDIPETVPLSTVNRQCSSGLQAVASIAAGGIRNGSYDIGMA CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVABR FGISREKQDTFALASQQAARAQSKGCFQAEIVPVTTHVDDKG TKRSITVTQDEGIRPSTTMEGLAKLPAFKKDGSTTAGNSSQVS DGAAILLARRSKAEELGLPILGVLRSAVVGVPDIMGIGPAY AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCEKRLPP*EG *TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC PCAIGSWNGSPLPVFEYPWGT |
| 5893 | 3 | 1653 | ILSKRRQCQAKTKELMAKKVAVIGAGVSGLISLKCCEVDEGLEPT CPERTEDIGGVWRFKENVEDGRASIYQSVVNTSKEMSCFSDFP MPEDFPNFLHNSKLLLEYFRIFAKKFDLLKYIQPTTVLSVRKCP DFSSSGQWKVVTQSNGEKQSAVFDAMVVCSGHHILPHIPLKSF GMRERFKQYFHSRQYKHPDGFEKRIILVIGMGNLGS DIAVELSK NAAQVFISTRHGTWMSRISEDGYPNDSVFHTRFRSMLRNVLP TAVKWMIBQQMNRWFNHNENYGLEPQNKYIMKEPVLNDVPSRL CGAIVKSTVKELTETSAIFEDGTVEENIDVIFATGYSFSPFF |

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|------------|--|--|--|
| | | | LEDSLKVENNMVSLYKIFPAHLDKSTLACIGLIQPLGSIFPT AELQARWVTRVFKGLCSLPSEBTMMMDIIKRNEKRIDLFGESQS QTLQTNVVDYLDLEALEIGAKPDFCSLLFKDKPLAVRLYPGPCN SY*YRLVGPQWEGARNAIPTQKQRIKPLKTRALKDSSNFSVS FLKILGLLAVVVAFF\COLQWS |
| 5894 | 174 | 1673 | RYSPPKVLQNKESLKLGMATLVAHSLAPLNKKKEGLRVVRE DHYSTWEGFKLQGNKGLGQEPLCKQFRQLRYEETGPREALS RLRELCCQWLQPEHTKHEILELLVLEQFLIILPKBLQARVQEH HPESREDVVVLEDLQDLGETGQQVDPDQPKKQKILVEEMAPL KGVEQQVRHECEVTKEPEKEGEETRIENGKLIIVVTDSCGRVES SGKISEPMEAHNEGSNLERHQAKPKIEYKCSEREQRFIQHLD LIEHASTHTGKKLCESDVCQSSSLTGHHKVL*ERKVIQC/HGV LGKAFQSSHLVRHQKIHLEKPYQCNECGKVFSONAGLLEHLR IHTGEKPYLCIHCGKNFRSSHLNRHQRIHSQEPCCKECCGKT FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG EKPFKCNICQKAFRLNSHLAQHVRIHNEKPYQCSECGEAFRQR SGLFQHQRYHHKDKLA |
| 5895 | 2967 | 86 | HPSSLGAIPFPFPSSPWPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGK\EDVLGSVRRTLTHIDHSL RQ\NCPFLAGETESLADIVLWALYPLLDQPAYLPEELSALHSW FQTLSTQ\EPQCR\AARLVLKQ\QGVLA LR\PYLQKQPQPSA EGKGLSPIEPPEELATLSEETAMAVTAWEGLESPLPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEC DKYHI IHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCP VVQSSQHLFLDLPKLEKRLEEWLGR LT PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEVLYNEDG K\FSKSRGVGVFRDM\AHD TGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQAGT VTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAEVAKL DDLKQLA VAE KPPEAPKGGKKK |
| 5896 | 2967 | 86 | HPSSLGAIPFPFPSSPWPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGK\EDVLGSVRRTLTHIDHSL RQ\NCPFLAGETESLADIVLWALYPLLDQPAYLPEELSALHSW FQTLSTQ\EPQCR\AARLVLKQ\QGVLA LR\PYLQKQPQPSA EGKGLSPIEPPEELATLSEETAMAVTAWEGLESPLPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEC DKYHI IHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCP VVQSSQHLFLDLPKLEKRLEEWLGR LT PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEVLYNEDG K\FSKSRGVGVFRDM\AHD TGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQAGT VTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA |

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|------------|--|--|--|
| | | | LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGGKKK |
| 5897 | 2967 | 86 | <p>HPSLLGAIFFYPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDGNYLFTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGGKG\EDVLGSRVRLTHIDHSLRQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLAALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWKGLSPLPRLPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFAYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSPKRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDAITIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSVLPSSALGAEDNYTL\VSHLIATEYLYNEDG K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNN\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQAGTGTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSI LLTNFLCTLPGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGGKKK</p> |
| 5898 | 2967 | 86 | <p>HPSLLGAIFFYPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDGNYLFTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGGKG\EDVLGSRVRLTHIDHSLRQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLAALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWKGLSPLPRLPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFAYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSPKRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDAITIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSVLPSSALGAEDNYTL\VSHLIATEYLYNEDG K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNN\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQAGTGTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSI LLTNFLCTLPGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGGKKK</p> |
| 5899 | 326 | 1078 | <p>NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKQIKHMMAFIEQ EANEKAEIDAKAEFEFNIEKGRVQTRQLKIMEYEEKKEKQIE QQKKILMSTMRNQRALKVLRANDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLOGLLRLLEPVMIVRCRP\QDLLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWVSGNQRIKVSNTLESRLDSAKQKMPERIMALFGANTNRKFFI</p> |
| 5900 | 64 | 1409 | <p>KAASRDSPCLEFCFLCGVSSHDLQHRMWHYHRLSHLSRLQDLLK GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHPEL KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTI RLDETTLFFTWPDGHVTKYDLNWLKNSYEGQKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLTENEGLKKFLQNFLLYGIAFVEN VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA LDRHTDTTYPQEPGCIQVPHCLKHEGTGGRTLLVDGFYAAEQVL</p> |

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|------------|--|--|---|
| | | | QKAPPEEFELLKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG/YKELYLRVNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPENEFWVKLPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVLNTARLLGLQA |
| 5901 | 1 | 2121 | VAIEQTSLSKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL KTHLDTVLPKLTCPQCNEFPNQESLLKHVTIHFMITSTYYICE SCDKQFTSVDDLOKHLDMHTFVFFRCTLCQEVFDSKVSILQLHL \AVKHSNEKKVYRCTSCNWDNRNETDLQLHVKNHLENQSKVHK CIPGSESGTEVELQCHITTHSKYCNCKFCSKAFHAIILLEKHL REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH DGSEEDVDTSEPMYGCDCGAAVTMETLLQNHQLRDHNIRPGES AIVKKKAELIKONYKCNVCSRTFFSENGLRHMQTHLGPVKHYM CPIOGERFPSSLTTEHKVTHSKSLDTGNCRICKMPLQSEEEFL EHCQMHFDLRNSLTGFRVCVCMQTVTSTLELKHGTFFHMQKTGN GSAVQTTGRGQHVQKLYKCAKCLKEFRS KQDLVKLDINGLPYGL CAGCVNLSKSASPGINVPPGTNRPGLGQENENLSAIEGKGVGGL KTRCS*LATFKF*VLKVELPEPHKPFHRGVSRRPDSNSTQLKTP QVSPMPRISPSQSDEKKTQCIKCMQVFYNWDIQQVHVANHMID EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFFKCPVCFTV FVQANKLQQHIFSAHQEDKIYDCTQCPQKFFQTELQNHMTMQ HSS |
| 5902 | 712 | 209 | LKNRRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMFGYMTDTGT VEPLQTVETQGGDLQSLLFHFLDEWLYKFSADFFIP\GWGE EFSLSKHPQGTVEVKAITYSAMQVYNEENPEVFVIDI |
| 5903 | 2106 | 735 | DTPGPSLPSTTAPFSLRSLSPFSPRSYLLPFGDPQLQGRGLPTT PALFALSAPVPGAASPMPPSGLRLLPLLLPLLWLLVLTGPRPAA GLSTCKTIDMELVKRKRIEAIHQILSKRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESAEPEPEPEADYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLLRL KLVQEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRSGEIEGFRLSAHCSDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSE HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFCL GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS |
| 5904 | 3 | 1126 | MMEIENAINTFKEEQRLIYEELIKEEKTNNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPTSLPEEVLDPEKFLQQTGG RQGAWDYDHDHONFVKVRNKHGKPTFMEEVLEHLPGKTQDEVQQ HEKWKYQKFLALEERKKESIQIWKTKKQKREBIFKLKEKADNTP VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKASQL KEEEEEKKEKHQKERQRFKLKLLLESYTQQKKEQEFLRLEKEI REKAKEAEKRKNADEISRFOERDLHKLKILDROAKEDEKSO KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR |
| 5905 | 287 | 2912 | MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLPVWSQCLQNFLLHGTKNVTNSSLRLPR QNSDGGQKNKPREHIDCGDIVWSLAPGSSVPEKQSRVCVNIENH RFRFGDQQLLATGLNSGRIKIWDVYTGKLLNLVDHTGTVVRDL TFAPDGSLLIVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAPSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFLVLIFF*K*CIVSQVK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFLAVNIFACISICFSS*A QVGDPSSL*TSYDLKGRQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTFLISVYFS*LVFGINGPQYSFVVKLHCLYFMFRLI FKLTFRNRI*NRICMSALINLKTDFNLMTLSIFFKLLIYNA* YNLN*I*QF*YKMFVLCMSE*SYNICLFIAGF\LWNMDKYTM |

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|------------|--|--|---|
| | | | IRKLEGGHHHDVVACDFSPDGLLATASYDTRVYIWDPHNGDIIM EFGHLFPPTPIFAGGANDRWVRSVSFSDGLHVASLADDKMVR FWRIDEDYPVQVAPLSNGLCCAFSTDGSLVLAAGTHDGSVYFWAT PRQVPSLQHLCRMISIRRVMTQEQVQLPISKLEFLSYRI |
| 5906 | 146 | 2038 | REGAGSGRMASGA\YNPYIEITEQPRQGRMFRYKCEGRSAGSI PGEHSTDNNRTYPSIQIMNYGKGV\RITLVTK\NDPYKPHPH DLVGKDCRD\GYEAEFGQE\RRP\LFPQN\LGIRCVKKKEVKE A\IITR\IKAGINPFDVP*KQLNDIEDCDLDDVRLWFRVFLPDG HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCVRNKNCGSVRGG DEIFLLCDKVQKDDIEVRFLNDWEAKGIFSQADVHRQVAIVFK TPPYCKAITEPVTVMQLRRPSDQEVSESMDFRYLPDEKDTYGN KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLLELLTSGDPPTLAS QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLPSHDAVREMP TGVSSQAESYYPSPGPISGLSHHASMAPLSSSSWSSVAHPTPR SGTNTPLSSSFSTRTLPSNSQGIPLRLIPVGNLNASNACIYNN ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTSSDSMGET DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT VFVSQSDAFEGSDFCADNSMINESGPSNSTNPNSHVFDQDSQY SGIGSMQNEQLSDSFYEFFQV |
| 5907 | 99 | 1873 | TYLLSSWS*NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK KATSKVPSAPHFVHPNDHANREAEKKKWVEEMREKQQAAREQE RQKRTIESYQCDVLRQEEFEHKEEVLQELNMFQLDDEATR AYYKEFRKVVEYSDVILEVLDARDPLGCRFCMEEAVALRAQGNK KLVLVLNKIDLVPKEVVEKNLDYLRNELPTVAFKASTQHVKVNL NRCSVPVDQASELLKSKACFGAENLMRVLGNYCRLGEVTRHIR VGVVGLPNVKGSSLSNLKRSRACSVGAVPGITKFMQEVYLDKF IRLLDAPGIVPGPNSVGTILRNCVHVQKLADPVTVPVETILQRC NLEEISNYGVSGFQTTEHFLTAVAHRLGKKKGGLYSQEQAOK AVLADWVSGKISFYIPPPATHTLPTLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGCTNPNRHQMGWAKRNVDRHPKSNMSMVDVC SVDRRSVLQRI METDPLQQQALASALKNNKKMQKRAKIASKL SDSMMSALDLSGNADGVDG |
| 5908 | 247 | 975 | HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEETHPHTRA HTRTLRATLRRPPRSHSTRLRFPMLDGDGGLASWK/PMRER* GWRPAPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHVKTGTCEVVALHRCCKNKNKIEERSQT VKCSFPQGVAGTTRAAPS CVDASIVEQKWWCHMQPCLEGBECK VLPDRKGWSCSSGNKVKTRVTH |
| 5909 | 1 | 5002 | PAIPGSTIIWAPGSHSAARADGRHGSLSQSQAPGALCGARAPP SSNLRADRSIMICARAGKNLYHNRLGLAAMAPPSSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTI PRSTDLDLVTSDSR STLMGRSSYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIWKIDASSYFVEPETKICFKYVHGV SGALRATTSPVTVKNSAAPIFKSIGADETVQGGSRRLISFSL DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGTNTVNIWQAEQFSFVSLPTDVLIEVVKDFAKSRPIIKRFL GKLSMPVQRLLEHAIGDRVSYTLGRRRLPTDHVSGQLQFRFEI TSSIHDPDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVDPDRGNQSIELSRPAEEAAVITEAGDOGM VSVGPEGAGELLAQVQKDIQAPSAEELAEQLDLGREASALLLE DGEAPASTKEEPLLEEATTQSRAGREEEKEQEEGDVSTLEQG EGRQLRASVKRKSRLPVSLETVIASACGDPETPRTHYIR IHTLLHSMPSAQGSAEEEDGAEESTLKDSSEKDGLESDTV AADPSALEEDREEPEGATPGTAHPHSGGHFPLSANGAAQDGD HPSTGSESDSSPRQGDHSCGCDASCCSPSCYSSSCYSTSCYS SSCYASCYSPSCYNGNRFASTRFSSVDSAKISESTVFSSQDD EEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSCHVER SPEGLESVPAGPSNRREGECPILHNSQFVSQPLSLRPEIHHYPT IDEPLPNWEARIDSHGRVYVDHVNRTTWTQRPATAATPDGMR RSGSIQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGG |

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|------------|--|--|--|
| | | | GGGGSSEABSSQSSLDLRREGSLSPVNSQKITLLQLSPAVKFI TNPEFFTVLHANYSAVRVFTSSTCLKHMILKVRDARNFERYQH NRDLVNFNMFADTRLELPRGWEIKTDQOGKSFVDHNSRATTF IDPRIPLQNGRLPNHLTHROHLQRLRSYSAGEASEVSRNRGASL LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFRLQPNIFEMLE RQPSIARNHTLREKIHVIRTEGNHGLEKLSADLVILLSLFEE EIMSYVPLQAAAFHGPYSFSPRCSPPSSPQNSPGLQASARAPSP YRRDFEAKLRNFRYKLEAKGFGPGKIKLIIRDHLLBGTFNQ VMAYSRLQRLNLYVTFGEEGLDYSGPSRBEFFLLSQELFNP YYGLFEYSANDTYTVQISPMFAFVENHLEWFRFSGRILG\LALI HQYLLDAFFT\RPFYKALL\RLPC\DLSDLEYLDEBFHQSLOW MKDNNITDILDLTFTVNEEVFGQVTERELKSGGANTQVTEKNKK EYIERMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVDARELE LVIAGTAEIDLNDWRNNTTEYRGYHDGHLVIRFWAAVERFNNE QRLRLQFVTGTSSVPYEGFAAPPWEPMLRRPLP*KKWGKITS LPPRG\HTCLQPDWDLPTVSPRTPLMYEK\LLTA\VEETSTFGT |
| 5910 | 1526 | 446 | VAEFAAMEPGRQIKLDPRTADLLEVLKTNVGTSPACFSQPPT AAQLLRALGPVELALTSILTLLALGSI AIFLEDAVYLYKNLTCP IKRRTLLWKSSAPTIVSVLCCFGLWIPRSLVLVEMTITSFYAVC FYLLMLVMVEGPGGKEAVLRLTRDTMMVHTGCCCCCPCCPRL LLTRKKLQ*R*CWALSNTPS**R**PWWACFSPTASMTQQTFL RGAQLYGSTLSSA/CSTLLALWTLGIISQARLHLGEQNMGAKE ALFOVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH LLILETFLMTVLTRMYRRDKHKVGYETFSSPDLDLNLKALRWM AWTMKGCCTH |
| 5911 | 109 | 595 | QLPLAPCTIQGKLEMRSPKQSFIRSSSHGAGLLVKNPSTPVF CGHRRGGAFFKYKPTPVVGPEQRPTGQKHMRRGGVSLSPRLCS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVQGAGLELL/NVVIHLPRPPKVLGLQA |
| 5912 | 924 | 277 | MILNKALMLGALALTVMSPCGGEDIVADHVASYGVNLYQSYGP SGQYSHEFDGDEEFPYVDLERKETVWQLPLFRFRFRFPDQFALT IAVLKHNLMNIVIKRSNSTAATNEVPEVTVFSKSEPTLGPNTLI CLVDNIFPPVNVITWLSNGHSVTEGVSETRPSSPKSDHFLQDQ VTSPSPFPE**DL**TAKVEQLGAWFEPLLKHGABIPPTL |
| 5913 | 46 | 1198 | QLRMAGAEGAAGRQSELEPVVSLVDVLEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEPEPAGICLACSIECHGS HKLFEPLYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCIKRPYPDPDEIIPDEMIQCVVCEDNPHGRHLGAIPPE SGDFQEMVCCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGRHQDSTLKEVDVPEQKDDVREVKVEQNSEP CAGSSSEDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSLCTCQDCMKMYGDLVLFLTDEYDTVLAYENKGI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ**FED |
| 5914 | 960 | 124 | NLGGSSELPPEALFIQVASMNRVDFYLASIEDMLVAI/GGRN ENGALSSSVETYSFKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMSLGD IYSIGGSDDNIESMERFDVLGVEAYSQPCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP**SLGQRTKRKAKARGTRTGASDFSCASWDH PHRLPGLCRPAATS |
| 5915 | 1604 | 703 | FPCRPTPLKLRRRRKRARIQAPHCHSRPRTCPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLRPLGSPFCPT QEDFPALGGPCPPRPPSPGFSVAVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS PRELPGEPSAHPVHQGLPAERRGFLQRVQEPRLRGVQTGPDLS PVLQELPGPAGGEFPEGL**AAGPAAH |
| 5916 | 256 | 633 | SPRWEIFGFWHRWESFSLGEWPSRIPEPSPDSTKGTSGKGR TVTGAVHRHLNHVAGIIPWVLSQLKPTAATAQDQWTSQQYPDH PTRLLIQ**NQATADKNN**TALLQPHQRL\VSPRMAEA |
| 5917 | 1343 | 827 | AHQILTYLEP/ICLVVNYNKILTIVFLTKSVLBI**KFIHTPQTYR |

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|------------|--|--|---|
| 5918 | 13 | 1247 | <p>F*NDFFGIKEVYVSRRLRRTSF/RLAVTFLEQAVVSKECPVDQ FMEHLPLSLSLASDPVPNVRLAKALRQMLLEKAYFRNAGNP HLEVIEETILALQSDRDQDVSFPAALEPKRRNIIDTAVLEKQN</p> <p>EGAQVARRRRRRQWRAGRCGRGGRRAERTGGRGPPGRPRPLP PGPARRRRRRMTFPYGDALSGLGGGASGGTFASPGRLFP APPTAAAGSMKKDALTLSEQVAAALKPAPAPASYPPA\ADG APSAAPPDGLLASPDGLLKLASPELERLIQSNGLVTTPTSS QFLYPKVAASEEQEFAEGFVKALEDLHKQNLGAGRAAAAAA AGGPGSGTATGSAPPCELAPAAAAPEAPVYA\NLSSY\AGGCRGL RGGAAT\VAFAAEVPPPPPPPPGALGPRRP/RLALQGRRPQT PDVP\SFGESE\PLSPIET\DTPRRI\KAKRKRL\RNPIRAPK PASRKLGAQSRALERESDPS*SPHGLSLASTASLLREQVAQLK QVLSHVNSGCOLLPQHQPVPAY</p> |
| 5919 | 1 | 4254 | <p>TSVQGDSTPTSTSSQGSINMHWISQAIHGSTTTSTSSSTQSG GSGAAHRLADVMAQTHIENHSAPPDVTTYSEHSIQVERPQGST GSRTAPKYGNAELMETGDGVVSSRSVSAKIQQLVNTLKRPRRP LREFVDDFEELLEVQPPDPNPQKPEGAQMLAMRGEOLGVVTNW PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM KVAYSILHKLGTQEPMPVRPGRVALVFPNNDPAAAFMAAFYGC LAEVVPVPIEVPLTRKDAGSQIGFLLGSCGVTVALTSDACHKG LPKSPTEGIPQFKGWPKLLWFVTESKHLSPKPRDWF\PHIKDAN NDTAYIEYKTC\DGSVLGVTVTRTALLTHCQALTOACGYTEAE TIVNLDFFKDVGLWHGILTSVMNMHVVISIPYSLMKVNPLSWI QKVCQYKAKVACVKSMDHVALVHRDQORDINLSSRLMLIVADG ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRP DDSNQPPGRGVLSMHGLTYGVIRVDSEELSVLTQDVGVLVMPG AIMCSVKPDGVPLCRTDEIGELCVCAVATGTSYGLSGMTKNT FEVFAMTSSGAPISEYFFIRTGLLGFVGPGLVFFVVGKMDGLMV VSGRRHNADDIVATALAVEPMKFVYRGRVAVSVTVLHDERIVI VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVCYCLALVPANTLP KTPGLGGIHLSETKQLFLEGLHPCNVLMPHTCVTNLPKPRQKQ PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE VLQWRAQTTPDHILYTLNCRGAIANSLTCVQLHKRAEKIAVML MERGHLQDGDHVALVYPPGIDLIAAFYGCYAGCVPIITVRPPH QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAADV TWPLILDITDD*PKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV KMSHAATSFAFCRSIKLQCELYPSREVAICLDPYCGLGFLVWCLC SVYSGHQSLIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL CTKGLGSQTESLKARGLDLSRVRTCVVVAERPRIALTQSFSKL FKDLGLHPRAVSTSPGCRVNLAIQLQGTSGPDPTVYVDMRALR HDRVRLVERGSPHSLPLMESGKILPGVRIIANPETKGLGDSH LGEIWHSAHNASGYFTIYGDESQSDHFNRLSFGDTQTIIWAR TGYLGLFRLRTELTDANGERHDALYVVGALDEAMELRGMRYHPID IETSVIRAHKSVTECAVFTWNTLLVVVVELDGSQEALDLVPLV TNVVLBEHYLIVGVVVVDIGVIPINSRGEKQRMHLRDGFLADQ LDPIYVAYNM</p> |
| 5920 | 1381 | 1499 | <p>QLGAVAHAGVSRIPP*LPFPLHPTFLSLWCLHHKLP/HPPGASM VRPPVPPRRPPAHISSVRQASTQVPTVPHTQVAVANIGTQTGP SGVGCTPGRPLLPCKCSSAAHSTYRVQEPVHIPGQEPLTASM LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLEIDNSEL LIMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH</p> |
| 5921 | 727 | 157 | <p>VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV GSSVNSDDEISSSDSADSCLNPTTASFTPTSILKRQKQLR RKNVRFDQVTVYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT LCEFAQEQEVNHRILREHLKEEKLHAKMKLTKNGTIVESVAD GLTLDDVSDDEDIDVENVEVDYFFLQPLPTKRRRALLRASGVHR IDAEKQELRAIRLSREECGDCRLCYDPEACACSQAGIKCQVD RMSFPCCSRDGCNMGRIEFNPIRVTRHYLHTIMKLELESKR Q\GAAQPPQ*GALPDCQLQPDRTGL*DPWSIGSKLSFTGKG AAATHLILRVINRGAEGKRK</p> |
| 5922 | 2475 | 495 | <p>SYSNWGLFPPSVFIQVPRSRGTGNLKPILFYSYYE\CMETLKG\T</p> |

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|------------|--|--|--|
| | | | CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFETRTGLLLGDT SKIITRTEEKEIPKQITLRFDAACAINSKKLEIGCGSLN*ERS* RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDVSYLQKGEAN PSCAAGHCNPLELIITNPLDPHKKGERVTLGINRTGLKPQVVI LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIPI*KAE ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNICGKLYNSTTK TIT*DLNHTKKNPFSKFSKLKTA*AHAEH*DWTPVSGLY*IC RHRAYFRLPNKWADSCVIGTIKPSFLLPIKMGELLGFSVYASR EKKGIVIGNWKDNEWPRERI IQYYGPATWAQDGSWGYR/TP/VY MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLLA DYLLVAEGGVCRKFNLTNCCQLINDQGVVKNIVRDMTKLAHP IQVWHKFDPESLFGKWPAIGGFKTLIVGVLLVIRTCLLLPCVL PLLFQMIKGIVATLVHQKTSAHVNYMNHYSISQRDSKSEDESE NSH |
| 5923 | 137 | 638 | QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL QQENRELWISLEEHDQDALELIMSKYRKQMLQLMVAKKAVDAEPV LKAHQSHSAIESQIDRICEMGEVMRKAVQVDDQDFCKIQEKLA QLELENKELRELLSISSESLQARKENSMDTASQAIK |
| 5924 | 274 | 2146 | EKGKVKDAGAEQWISLSLSCCKGSWETQFSNHLNSLTPPTSVRRM PLITTVTLKKMVARHHMKLLCSKAFSTQLOQKIFLHSGMGIHQ SVCMKLPNTSHIISILMGQPMALVQLETLAPLTII IQFQOTD HMKFWKNLPLHSHHLTPSVPTQVTPKKTGSPEIKLKITKTIONG RELFESSLCGLDLNEVQASE\Q*NQSIERSKEKRKSKNHDSR SEERKSHKIPKLEPEEQNRPNERNVDTVSEKPREEPVLKEGSPS ANTIFCSNNGSVHW\FKPQVGDVWSKVGTYPWWPCMVSSDPQL EVHTKINTRGAREYHVQFNSQPERAWVHEKRVREYKGHKQYEE LLAEATKQASNHSEKQKIRKPRPQEREAQWDIGIAHAEKALMT REERIEQYTFIYIDKQPEEALSQAKKSVAKEVKKTRRPRSVL NTQPEQTNAGEVASSLSSTEIRRHSSRRHTSAEEEEPPPVKIAW KTAARKSLPASITMHKGSLLDLQKCNMSPVVKIEQVFALQATG DGKFIQDFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS VSSPEATSGSTGSVEKKQQRRISTRSESEKSTEVPVKKIKKE QVGFLHVES |
| 5925 | 216 | 1911 | MMTAESREATGLSPQAAQEKDGIIVIVKVEEEDBDHMGQDSTL QDTPPPDPEIFRQRRFRFCYQNTFGPREALSRLKELCHQWLRF EINTKEQILELLVLEQFLSILPKELQVNLQEYRPSDGEEAVTLL E DLELDLSGQVPGQVHGPEMLARGMVPLDPVQESSFDLHHEAT QSHFKHSSRKPRLLQSRALPAHI PAPPHGSPRDQAMASALT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSF PQGGENRNEEESTSKAETSEDSASRGETTRGSQKBFGEKRDQ GKTGERQQKNPEEKTRKEKRDGPAIGKDKKTTITGERGPREGK GLGRSFSLSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK I IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKEHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSLTLLHRIHARERASEYSPASLDAPGAFKSCV |
| 5926 | 2 | 233 | DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS |
| 5927 | 4146 | 1248 | KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAKYGIPLA YKKYGDKKLHEKKPLQKHQAQHTPEKRVNTGEERRKISEEAA RRRLEFIEKEKKQKQDIISLMKAEQMKRQBERLERINRAREQG WRNVL SAGGSGEVKAPFLGSGGTIAPSSFSRGGQYEHYHAI FQ MQQQAEDNEAKWKREIYGRGLPERQKQLAVERAKQVEEFLQR KREAMQNKARAEHMGILQNLAAMYGGRPSSSRGKPRNKEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGESEEDM RKK\IESLKAHANARAALVKEQLERKRKEAYBREKKVVEEHLV AKGVKSSDVSPLQGHETGGSPSKQQMRSVISVTSALKEVGVD S SLTDTRETSEEMQKTNNAISSKREILRLNENLKAQEDEKQKQ N LSDTTEINVHEDAKEHRKEKSVSSDRKKWEAGGLVPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE |

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|------------|--|--|---|
| | | | LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPFSEAS PQMSLKLEGNLEPPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVS EDG VSSTVDQLSDIHIEPGTNDQS QHSCDVKSVQPEFFPHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPKKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLM DVPTVGDVVRQDNLEIDEI EDENIKEGPSDS EDIVFEETD TDLQELQASMEQLLREQPGEEYS EEEEVLKNSDVEPTANGTDVAEDDNPSSESALNEEWHSDNSD GEIASECECD SVFNHLEELRLHLEQEMGF EKFFEVYKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE |
| 5928 | 4146 | 1248 | KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAKYGTPLA YKKGDKKLHEKKPLQKHQAQHTPEKRVNTGEERRKISEEAA RRLEFIEKEKKQKQDIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSRQYEHYHAI FDQ MQQRAEDNEAKWKREIYGRGLPERQKQLAVERAKQVEEF LQR KREAMQNKARAEHGMILQNLAA MYGGRPS SSRGKPRNKEEV YLARLRQIRLQNFNERQ QIKALRGEKKEANHSEGEQEGSEADM RRKK\IESLKAHANARA AVLKEQLERKKEAYEREKKVWEEHLV AKGVKSSDVS PPLGQHETGGS PSKQMSVISVTSALKEVGVD SLD TRETSEMQKTNNAISSKREILRLNENLKAQEDKKGQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIFLDELTL DTSFSTTERHTVGEVIKLGPNGPSRRAGKSP TDSVLKILGEAE LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPFSEAS PQMSLKLEGNLEPPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVS EDG VSSTVDQLSDIHIEPGTNDQS QHSCDVKSVQPEFFPHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPKKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLM DVPTVGDVVRQDNLEIDEI EDENIKEGPSDS EDIVFEETD TDLQELQASMEQLLREQPGEEYS EEEEVLKNSDVEPTANGTDVAEDDNPSSESALNEEWHSDNSD GEIASECECD SVFNHLEELRLHLEQEMGF EKFFEVYKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE |
| 5929 | 3 | 1558 | LDFSM TQLPAYVAILLFVYSRASQD TFTAAYVEHAAILPNAT LTPVSRREALALMNRNLDILEGATISAADQGAHI I VTPEDAIYG WNFN RDSLYPYLEDIPDPEVNWIPCNNRRNFQQT PVQERLSCL\ AKNNSIYV VANIGDKKPCDSDPQC PPDGRYQYNTDVVF\DSQ KLVAR YHKQNLFMGENQFNVPKEPEI VTFNTTFSFGIFTCFDI LFHDPAVTLVKDFHVD TIVFPTAMNVLPHLSAVEFHS AWAMGM RVNFLASN IHYP SKKMTGSGIYAPNSSRAFYDMKTEEGKLLLS QLDSHFSSHSAVNWTSYASSIEALSSGNKEFGTVFFDEFTFVK LTGVAGNYTV CQKDLCHLSYKMSENI PNEVYALGAFDGLHTVE GRYVLQICTLLKCKTTLNLT CGDSAETASTREFMPSLSGTFTGTQ YVFP EVLLSENQLAPGEFQVST DGRFLSLKPTSGPVLTVTLFGR LYEKD WASNASSGLTAQARIIMLIVIAPIVCSLSW |
| 5930 | 113 | 6082 | RGNCFWIVFF TMAQTGLEDPERYLFV DRAVIYNPATQADWTAK KL VVIPSERHGF EAASIKEERGDEV MVLEANGKKAMVNKDDIQ KMNPKFKSKVEDMAELTCLNEASVLHNLKDRYSSGLIYTYSGLF CVVINPYKNLP IYSENI IEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDNH IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFI RINF DV TGYIVGANIETYLLEKSRVRQAKDERTFHI FYQLLSG\AGEHL KSDLLLEGFN NYRFLSNGYIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVSSVLQFGNISFKKERN TDQASMPENTVAQKL CHLLGMNVMETRAILTPRIKVG RDYVQKAQTKEQADFAVEALA KATYERLPRWLVRINKALDR TKRQGASFIGILDIAGPEIFELN SFEQLCINYTNEKLQQLFNHMTF ILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGV LALLDEECWF PKATDKTFFVEKLVQEQ GSHSKFQKPRQLKDKADFCI IHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKG MFRIVGQLYKESLT KLMTALRNTPNFVRCI IPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRI VFQEFQRQRYEILTP |

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|------------|--|--|--|
| | | | <p>NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIFFQAVCRGYLARKAFKKQQQLSALKVLQR NCAAYLKLRLHWQWVRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAACKQEELEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEESSEKAKNLAKIRNKQEVMSIDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSSELEALKTELEDTLDTAAQCELRTKRE QVVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKLACEVKVLQVQVKAESHEKRRKKLDAQV QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEAEKKGKIK FAKDAASLESQLODTQELLQEETRQKLNLSRIRQLEEEKNSLQ EQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA KKLLKDAEALSQRLEBKALAYDKLEKTKNRLQQLDLDLTVDL HQRQVASNLEKKQ\KKFDQLLAEKKSISARYAEERDRAEAEARE KETKALSARALEEAEAEKEEFERQNKQLRADMEDLMSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEEELEDELQATEDAKLRLEV NMQAMKAQFERDLQTRDEQNEEKRLLIKQVRELEAELEDERKQ RALAVASKKMEIDLKDLAEQTEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSEKSEKKLSLEAEILQLQEEELASS ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE ELEEEQSNMELLNDRFRKTTLQVDTLNAELAERSAAQKSDNAR QQLERQNKELKAKLQLEGA VKSKFKATISALEAKIGQLEEQLE QEAKERAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMQLKRQLBEAEBEATRANASRRKLQRELDDEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLLEGASLELSDDDTESK TSDVNETQPPQSE</p> |
| 5931 | 113 | 6082 | <p>RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWVPIPSERHGFPAASIKEERGDEVMLAENGKKAMVNDKDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTSGLF CVVINPYKNLPIYSENIEMMYRGKKRHEMPPIYATSESAYRCM LQDREDQSILCTGSGAGKTENTKKVIQYLAHVASSHKGRKDNH IPGE\LERQLLQANPILESFGNARTVQNDNSSFQKGFIRINFDV TGYIVGANIETYLEKSRVRAKQDERTFHFIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVSVVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVG RDYVQKAQTKEQADFAVEALA KATYERLFRWLVRINKALDRTRKQGSFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGV LALLDEECWFPKATDKTFVEKLVQEQ GSHSKFPKPRQLKDKADFCIIHYAGKVDYKADWLKMNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMTALRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGRICRQGFNPNRIVQEFQRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIFFQAVCRGYLARKAFKKQQQLSALKVLQR NCAAYLKLRLHWQWVRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAACKQEELEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEESSEKAKNLAKIRNKQEVMSIDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSSELEALKTELEDTLDTAAQCELRTKRE QVVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKLACEVKVLQVQVKAESHEKRRKKLDAQV QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEAEKKGKIK FAKDAASLESQLODTQELLQEETRQKLNLSRIRQLEEEKNSLQ EQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA</p> |

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|------------|--|--|--|
| | | | KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQEELDDLTVDLH HQRQVASNLEKKQ\KKFDQLLAEKKSISARYAEERDRAEAEARE KETKALSARALEEAEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEEELEDELQATBDALRLLEV NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQQAQMK DYQRELEEARASRDEIFAQSKSEKLLKSLEABILQLQEELAS ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE BLEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQEEGAVKSKFKATISALEAKIGQLEEQLE QEAKEERAANKLVRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMKQLKRQLEEEEAATRANASRRKLQRELDDEANEGLSR EVSTLKNRLRRGGPISFSSSSRGRRLHLEGASLELSDDDTESK TSDVNETQPPQSE |
| 5932 | 33 | 572 | RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGWLWKAENMG FGATLAVGLTIFVLSVVTIIICFTSCCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPQPPSPVPSYQGYHTMPPQPGMPAAPP FMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYPNAYMDA PKAAL |
| 5933 | 1 | 3190 | GTRKLMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPS SDMPSRTRPKSPRKHNYRNESARESLECDSPHQNLSRPLENKLK AFSIGKMSTAKRTLSKKEQEELKKKDEKAAAEIYEEFLAAFE SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKEKEKKKSNELEFKEELKQI QEERDERHKTGRLSRFEPPQSDSDGQRRSMDAPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLLKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGAVPPIPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLQAIIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPLYLHGMSEEQ ETEAFVEEPSKKGALKEEQDKLEELRGLTPRKNDIGDAMVFC LNNAEAAAEIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA KVANASYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQKRM TCFRAWEDWAIYEPFLIKLQNIIFGLVNIIEEKETEDVPPDL GAPIEEELDGAPLEDVVGIPIDATPIDDLGVPKSLDDDLG PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQVTSKWELFD QHEESEEEENQNEEESDEEDTQSSKSEEHLYSNPIKEEMTE SKFSKYSEMSEBKRAKLEIELKVMKFQDELESGKPKKPGQS QEQVHYRDKLLQREKEKELEERERERDKKDEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPPSPKERSER SHKESRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSP KKSGKRSRSQSRSPHRSHKSKGKTNTGRKFFKAVTYWKCDLF LCPERSVF |
| 5934 | 1 | 3190 | GTRKLMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPS SDMPSRTRPKSPRKHNYRNESARESLECDSPHQNLSRPLENKLK AFSIGKMSTAKRTLSKKEQEELKKKDEKAAAEIYEEFLAAFE SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKEKEKKKSNELEFKEELKQI QEERDERHKTGRLSRFEPPQSDSDGQRRSMDAPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLLKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGAVPPIPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLQAIIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPLYLHGMSEEQ ETEAFVEEPSKKGALKEEQDKLEELRGLTPRKNDIGDAMVFC LNNAEAAAEIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA KVANASYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQKRM TCFRAWEDWAIYEPFLIKLQNIIFGLVNIIEEKETEDVPPDL GAPIEEELDGAPLEDVVGIPIDATPIDDLGVPKSLDDDLG |

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|------------|--|--|---|
| | | | PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNEESEDREDTQSSKSEEHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKQFDELESGKRPKPKQGSF QEVEHYRDKLLQREKEKELERERERDKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKRSERSER SHKSSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP KKGKKSRSQSRSPHRSHKSKGKTNTGRKFFKAVTYWKCDF LCPERSVF |
| 5935 | 3 | 4493 | SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL SDSGSFVSSRARREKSKKGRQEAERLKKAKAGERKYKYEVEDF TGVEEVDEEQYSLVQARQDDDWIVDDGIGYVEDGREIFDDD LEDDALDADEKGDGKARNKDKRNVKLAFTKPNNIKSMFTACA GKKTADKAVDLSDGLLGDIQLDNTETPQTTPPPVMILKKKRS IGASPNNFVHTATAVPSGKIASPVSRRKEPLTPVPLKRAEFAG DDVQVESTEEQESGAMEFEDGDFDEPMEVEVDLEPMAAKAWD KESEPAAEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS VQEVQVDSSHLPLVKGADBEQVFHYWLDAYEDQYNQPGVVFLF GKVIWESAETHVSCVMVKNIERLTLYFLPREMKIDLNTGKETGT PISMKDVEEYEFDEKIATKYKIMKFKSKPVEKNYAFEPIDVPEKS EYLEVKYSAEMPQLPDQLKGETFSHVFGTNTSSLELFLMNRKIK GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDVSPPLV VMAFSMTQMNAKNHQNIIAMAAALVHHSFALDKAAPKPPFQSH FCVVSKEPKDCIFPYAFKEVIEKKNVKEVAATERTLLGFFLAKV HKIDPDIIVGHNIYGFELVLLQRINVCKAPHWSKIGRLKRSNM PKLGGRSFGERNATCGRMICDVEISAKELIRCKSYHLSLVQQ ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC ELNVLPLALQITNAGNIMSRTLMGGRSERNEFLLHAFYENNY IVPDKQIFRKPQQLGDEDEEIDGDTNKYKGRKKGAYAGGLVL DPKVGFDYDFILLDFNSLYPSIIQEFNICFTTVQRVASEAQKV TEDGEQEIQPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD LNPDLILQYDIRQKALKLTANSYMGCLGFSYRFYAKPLAALV YKGREILMHTKEMVQKMNLEVIYGDTSIMINTNSTNLEBVKL GNKVKSEVNKLYKLEIDIDGVFKSLLLKKKKYAAALVVEPTSD GNYVTQKELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV ENIQRLIEIGENVLNGSVPSQFEINKALTKDPQDYPDKKSLP HVHVALWINSQGGKVKAGDTVSYVICODGSNLTASQRAYAPEQ LQKQDNLTIDTQYLAQQIHPVVARICEPIDGIDAVLIATGWEL DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKPCPC TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN KLIMDIRRFIKKYDGLWICEPTCRNTRHLPLQFSRTGPLCP ACMKATLQPEYSDKSLYTQLCFYRIFDAECALEKLTDTHEKDK LKKQFFTPKVLQDYRKLNKTAEQFLSRSGYSEVNLSKLFAGCAV KS |
| 5936 | 1124 | 139 | RGEEQDAEFRRFACLGFERLQEFSLRLRAVHRSRAWTCYLAI RMLMATCCPSPTTTACTGPWQRAPLRLLVQKREADSSGLAFAS NSLQRRKKGLLLRPVAPLRTPLLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN SHN\LIVTVKPAQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPLSD QEQASSGWGSRIRGDGSGFSL |
| 5937 | 31 | 1600 | PTSLKSTVOLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWMLRSSLKQYSFEALREKSNYSIDPDVKNDFAPI LHLADQYDPLYSKRFSIFLSEVSENKLLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPFVKLPS AVSQVLNKLRLVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFLKLNKELYLSGCVLPEQLSTMQLEGFQDLKLNRLTYL KSSLSRIPQVVTDLPLSLQKLSLDNEGSKLVVLNLLKMMVNLKS LELISCDLERIPHSIFSLNHLHLDLRENNLKTVEEIIISFQHLQ NLSCKLWHNNIAYIPAIGALSNLQSLDHNHNIENLPLQLFL CTKLHYLDLSYNHLTFIPPEIQYL\SNLQYFAVTNNNIEMLPDG |

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|------------|--|--|--|
| | | | LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL PPELEGCSLKRNC LIVEENLNTLPLPVTERLQTCCLKC |
| 5938 | 395 | 1865 | YKGEFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK MTVMILLLLSLYPGFTSQKSDDDYEDYASNKTWLTPTKVPBGDV TVILNNLLLEGVDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME YTIDIFFAQTWYDRRLKFNSTIKVLRNLSNMVGIWIPDTFFRN SKKADAHWITTPNRMRLIWNDRVLYSLRLTDAECQLQLHNP MDEHSCPLEFSSYGYPREIIVYQWKRSSVEVGDRSWRLYQFSF VGLRNTTEVVKTTSGDYVVMVYFDLSRRMGYFTIQTYPCTLI VVLSWVSFWINKDAVPARTSLGITVLTMTLSTIARKSLPKVS YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK KNPAPTIDIRPSATIOMNATHLQERDEEYGYECLDGKDCASF FCCFEDCRTGAWRHGRIHRIAKMDSYARIFFFTAFCFLNLVYW VSYLYL |
| 5939 | 66 | 1404 | IRPGYLKEVQENSPGHRAGLEFFDFIVSINGSRLNKDNDTLKD LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGV SIR FCSFDGANENVVHVEVESNSPAALAGLRPHSDYIIGADVTMNE SBDLFSLIETHEAKPLKLYVNTDTDNCREVIITPNSAWGGEGS LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTF VQLSSVNPSPSPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV PTVP\LLPPQVNVQSLTSVPPMESSYLHLPLGMPFTRQGLPNLPQ PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I AFLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT TTAADAASSLTVDVTPPTAKAPTTVEDRVGDS TPVSEKPVSA V DANASESP |
| 5940 | 145 | 717 | RRSASRSASPROSAGTAVTTGTTRAGGTCLAAHHRMRWRADGRS LEKLPVHMLGVITEVEQEPSFSDIASLVVWCMVAGISYISVYDH QGIFKRNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPDLDVDT LA\VTYLVQMVVLLILI |
| 5941 | 13 | 6147 | MCLGRMGASSPSPPEVGPFPAPGLPFCGGSSLLAVVLLALPVA WQCNAPAW\LPFARPTNLTEFEFP IGTLYNCECRPGYSGRPF SIICLKNSVWTGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQ IKYSC TKGYRLIGSSSATCIIISGDTVIWNETPICDRIPCGLPP TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL NEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTORDKDNFSPGQEVFYSCBPGYDLRGAASMRCTPQGDW SPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLGAKVDFVCEG FQLKGSSASVCLAGMESLWNSVVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNG VVSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPF SITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVH VITDIQVGSRIYNSCTTGHRLIGHSSAECILSGNAHWSTKPP I CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLSLNEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTORDKDNFSPGQEVFYSCBPGYDLRGA A SMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLG A KDFVCEG FQLKGSSASVCLAGMESLWNSVVPVCEQIFCPS P PVI PNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNAS D FPIGTSLKYE CRPEYYGRPF SITCLDNLVWSSPKDVCKRKSK T PPDPVNGMVHVITDIQVGSRIYNSCTTGHRLIGHSSAECILSG N TAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK C T PPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGP RRVKCQ A LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPAAPCAVKS CDDFLGQLPHGRV LFPNLQLGAKVSFVCEG FRLKGSSVSHCVLGMRS LWNNSVP VCEHIFCPNPPAILNGRHTGTPSGDIPYKGEISYTCDPHPDRGM |

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|------------|--|--|---|
| | | | TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFISISLENLWVS SVEDNCRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRLL IGSPSTTCLVSGNNVTWKKAPICEIISCEPPPTISNGDFYSNN RTSFHNGTVVTYQCHTGPDEQLFELVGERSIYCTSKDDQVGWV SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFCRQPG FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ DNFSPGQEVFYSCFPSYDLRGAASLHCTPQGDWSPEAPRCTVKS CDDFLGQLPHGRVLLPLNLQLGAKVSFVCEGFRLLKGRSASHCV LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI PYGKE VSYTCDPHPRGDMTFNLIGESTIRRTSEPHONGVWSSPAPRCEL PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGYLLVK GFI FCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY GDYVTLKCEDGYTLEGS PWSQCQADDRWDPLAKCTSRTHDALI VGTLSGTIFFILLIIFLSWII LKHKRGNNAHENPKEVAIHLHSQ GGSSVHPRTLQTNEENSRLVP |
| 5942 | 4509 | 688 | YLYVVRMRANFLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRL DK\AQMRIFBERTGYFSSDGLRTASHYIKYNTIETFNELFDA HKTEGDI FAIVSKAEEDQIKVREEEIEELDTLLSNFCBLSTPG GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA LFEIALRKRWPTMTYRLNLKSAIDKRLNGWASPLRQFSILP PH MLTRLEEKLTVDKLDKMRKDEIGHILHHVNIIGLKVKCVHQIP SVMMEAFIQPI TRTVLRVTL SIYADFTWNDQVHGT VGE PWWI WV EDPTNDHIYHSEYFLALKKQVISKEAQLLVFTIPIFEPLPSQY I IRAVSDRWLGAEAVCI INFQHLILPERHPPHTELLDLQPLPITA LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTSGKT VAAELAI FRVFNKYPTSKAVYIAPLKALVRERMDWKVRIEEL GKKVIELTGDVTPDMKSIKADLIVTTPEKWDGVSRSWQNRNRY QQVTILI IDEIHLGEEERGVL EVIVSRTNFISSHTEKPVRIYV LSTALANARDLADWLNLIKQMGLENFRPSVRPVPLEVHIQGFPGQ HYCPRMASMNKPAFQAIRSHSPAKPVLI FVSSRRQTRLTALELI AFLATEEDPKQWLNMDEREMENI IATVRDSNLKLTAFGIGMH AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNPPAHLV I IKG TEYDYGKTRRYVDFPITDVLQMMGRAGRPOFDDQKAVILVHDI KKFYKFLYEPFPVSSLLGLVSDHLNAEIAGGTITSKQDALD YITWTYFFRRLIMNPSYVNLGDVSHDSVNKFLSHLIEKSLIELE LSYCIBIGEDNRSIEPLTYGRIASYYLKHQTVKMFKDRLKPEC STELLSILSDAEYTDLPVRHNEHDHMSLAKCLPIESNPHSF DSPHTKAHLLQAHLSRAMLP CPDYDTDTKTVLDAQALRVQAML DVAANQGWLVTLNITNLIQMVIQGRWLKDSLLTLPNIENHHL HLPKKWKPI MKGPHARGRTSIECLPELIHACGGKDHVFSMVS ELHAAKTQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQYVQLQVSLQRVHFGFHKGKPECAVT PRFPKSKDEGWFLILGEVDKRELIALKRVG YIRNHHVASLSPYT PEIPGRYIYTYFMSDCYLGLOQQYD/NLSQRYTSESFCTGQHQ GL |
| 5943 | 1 | 2274 | DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTLWLPNHVFLRLR EGLKNQSPTEAEKPASSSLPSSPPQLLTRNVVFLGGELFLWD GEDSSFLVVRLRGPGSGG\BEPALSQYQRLLCINPPLFEIYQVL LSPQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVILSEABEESLVLNKGRAYTASLGETAFAVDFGPLA AVPKTLFGQNGKDEVVAYPLYIYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AARDNYGYDACAVALCPVNPILVIATESGML YHCVVLEGEEDDHTSEKSWDSRIDLIPSLYVFECELELALKL ASGEDDPFDSFSPVKLHRDPKCPSPRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTBQKCFVEHILCTKPLPCRQAP IRGFWIVFDI LGPTMICITSTYECLINPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHRSILQRSVANPAFLKASEKD IAPPPECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK |

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|------------|--|--|--|
| | | | KLLHSFHSSELVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK KDYQQQKMEKVLSPKPTIILSAYQRKCIQSILKEEGEHIREMV KQINDIRNHVNF |
| 5944 | 167 | 3428 | FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNIT ITTSKKRKNRKNKITPENVOIIFDDPLPISYSQPEKVNGESKS SSTSESGDSNDNRISCSDESSNSNRKSDNHSAPVTTTVSS KKQPSVLVTPPKEERKSVSGKASIKLSETISEGTSNSLSTCKTS GPSPLSSPNGKLTVASPKRGQKREBGWKEVVRSSKKVSVFSTVI SRVIGRGGCNINAIREFTHAIDIDKQKDKTGDRITIRGGTES TRQATQLINALIKDPDKEIDELIPKNRLKSSANSKIGSSAPTT TAANTSLMGIKMTTVALSSTSQTATALTVPASSASTHTIKNP VN\NVRPGFPVSFP\LAYPPQFAHALLAQTFQQIRPRLPMT HFGGTFPPAQSTWGFPPVRLSPARATNSPKPHMVPRHSNQNSS GSQVNSAGSLTSSPTTTSSASTVPGTSTNGSPSSPVRRQLF VTUVKTSNATTTTVTASNNNTAPTATYPMPTAKEHYFVSSP SSPSPPAQPGGVSRNSPLDCGSASPKNKVASSEGEAGSFPVVFET TNRTPPNSSSSSGSSAHSNQPPGVSQEPRLPQQSQVPPFP EVRMTVPPLATSSAPVAVFSTAPVTYPMPTQPMGCPQPTPKMET PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSVQ LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT SAHAFWGGSVSSQSTPESMLSGKSSYLPSNDPLHQSDTSKAPG FRPPLQRPAPSPSGIVNMDSPIYGSVTPSSSTHLGNFASNISGGQM YGPAPLGGAPAAANFNQRHFSPLSLTPCASSANDSSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSDRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK VGGMPFVSYGNAMIPVAPIDPAGGPIFNGPHAADPSWNSLIK MVSSSTENNGPQTWTGFWAPHMNSVHMNQLG |
| 5945 | 1461 | 197 | GVTHLFLFGKRKLNGTAEDLKGQADFFLLVSEAVVATGSPRA WLTCLILPLPGIIFSVLPKAMSRPLITFTPATDPSDLWKDQQQ QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQORSQTEPARER KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTIRILRAA QEGDLPELRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG AAVSLLGRGAAWVGVCELSGRDAAQLAEAGFPEVARMVRESH GETRSPENRSPTPSLQYCENDTHFQDSNHRSTAHLLSLSQGP QPPNLPGLGVPISSPGFKLLRGGWEPGMGLGPRGEGRANPIPTV LKRDOEGLGYRSAPQPRVTHFPADWTRAVAGRE\TPPRVATLSW REERRREE\KDRAWERDLRTYMNLEF |
| 5946 | 541 | 1666 | ILGSYSYIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLF SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDV/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYLTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLKIAQISELAFPTASQ KIALNAHSSLSKISFSSLPNIYVTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPAALMTAIDGRHDVCIRVESKLIKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAWSAEPCVLKIQSLFVL DENSYPQQDFSLDFYPDIVKHGANARL |
| 5947 | 3 | 1317 | RGIPDRRRRGPIGRVNMDELNVKKMGLGHEQGFGAPCLCKCEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKQNVISINTVYEW PPVQNALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKYKSEALGVGDVXLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCKLSMKEG DPAIYAERAGYDKLWHPACFVCSSTCHELLVDMYIFWKNKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAEQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCOGCHNAIDPEVQRVTYN NFSWHASTECLSCSSCKCLIGQKFMPEGMVFCVVECKKRMS |
| 5948 | 39 | 3370 | YRERYPVSGSVLRSALFVCWDFLSGLTEGSLLEGGFFSGPIDQ GNHYQMRKGRCHRGSAARHSPSPSVKHSPTRETLTYAQORM VEIEIEGRHLRISIFDPLEIILEDLTAQEMSECSNSENSERP PVCLRTKRRHKNNRVKKNEALPSAHTPASASALPEPKVRIVEY |

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|------------|--|--|--|
| | | | <p>SPPSAPRRPPVYKFKIEKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDGCVPAVSQSMFEFLMDRFKESHENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDCMCNLAVHQECYGVPIPEGQWLC/ RAHCLQSRARPADCVLCPNKGGAFFKTTDDDRNGHV\VCALW\IP E\VGFAVTVFIEPIDGVNIPPARWKLTCNLCKEKGR/VGACI QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPICAVLPTVCAPYIPQRLNRIANQVAIQKKQ FVERAHSYWLKRLSRNGAPLLRRLQSSLQSQRSSQRENDDEM KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLAAGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLDPANRAHLGLEEQRLRELLDMLDLCAMKSSG SRSKRAKLLKKEIALLRNLSQQHSQPLPTGPGLEGFEEDGAAL GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTSDEKLFVLFFDNKRWSQ WLPKSKMVLGIDETIDKLKMEGRNSSIRKAVRIAEDRAMNHL SRVHGEPTSDLSID</p> |
| 5949 | 39 | 3370 | <p>YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLEPGFFSGPIDQ GNHYQMRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQARM VEIEIGRLHRISIFDPLEIILEDLLTAQEMSECSNKNSESRP PVCRLTKRHKNNRVKKNEALPSAHGTPASASALPEPKVRIVEY SPPSAPRRPPVYKFKIEKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDGCVPAVSQSMFEFLMDRFKESHENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDCMCNLAVHQECYGVPIPEGQWLC/ RAHCLQSRARPADCVLCPNKGGAFFKTTDDDRNGHV\VCALW\IP E\VGFAVTVFIEPIDGVNIPPARWKLTCNLCKEKGR/VGACI QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPICAVLPTVCAPYIPQRLNRIANQVAIQKKQ FVERAHSYWLKRLSRNGAPLLRRLQSSLQSQRSSQRENDDEM KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLAAGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLDPANRAHLGLEEQRLRELLDMLDLCAMKSSG SRSKRAKLLKKEIALLRNLSQQHSQPLPTGPGLEGFEEDGAAL GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTSDEKLFVLFFDNKRWSQ WLPKSKMVLGIDETIDKLKMEGRNSSIRKAVRIAEDRAMNHL SRVHGEPTSDLSID</p> |
| 5950 | 1166 | 373 | <p>ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR CLCRQHRPVQLCAHRTCREALDVLAKTVAFRLNLPSPWQLPPQ DQRRLLQGCWGPFLFLGLAQDAVTFEVAEAPVPSILKKILLEP SSSGSGQLPDRPQPSLAQVWLQCCLESFWSLELSPKE\YACL KGPIILFNPDPGLQAASHIGHLQEAHWLCEVLEPWCAPQGR LTRVLLTASTLKS IPTSLGLDLPFRPIIGDVIDAGLLGDMLLLR</p> |
| 5951 | 143 | 5449 | <p>WNVPKSLVQLFKFSDEEHEQNDISIGKTGETGVEEMIATR VBQDSKETVLSHEDDHILEDAGSSDISSDACTNPNKTENSLV GLPSCVDEVTECNLELKD TMGIADKTENTLERNKIEPLGYCEDA ESNRQLESTEFNKNLEVVDTSTFGPESNILENAICDVPQNSK QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP VHSKQNM TTDAPKKIVAAYEVHSKTKVNVKSVKRN TDVPS QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQHSVLKKTQ</p> |

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|------------|--|--|--|
| | | | <p>DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTHGVSHSSQK QCHKPQQQAPAMKTNHSHVKELEHPGVEHFKEEDKLKKPEKN LQPRQRSSSKSFLDEPPLFIPDNIAITRREGSDHSSSFESKYM WTPSKQCGFCKKPHGNRFMVGCGRCDWFHGDVGLSLSLQAQVM GEEDKEYVCVKCAEEDKKTEILDPTLENQATVBFHSGDKTME CEKLGSLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD NEIKKWQLAPLRKMGQPVLPRRSSEKSEKIPKESTTVTCTGEG ASKPGTHEKQEMKKKKV\KGVNLNVHPAASAKPSADQIRQSVR HSLKDILMKRLTDSNLKVPEEKAATKIEKELFSFFRDTDAK YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS KELAAWRRRENRTIEMIEKQREVERRPITKITHKEIEIESD APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS QHRQHLFDLNCCKICIGRMAPPVDDLSPKKVKKVVGVARKHSDNE AESIADALSSTSNILASEFFEEKQESPKSTFSPAPRPPEMPGT EVESTFLARLNFVWGFINMPVAKFVTKAYPVSGSPEYLTEDL PDSIQVGGRIISPQTVDYVEKIKASGTKEICVVRFTPVTEEDI SYTLFAYFSSRKRYGVAANNMKQVKDMLYLIPLGATDKIPHLV PFDGPGLELHRPNLLGLIIRQKLKQHSACASTSHIAETPESA PPIALPPDKKSKIEVSTEEAPEEENDFFNSPTTVLHKQRNKPPQ NLQEDLPTAVEPLMEVTKQEPKPLRFLPGVLIGWENQPTTLEL ANKPLPVDDILQSLGTTGQVYDQ\AQSVMEQNTVKEIPFLNEQ TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEITSVVG SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE KTLKRLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN LVANTARSPQFINLKRDPQQAAGRSQPVTTSESKDGDSCRNGEK HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRFGSAVATSHFE VGNTCPSEFPKSKITFTSRSTSPRTSTNFSMPRPQQPNLQHLKS SPPGFPFPFPFPFPQSMFGFPFPHLPPLLPPLPPGFG\FA\QNP VWPPPVV\HLP\GQPMRMMGPLSQASRYIGQNFYQVKDIRPE RRHSDPWGRQDQQLDRPFNRGKGRQRFYSDSHHLKRERHEKE WQESERHRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD GKASRDSRNVDKKPKPKSEDYBKDKEREKSKHREGEKDRDRYH KORDHTDRTKSKR</p> |
| 5952 | 3226 | 639 | <p>PPARRSARDLFRALSMEARPSGSWNGALCRLL\LVTL\AFLIF ASDACKNVTLHVPKSLDAEKLVGVRNLKECFATANLIHSSDDPF QILEDGSSVYTTNTILLSSEKRSFTILLSNTENQEKKKIPVFLHE QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFLFLQVQ QSDTAQNYTIYYISIRGPGVDQEPNLFYVERDGTNLYCTRPVDR EQYESFEIIAFATTPDGYTPELPLPLIKIEDENDNYPIFTEET YTFTIFENCVRGTIVGQVCATDKDEPDTMHTRLKYSIIIGQVPPS PTLFSMHPTTGVIITTSQDLRELIDKYQLKIKVQDMGQYFGL QTTSTCIINIDVDNHLPTFTRTSYVTSVEENTVDVEILRVTV DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLGVVVKPL NYEBKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL TDPTGWVTIDENTGSIKVFRLDREAETIKNGIYNITVLASDQG GRICGTGLGIIQLQDVNDNSPFIKKTVIICKPTMSSAEIVADVP DEPIHGPPDFSLSSSTSEVQRMWRLKAINDTAARLSYQNDPPF GSYVVPITVRDRLGMSVSTSLDVTLCDCITENDCTHRVDPRIGG GGVQLGKWAIIALLGIALFFCILEFTLVCGASGTSKQPKVIPPDD LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAGVCGTVGSG IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC RVTYSEBWSFTQPRLGEEISIRGHTLIKN</p> |
| 5953 | 330 | 811 | <p>PLLCNPDPGWYVWVKQSEISKESQEMDARPKLDLGFKEGQTIK LCIGNITNKKGGASKPRTARGGGLSLLPPPGGKVTIPPPSS/V KLPSTNHVTPPSIPKSNHGGSDADILLDLSDPAPVTTTAPTPVS VSNLWGDFTASSSVNPQAPQPSNVVQF</p> |
| 5954 | 32 | 2130 | <p>PPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL PEPSIRSVMQYLAERNEITFDKIFNQKIGFLLPKDFCLNEINE AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH</p> |

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|------------|--|--|--|
| | | | PFSKQAVEHVQSHLSKKQVSTLTFQPYIBEICESLRGDIQKFM ESDKFTRFCQWKNVELNIHLMNEFSVHRIIGRGGFGEVYGCRA ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI TCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYA TEIILGLEHMHNRFFVYRDLKPANILLDEHGHRIS\DLGLACD FSKKKPHASVGTGHYMAPEVLQKGTAYDSSADWFLGCMFLKLL RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL QRDVSKRLGCHGGGSQEVKEHSFFKGVWDQHVYLYQKYPPLIPP RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM HGYMLKLGNPFLTQWQRRYFYLFPNRLWEWRGEGESRQNLITM ILSVEETQIKDKKCLFRKGGKQFVLQCESDPEFVQWKKELNE TFEQAQRLRLRAPKFLNKPRTSGTVLEPKPSLCHRNNSGL |
| 5955 | 1726 | 444 | KREREFRLAVCPRLRYFSAYESSPGTELRCEGLCRSGQBFADCR PANRQDVLSGWINLPLVLQTKDPLKTPGRDLHGTRTAFIHHRQ VWKRCINIWDRDVLGVLNEIANSEEEVFVWKTASGWALALCR WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSGCCLRVFAWHPT NKPAVALLDSDSVRVYNASTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILITLDTSLSTRPSSGCAQVLSHPGHTPTVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLW SPDGSKILATTPSAVFRVWEAQMTWCERWPTLSGRGQTGCWSPD GSRLFTVLGEPLIYSLSPFERCGEGKG\ALEVQSQRRLWQICL RQQRHQMVRRLGERLTPWSGTPVGNVWLCL |
| 5956 | 1705 | 139 | GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKRRHRLKRHND CFVGEAVDVIFSHL IQNKYFGDVIDIPRAKVVRVQALMDYKVFVAVPTKVFGDKKPT FEDSSCSLYRPTTIPNODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQVLDLPLDLSLLKQGEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQDEWLSAIDCSBYLPQDMVVEISRSFPEQPDRTDLVK ELLFDAIGRYSSREPLNLHSDVHNGIARLVNGKTEIALEAT QLLLKLLDFQNRREEFRRLLYFMVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSXGKTDLVLVFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYQRIIDQRDYSNNTKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD |
| 5957 | 1479 | 451 | ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKNENIKNAMLIK GGNANATVTVKLVKDVYALKKPYGVLYKKKNITRPEDQTSLEFF SKKSDCSLFMGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCEGTKPMILIFAGDDFDVTEYRRLKSLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIIKHQSIQSFL |
| 5958 | 1 | 3138 | AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGAVYICPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFKPTPEKGPVGTCTYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGVITASVADI IA NYSFKDILRLKAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNGFYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGOIYLYLQVSSLL FRDPOILTGTETFGFRGSAMAHGLDNLQDGYNDIAIGVFPAGKD QRGKVLIIYNGNKDGLNTKPFKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSACFSLRVCASVTGQS IANTIVLMAEVQLD SLKQKGAIKRTFLDNHQAHRVFPVLIKQKSHQCDQDFIVYLRD ETEFDRKLSPINISLNSLDESTFKEGLEVKPIILNYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHMLIINAR NEGEGAYEAEFLVMIPEEADYVGIERNKNGFRPLSCYKMNVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS NKDNPDNSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNEPEE |

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|------------|--|--|--|
| | | | EPHKEEBVGPLVEHIYELHNTIGPSTISDTILEVGNPFPSARDEFL LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG GESAVLKVRSLWAHTFLQRKNDPYALASLVSEVKMPYTDQP AKLPEGSIAIKTSVIWATPNVSFSIPLWVILAILLGLLVLAAIL TLALWKCGLFDRARPPQEDMTDREQLTNDKTPEA |
| 5959 | 1 | 1166 | GTSGYAAQQLPSLLKEREPHLGLTNKVFASQWLNHRQVVCSTKC NTLFVVDVQTSQITKIPIILKDRPGGVTOQCGCIHAIELNPSRT LLATGGDNPNSLAIYRLPTLDPVCVGGDDGKDWIFSIWISDTM AVSGSRDGSMLWEVTDVLTKSADARNVSRVPVYAHITHKALK DIPKEDTNPDCNKVRALAFNNKNKELGAVSLDGYFHLWKAENTL SKLLSTKLPYCENVCCLAYGSWSVYAVGSQAHVSFLDPRQPSY NVKSVCSRERGSGIRSVSYEHIITVGTGQGSLLFYDIRAQRFL EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF FPNAVYTHCYDSSGTLKFVAGGPLPSGLHGNVYAGLWS |
| 5960 | 2853 | 870 | FVWSDGGFRPRRGPAVGAGAAHLSDPWAMTPTANRATNPLNKE LDWASINGFCQLNEDFEGPPLATRLLAHKIQSPQEWELQALT VLETCMKSCGKRFDHVEVGKFRFLNELIKVSPKYLGSRTSEKVK NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT TFPLPPPRPKNVI FEDEEKSMLARLLKSSHPEDLRAANKLIKE MVQEDQKRMEKISKRVNAIEEVNNVKKLTEMVMSHSQGGAAAG SSEDL\MKEL\YQRCRMRPTLFTPTGRVDTEDND\EALAEILQA NDNLTQVINLYKQLVRGEEVNGDATAGSI PGSTALLDLGLDL PPAGTTYPAMPTRPGEQASPEQPSASVSLDDELMSLGLSDPTP PSGSLDGTGWNFSQSSDATEPPAPALAQAPSMESRPPAQTSLP ASSGLDDLDLLGKTLTLLQSLPPESQQRWEKQQTPTRLTLRDLQ NKSSSCSSPSSSATSLHTVSPPEPRPPQPPVPTSLASITVP LESIKPSNLPVTVYDQHGFRILFHFARDPLPGRSDVLVVVSM LSTAPQPIRNIVFQSAVPKVMKVLQPPSGTELPAFNPIVHPSA ITQVLLLANPQKEKVRRLRYKLTFTMGDQTYNEMGDVDQFPFPET WGSLL |
| 5961 | 198 | 3147 | SGEPRPEPGNMATCIGEKTEDFKVGNLLGKGSFAGVYRAESIHT GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPISILELYNY FEDSNYVYLVELMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT GMLYLHSHGILHRDLTSLNLLLTRNMNIKIADFGLATQLKMPHE KHYTLCGTPNYISPEIATRSAGHLESVDVSLGCMFYTLIGRPP FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRNRPADRL SLSSVLDHPPMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS STISGSLFDKRRLLIGQLPNKMTVFPKNKSSDFSSSGDGNS FYTQWGNQETSNSGRGRV IQDAERPHSRYLRRAYSDDRSGTSN SQSQAKTYTMRCHSAEMLSVSKRSGGGENEERYSPTDNNANIF NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHFDLQKDTSKNA WTDTKVKKNSDASDNAHSVQQNTMKYMTALHSKPEIIQECVF GSDPLSEQSKTRGMEPPFWGYQNRRLRSITSPLVAHRLKPIRQKT KKAVVSLDSEEVVELVKEYASQYVKEVLQISSDGNITITYY PNGG\RGFPLA\DRPPSP\DNISR\YSF\DNLPKEYWRKYQYA SRFVQLVRSKSPKITFYTRYAKCILMENSPGADFEVWFYDGVXI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR ICLALESIISEERKTRSAFFPPIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRVMHSAASPTQAPILNPSMVTNEGLGLTT TASGTDISSNSLKDCLPKSAQLLKSQVFNKVGWATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLDPDIKQ KLQCLSSILLMFSNPTPNFH |
| 5962 | 20 | 2447 | RVCSSASTASQAVMADAWEEIRRLAADFQRAQFAEATORLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVGR GRVNIQVLDQVINVDLIHNRIIGDIIKSEKHVQLVLGQLIDEN YLDRLAEVNDKLQESGQVTISELCKTYDLPGNFLTQALQRLG RIISGHIDLNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRODKAVFVDPDIYS RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSIKKRYKTTQLL |

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|------------|--|--|--|
| | | | FLKAACVGGQLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA AILLQQVMRAFASKQASTVVFSDTVVSSEKF\INDCTELFREIMH QKAEMKNNPVHLITEEDLKQISTLESVSTSKDKDKDERRRKA TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDSDDESQSSHTGK KKPEISFMQDEIEDPLRKHIQDAPEEFISELAEYLKPLNKTY LEVVRSVFMSSTTSASGTGRKRTIKDLQEBVSNLYNNIRLFEKG MKFFADDTQAALT KHLKSVCTDITNLIFNFLASDLMMAVDDPA AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA AEACDIMVKRGDKKREKQILFQHRQALAEQLKVTEDPALILHLT SVLLFPQFSTHMLHAPGRCVPIIAFLNSKIPEDQHALLVKYQG LVVKQLVSQSKKTGGDYPLNNELDKEQEDVASTTRKELQELSS SIKDLVLKSRKSSVTEE |
| 5963 | 62 | 1130 | PWNPQDFPGRNGLMG\QKGEIGFP\GQGGKKGAPGMP\GLMGSN GSPGPGTSGSGSGKEPGIQGMPGASGLKGPATGSPGPGY MGLPGIQGKKGDKGNQGEKGIQGGKGENGRQGI PGQGIQHHG AKGERGEKGPVGRGAIGSKGESVDGLMGPAGPKGPGDPGPQ GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLQSGRIRNCDH CLSQHSGSPIPGPPGPIGPEGPRGLPGLPRDGVPLGVGVRGP GVRGLKGLPGRNGEKGSGQGFYGPGEQGGPPGPPGEGPPGISKEG PPGDPGLPGKGDGDKPGIQGQPPGPGICDPSLCSFVIARRDPF RKGPNY |
| 5964 | 3 | 2147 | SCRTRGRLSPLQPREAGSSRSRSEPPRPGMEECACQVOTTK RGDPHELRLNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNS PKIVQLLAGVADQTKDGLISYQEFLEFESVLCAPDSMFIVAFOL FDKSGNGEVT FENVKEIFGQTI IHHHIFPNWDCEFIRLHFHGNR KKHLNYTEFTQLQELQLEHARQAFALKDKSKSGMISGLDFSDI MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAPNSLLNM ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ LADLYNASGRLTLADIERIAPLAEGALPYNLAEQRRQSPGLGR PIWLQIAESAYRFTLGSVAVGATAVYPIDLVKTRMQRNGSG SVVGLMYKNSDFCKKVLRYEGFFGLYRGLIPOLIGVAPKAI KLTVNDVFRDKFTRRDGVSPLPAEVLAGGCAGGSQVIFTNPLEI VKIRLQVAGEITTGPRVSALNVLRLDGI FGLYKAKACFLRDIP FSAIYFPVYAHCKLLADENGHVGGNLNLAAGAMAG\VPAASLV TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG TAARVFRSSPQPG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK SRIADLPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA VVQPKAAVAATQ |
| 5965 | 1 | 1498 | MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG CGSYCAGAKASPLPGKMAMGLMGRRELRLQLSGRRVHVSAGP SQWLKGPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSISFA EVQVQAPPVVAATPSPTAVPEVASGETADVQTAEQSFELGL GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV TGQREARAIHNLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL YQKKHGKIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQGT GLWVFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW MRNVIRMMPLITLPI TMHFTAVFMYWLSNLFSLVQVSLRIP AVRTVLKIPQRVVHDLKLPREGFLESFCKGWNKNAEMTRQLRE REQMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS SSKPKSKYPWHDTLG |
| 5966 | 102 | 1925 | RSKQVMARLTKRQADTKAIOHLWAAIETIRNOKOIANIDRITK YMSRVHGMHPKETTRQLSLAVKDLIVETLTVGCKGSKAGIEQE GYWLPGBEIDWETENHDWYCFBCHLPGEVLICDLCFRVYHSKCL SDEFRLRDSSSPWQCPVCRSIIKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC KNCFYLANARPDNWFYPCIPNHELDWAKMKGFVPAKVMQKE DNQVDVRFHHHQRRAWIPSENIQDITVNIHRLHVKRSMGWKA CDELELHQRFLEGRFPWKSNEDRGEEEAESSISSTSNEQLKVT QBPRAKKGRNQSVFEPKKEPEPETEAUSSSQEIPTMQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF |

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|------------|--|--|--|
| | | | KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKECKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEMHYHCCWNTSYCSIKCQEHWAHAEHKRTRCRKR |
| 5967 | 102 | 1925 | RSKQVMARLT KRRQADTKAIQHLWAAIBIIRNOKQIANIDRITK YMSRVHGMHPKETTQRLSLAVKDGLIVETLTVGCKGSKAGIEQE GYWLPGEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL SDEFRLRDSSSPWQCPVCRSIIKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHFMYRRLVHSAVDVPTIQEKVNEGKYRSYEE FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC KNCFFLANARPDNWFPCPCPNHELDWAKMGFGFWPAKVMQKE DNQVDVRFPGHHHQRRAWIPSENIQDITVNIHRLHVKRSMGWKKA CDELELHQRFPLREGRFWKSKNEDRGEAEASSISSTSNELQKVT QEPRACKGRNRQSVEPKKEPEPETEAVSSSQEIPMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKECKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEMHYHCCWNTSYCSIKCQEHWAHAEHKRTRCRKR |
| 5968 | 81 | 1288 | VRFPRRGAPFTVLTGPRQGGVFLGPQRPGSEPDIPARGQPHFP RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL ENWLPSVYVPYYLPCEIFNMKLHYKREKPLQPVVWSQYPPQKL LEHRPTQLLTLPWLAPIVSEGTFFNPELLQHIYQPLNLTIGVT FAVGN/HFLESABEFFMRGYRVHYIIFTDNPAAVPGVPLGPHRL LSSIPQGHSHWEETSMMRMETISQHIakrahevdyLPCLDVD MVFRNPWPGETLGLDVAIHPSYAVPRQQFPYERRRVSTAFVA DSEGDFFYGGAVFGGOVARVYEFTRGCHMAILADKANGIMAAWR EESHLNRHFI SNKPSKVLSP EYLWDDRKQPPLSLKIRFSTLDK DISCLRS |
| 5969 | 1126 | 503 | DVGFINIKRRCDLDFLES PRKPSGRDRAPKORRI AANKCLC TGVREGEPPS/TTSQKVKEAGRDFTYLIIVVLFGISITGGLFYTI FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGEVVKGYGEVTRR GRRQHVRFTEYVKDGLKHTCVKPYIEGSEPGKQGTVYAQVKENP GSGEYDFRYIFVEIESYPRRTIIEDNRSQDD |
| 5970 | 316 | 4712 | SQDNIGHRLQLQKHGWKLQGLGKSLQGRDTPIPVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA KALEDLRANFYCELDKQYQKHQEFDNHINSYDHAHKORLKDOLK QREFARNVSSRSRKDEKKQEKALRLHLEAEQRKQAECAFGSGP MFKPTTAVVDEEGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTPKDEKSSDQGLQKV GDSGSSNLDGKKEDDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLFMRASEQMDGDNTHPKNAPES KKGSSPKPKSCIKAAASQGAETVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETS LATPA GKESQEGPKHPTGFFFPVLSKDESTALQWPELLIFTKAEPSSIS YSCNPLYFDKLSRNKDARTKGT EKPDKIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKSSKHKKRKHADTEEK SSKAESGEKSKRKRKRKRKNKSSAPADSERGPKPEPPGSGSPA PFRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSDDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSEDESDASSHRLHQ KSPSYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSRRSYSSSS DASSDQSCYSRQRSYSDSYSDYSDRSRRHSKRSHSDSDSYAS SKHRSKRHYSSDDDYSLSCSQRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSSTTAHWSQRSRSYSRDRSRSTRSPSQRSGR KRSWGHESEERHSGRDFIRSKIYRSQSPHYFRSGREGPGKK DDGRGDDSKATGPPSQNSNIGTRGSEGDSPEDKNSVTAKLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLP LIGKLPATRKPNKKCEESGLERGEQEQS ETEBGP GSSDALFGHQFP\SEETTGPLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDP TISHNYLPDPSDGNLTLESLSSSQPGPVSSSL LP IAPDLEHFPSYAPPSGDPSEIESTDGAEDA\SLAPLESQPI TF |

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|------------|--|--|---|
| | | | <p>TPPEMEKYSKIQQAQQHIQQQLLAKQVKAPPASAAALAPATPALQPIHIQQPATASATSIITTVQHAILQHHAATAAIGIHPHPHPQPLAQVHHIPQPHLTPIISLHLTHSIIPGHPATFLASHPIHIIPA SAIHPGPPTFHPVPHALYPTLLAPRPAATAALHLHLPLHPI FSGQDLQHPPSHGT</p> |
| 5971 | 53 | 2149 | <p>SFLYFVGVMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII PESVTQERRPPKLAFFMSRGVGDGKSSSHNPKATGTSDDPGNRN RSELYFTLNGSSVDSQPQSKSNWYIDEVAEDPAKSLTEISTD FDRSSPPLQPPPVNSLTENRFHSLPFLTKMPTNGSIGHSPL SLSAQSVMEELNTAPVQESPLAMPFGNSHGLEVGSLAEVKENP PFYGVIRWIGQPPGLNEVLAGELEDEDCAG\CTDGT/REGTRY FTCALKKALFVKLSCRPSRFASLQPVSNQIERCNSLAIWEAY LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIY YVCATKIMKLRLKILEKVEASGFTSEEDPEEFLNIFPHILRV EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVTIQQLLEWSFIN SNLKFAEAPSCLIIQMFRFGKDFKLFKKIFPSLELNITDLEDT PROCRICGLAMYECRECYDDPDISAGKIKQPKCTCNTQVHLHP KRLNHKYNPVS LPKDLPDWDWRHGCIPQNMELFAVLCIETSHY VAFVKYKGDSDAWLFFDSMADRDGGQNGFNIPQVTPCEVGEYL KMSLEDLHSLDSRRIQGCARRLLCDAIYVPTQSPMTSLYK</p> |
| 5972 | 440 | 1761 | <p>ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ EPPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF SHKTVFVSVLMGSCLLVTSGFSLYLGNVFPAMDYLRCAGSCI PSAIVSFTVSRNNANVINPQILFVSTFAVTTCLIWFGCKLVL NPSAININFNLILLLELLMAATVIAARSSEEDCKKKKGSMS DSANILDEVFPFARVLKYSVVEVIAGISAVLGGI IALNVDDSV SGPHLSVTFFWILVACFPASIAASHVAECPNKCLVEVLIAISSL TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLILLLV LLLQA/GPQHGRHPVRALQGGQCAAGCILGHPERPAGAPGWGG GQEPPEGVRQGESLESRRGANGFVTPRRGNRVAAPSLAPGMETH NP</p> |
| 5973 | 65 | 2007 | <p>NGDGKDLFGHIWAWRSNGIISNFRSPHAGMAEEDPAKSPKTG GRAPPGGAEEAGEPTTLQLRLRGITISKAVQNKVEGILQDVQKPSD NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHEE HTDTCPLKQSVYDAYRYCESLACCRPLSTANFGKIIREIFPDI KARRLGGRGQSKYCYSGIRRKTLVSMPLPLGLDLKGSSEPEMGP EVTPAPRDELVEAACALTCDAERILKRSFSSIVEVARFLLQOH LISARSAHVLKAMGLAEDEHAPRERSKPKNGLENPEGGAH KKPERLAQPPKDLARTGAGPLARGERKKSVESSAPANNLOV NALVARLPLLLPRAPRSLIPPIPVSPPIIAPRLSSGALKVATLP LSSRAGAPPAVPIINMILPTVPALPGPGPGGRAPPGGLTQPR GTENREVGIGGDQGPDKGVKRTAEVPVSEASQAPPAKAAQD IEDTASDAKRKRGRPLKKS GSGSGERNSTPLKSAAAMESAQSSRL PWETWGS GEGNSAGGAERPGPMGEARKGAVLAQG\QGDGTYSK GGRGPGSQHTKEAEDIPLVPSKVSIVKGSRSQKEAPFLAKGEV DTAQGNKDLKEHVLQSSLSQEHKDPKATPP</p> |
| 5974 | 4293 | 2200 | <p>LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENTGDKG\BID LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVNRR TV\ASIKNDPPS\RDNRVVG SARARPSQFPEQFSSAQONGSV\S DISPVQA AKKEFGPPSRKSNVCVEKLEKREKRRLQOQELR BKRAQDV DATNPNYEIMCMIRDFRGS LDYRPLTTADPIDEHRIC VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL ENQTRFRDYAFDDSAFNEMVYRFTARPLVETIFERGMATCFAYG QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQVQVVLGLQ REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR KGKLGKPSLIDLAGNERGADTSSADRQTRLEGAEINKSLALK ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISP G MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPNQI\DD LETQWGVGSSPQRDDLKLLCEQNEEVSPQLFTFHEAVSQMVEM</p> |

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|------------|--|--|--|
| | | | EEQVVDHRAVPQESIRWLEDEKALLEMTEEVDDYDVSATQLE AILEQKIDILTELDRKVKSFRAALQEEEOQASKQINPKRPRAL |
| 5975 | 4293 | 2200 | LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWENGDTKGK\EID LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNIKVNRR TV\ASIKNDPPS\RDNRVGSARARPSQFPEQFSSAQNGSV\S DISPVQAAKKEFGPPSRKSNVCVKEVKLQEKREKRLQQQLER EKRAQDVADATNPNYEIMCMIRDFRGSLDYRLTTADPIDEHRIC VCVRKRPLNKKETQMKDLVDITIPSKDVMMVHEPKQKVDLTRYL ENQTFRFDYAFDDAPNEMVYRFTARPLVETIFERGMATCFAYG QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKQ LELQVYATFFEIYSGKVPDLLNRKTKLRVLEDGKQQVQVVLGLQ REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR KGLHLHGKFLIDLAGNERGADTSSADRQTRLEGAEINKSLALAK ECIRALGRNKPHTPPFRASKLTQVLRDSPIGENSRTCMIAITISPG MASCENTLNTLRYANRVKELTVDPATAAGDVRPIMHHPNQi\DD LETQWGVGSSPQRDDLKLLCEQNEEVSFQLETFHEAVSQMVEM EEQVVDHRAVPQESIRWLEDEKALLEMTEEVDDYDVSATQLE AILEQKIDILTELDRKVKSFRAALQEEEOQASKQINPKRPRAL |
| 5976 | 20 | 2949 | VHHLHLTRVSVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF PEVSWMEVKDPMNKGAMLTNTGKYAIPITIDA\EAYAIGKKEKPP FLPEEPSSSSSEDDPIPELLCLICKDIMTDAVVPCCGNSYCD BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE TGTYKRLRKQLPSPPPPPIPPRPLIQRLQPLMRSEISRQODPL MIPVTSSSTHPAPSISSLTNSQSSLAPPVSGNPSSAPAPVPDIT ATVISVHSEKSDGPPFRDSNKLPAALASEHSGTSSIAITA LMEEKGYQVPLGTPSLLGQSLHLGQLIPTTGPVRINTARPGGG RPGWEHNSNKLGYLVSPPPQIIRRGERSCYRSINRGRHHSERSQRT QGPSLPATPVFVPVPPPPPLYPPPPHTLPLPPGVPPPQFSQFPF GQP\PPAGYSVPPPGFPAPANLSTPWVSSGVQTAHSNTIPTTQ APPLSREEFYREQRRLKEEEKKSKLDEFTNDFAKELMEYKKIQ KERRRSFSRSKSPYSGSSYSRSTYSKSRSGSTRSRSYSRSFS RSHRSYSRSPPYPRGRGKSRNYSRSRSHGYHRSRSRSPPYR RYHSRSRSPQAFRGQSPNKRNVPOGETEREYFNRYREVPPPYDM KAYYGRSVDFRDPFEKERYREWERKYREWYKYYKGAAQAQPR PSANRENFSPEFLPLNIRNSPFTGRREDVVGQSHRSRNIGS NYPEKLSARDGHNQDNTKSKEKESNAPGDGKGNKHKHKRKR KGESEGLNPELLETSSRSREPTGVEENKTDSLFPVLPDRDDAT PVRDEPMDAESITFKSVSEKDKREBDRPKAKGDKTKRKNDSAV SKKENIVKPAKGPQEKVDG\DVRLDLLNL\QLKKPKEETPKDL TILNHLPLRRMKSL\EP\EKLTLNQK\IPRNKTSQRGKSE EGLFQRCQIRKANN |
| 5977 | 1363 | 1336 | FLEDRGQVLSHFQCLSLHSINHLHPGAGVAAGPATGW/REYLT PVLKESKPKETGVITPEEFVAAGDHLVHHCPTWQWATGEELVKV AYLPTGKQFLVTKNVPCYKRCQMEYSDELEAIEEDDGDGGWV DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEDEDEG EADMEEYESGLLETDEATLDRKIVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFYDEQROPLTVEHMYEDISQDH VKKTVTIENHPLPPPPMCSVHPCRHAEMVKKIIETVABGGGEL GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM |
| 5978 | 160 | 3213 | RDGARRWGGCCSPLTWAPGFYRRFDLATSGRRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIAVFRFCICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRELVCNRAAEVVTQQLDTLQ LCSLTKEENEKDKCENHHEKLSVFCWTCCKKICHQCALWGGMH GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLIITLMGQKTSLT QETELLESLLQVEVHQLRSCSKSELISKSSSEILMMFQOVHRKPM ASFVTTTPVPPDFTSELVPSYDSATFVLENFSTLQRQADPVYSPP LQVSGLCWRLKVYPDGNVVRGYLSVFELESLAGLPETSKYEYR VEMVHQSNDPTKNIIREFASDFEVGECWGYNRFRLLDLANEG YLNQNDTVILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ INNLERLTIELSRTQKSRDLSPPDNHLSQNDDALETRAKKSA |

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|------------|--|--|--|
| | | | CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSGDGL DLDLVYEDEVNQLDGGSSSSASSTATSNTEENDIDEETMSGENDV BYNNMELEEGELMEDAAAAGPAGSSSHGYVGSSSRISRRLHCSA ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA SYSRKDKDQRKQAMWRVPSDLKMLKRLKTMMAEVRCKMTDVKX TLSEIKSSSAASGDMQTS\LFSAQAALAACGTENSGRLQDLGME LLAKSSVANCYIRNSTNKKSNPKPARSSVAGSLSLRRVDPGE NSRSKGDQCQTLESGSPGSSQSGSRHSSPRALIHGSIIGDILPKTE DRQCKALDSDAVVAVFSGLPFAVEKRRKMVTLGANAKGGHLEGL QMTDLENNSETGELQPVLPBGASAAPEEGMSSSDIECDTENE QEEHSTVGGFHDSEFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT DENSGR |
| 5979 | 212 | 3665 | LPDNTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK LFTAKLVNENVECGNNTCTNNEVHNLTECKNASVISHSNSTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC DTQNTYRFPQCGNMIFDNKEIKLENLEPEHEKCDSEILYNCHK FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPQORSFHN FTLCYIKETEKDCLNLDKNLIKYLQNLKPYTKYVLSLHAYIIA KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMSTSDNSMHVKCRP DRNGPHERYHLEVEAGNTLVNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPFILHHS\SYNSKALIAFLAFLIIVTSIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADDEGRFLAEFQSI\PRVFSKFPKEARKPFNQKNRYVD ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVIMVTRCEEGRNKKCAEYWPMEEGT RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKKATGREVTHIQ FTSWPDHGVDPEDPHLLKLRRRVNAFNSNFFSGPIVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGVVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVNLSLHPYLHNMKKRDPPEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHSDSESSDDSDSEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMI\FQRKVKVIMVLTTELKHGDQEICAQYWG EGKQTYGDIIEVDLKD\TKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNSVVEQLPAEPKELISMIQVVKQLPQKNSSEGNKHKHSTPL LIHCRDGSQQTGIFCALLNLLSEAEETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCNVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQQS |
| 5980 | 3 | 2363 | DAWGCKLRLRLRPTGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVIMHALLQEVDDVVVAPCOGLR PTVDVLGDLVNDLFPVITYALHKDELSEDEQELQEIIRKYFSFP VFFFKVPKLGSEIIDSSSTRMESERSPLYRQLIDLGLYSSSHWN CGAPGQDTKAQSMLEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKNELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIIPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGT ERCLQSLEKSQDVSVHITSNYLKQILNAAHYHEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRLQDVLLHRRKPKLGQELGRGQYGVVLYCDN WGGHFFCALKSVVPPDEKHWNDLALFHYMRSLPKHERLVLDLHG SVIDYNYGGSSIAVLLIMERLHRDLTYGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLVNLLDKQNRKIDTDLGFCCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLEACWDG DPLKRPLLGIQVPMLOGIMNRLCKS\NSEQPNRGLDST |
| 5981 | 1 | 2519 | GRRHSAAMERPWGAADGLSRWPHGLGLLLQLLPSTLSQDR DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\DEECGRVRDFVAKLANNTQHVFDDLRGSVSLSWVGDSTGV ILVLTTFHVPLVIMTFGQSKLYRSEYDGKNFKDITDLINNTFIR |

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|------------|--|--|---|
| | | | TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD LPFHPLTQMYSPOQNSDYLLALSTENGLWVSKNFGGKWEIHK VCLAKWGSNDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDDQGTWSMAQLP SVGQEQQFYSILAANDDMVFMHVEPGDTGFGTIFTSDDRGIVYS KSLDRHLYTTTGGGETDFTNVTSLRGVYITSLSEDSIQITMITF DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP MAPLSEPNAGVIVIAHGSVGDAISVMVPDVYISDDGGYSWTMML EGPHYTILDSGGIIAIEHSSRPINVIKFSTDEGQCQWQTYTTF RDPYFTGLASEPGARSMNISIWGFTEFLTSQWVSYTIDFKDI LERNCEEKDYTIWLAHSTDPEYEDGCILGYKEQFLRLKSSVC QNGRDYVVTQPSICLCSLEDFLCDFGYRPPENDSKCQEPEL GHDLFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVLDLKKK CTSNFLSPEKQNSKNSVPIILAIVGLMLVTVVAGVLIVKKYVC GGRLVLHLYSVLQQH\AEA\NGVDGVDALDTASHTNKGHYHDDS DEDLLE |
| 5982 | 56 | 2316 | ATRPGRSSWCRQFSRTASAPGRSNMLRI PVRKALVGLSKSPK GCVRTTATAASNLIIEVFVDGQSVMEPGTTVLQACEKVGMIIPR FCYHERLSVAGNCRMLVEIEKAPKVVAACAMPVMKGNILTNS EKSKKAREGVMEFLANHPDLCPI CDQGGECDLQDQSMFQNDP SRFLEKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD LGTTRGRNDMQVGTIYEKMFMSLSGNIIDICPVGALTSKPYAF TARPWETRKTESIDVMDAVGSNIIVSTRTGVEVMRILPRMHEDIN EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV AGMLQSFQGDVAAIAGGLVDAEALVALKDLNLNRVDSDTLCTEB VFPTAGAGTDLRSNYLLNTTIAGVEEADVLLVGTNPRFEAPLF NARIRKSWLHNDLKVALIGSPVDLTITYDHLGDSPKILQDIASG SHPFSQVLKEAKKPMVVLGSSALQRNDGAAIILAUVSSIAQKIRM TSGVTGDWKMNIHLRIASQVAALDLGYKPGVEAIRKNPPKVLV LLGADGGCITRQDLPKDCFIYQGHGVDVGAPIADVILPGAAYT EKSATYVNTGRAQQTKVAVTPPGLAREDWKIRALSRAGMTL PYDTL\DOVRNRLEEVSPLVRYDDIEG\ANYFQQANELSKLVN QQLLADPLVPPQLTMKDFYMTDSISRASQTMACKVAVTEGAQA VEEPSIC |
| 5983 | 248 | 1763 | EARGDGGRRRRHRASRRRAGRGEF\AGLKSQGGRAVFKRAVARGG RQ\YSAALALEPAGSEIADDDLSILYSNRAACYLKEGNCSGCTQ DCNRALELHPFSMKPLLRAMAYETLEQYKAYVDYKTVLQIDC GLQLANDSVNRLSRILMELDGNWREKLSLIPAVPASVPLQAWH PAKEMISKQAGDSSSHRQGGITDEKTFKALKEBGNQCNDKNYK DALSKYSECLKINNKECAIYTNRALCYLKLQCFEAKQDCDQAL QLADGNVKAFYRRALAHKGLKNYQKSLIDLKLVILLDPSII EAK MELEEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPPGRPA GEVSTGLASEKGGKSSRPEDPEKLP IAKPNNAVEFGQIINAL STRDKKEACAHLLAITAPKDLPMFLSNKLEGDTPLLLIQSLKNN LIEKDPSLVYQHLLYLSKAERFKMMLTLISKQKELIEQLFEDL SDTPNNHFTLEBDIQALKRQYEL |
| 5984 | 755 | 1193 | SSVCMACTYVSNLGGKQRSVSFLASGLMRVSTGPFLRLHHSFVL TGDVGRRICRLVLGLFTKGTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTORSTVFVWQRCSLVGPFQVTVFTMY FHHSLSRSIRFSSG |
| 5985 | 22 | 1408 | RRVARPGTAEPFAKARRTVRRGRARRDLACAERKAGVSEBGDSGR RRPNPSPSAAGMSHIQIPPLTELLQGYTVEVLRRQPPDLVE FAVEYFTRLREARAPASVLPATPRQSLGHPPEPGPDRVADAK GDSESEDEDEDLEVPVPSRFNRRVSVCAETYNPDEEEDTDPRVI HPKTDQRCRLQEAACKDILLFKNLQEQLSQVLDAMFERIVKAD EHVIDQDDGDNFYVIERGTIDILVTKNQTRSVGQYDNRGSGF ELALMYNTPRAATIVATSEGSWLGLDRVTFRRIIVKNNAKRRKM FESFIESVPLLSLEVSERMKIVDVIGEKIYKR/DGERIITQGE K\ADSFYIIESGEVSIILRSRTKSNKDGNGQVEIARCHKQGYF GELALVTNKPRASAYAVGDVVKCLVMDVQAFERLLGPMCDIMKR NISHYEBQLVKMFGSSVDLGNLQ |

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|------------|--|--|---|
| 5986 | 1806 | 484 | DAWKSTSLTFHWKLGRRHRRGLAHPKNHLSPOQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPVPSPGPPMEED GLRWTFKSPLDPSGLLSCITLPGNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDDLGMMAEEAERPGEK\AQHSPRLRE EHVTCVQSILDEFLOT\YGSILPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHLVTMDLGLTYG QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFF\DKLRTKGYDG VWRWTKNVDIFNKELELLPIHLEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLAQEAVKDRDLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSTQDMPKLRQIYKELCHCKL TV |
| 5987 | 1806 | 484 | DAWKSTSLTFHWKLGRRHRRGLAHPKNHLSPOQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPVPSPGPPMEED GLRWTFKSPLDPSGLLSCITLPGNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDDLGMMAEEAERPGEK\AQHSPRLRE EHVTCVQSILDEFLOT\YGSILPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHLVTMDLGLTYG QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFF\DKLRTKGYDG VWRWTKNVDIFNKELELLPIHLEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLAQEAVKDRDLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSTQDMPKLRQIYKELCHCKL TV |
| 5988 | 1292 | 410 | FKYFSLFGLLESSHSRDRHNLVLMFLATHNLVWVFTCRFQ RLDCIYNAGIMPNPQLNIKALLFGLFS\ABGLLTQGDKITADG LQEVFETDVFHGFILIRELEPLLCHSDNPSQLIWTSSRNARKSN FSLEDFQHSKGEKYSSSKYATDLSVALNRNFNQQLYSNVAC PGTALTNLTGILPPFIWTLMPAILLLRFPANAFTLTPYNGTE ALVWLFHQKPSLNLPIKYL SATTGFRNYIMTQKMDLDEDTAE KFYQKLELEKHIRVTIQTNDQARLSGSC |
| 5989 | 194 | 2610 | AMDFFQHSQHVLEQLNQQRQLGLLDCDTFVVDGVHFAKHAVALA ACSEYFKMLFVDQDVVHLDISNAAGLGQVLEFMYTAKLSLSP NVDDVL\AVATFLOQMODIITACHALKSLAEPATSPGNAEALAT EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPRDLKEERGGQQAQ SAASGAEQTEKADAPREPPVELKPDPTSGMAAAEAALSESS EQEMEVEPARKGEEBQKEQEEQEEGAGPAEVKEGGSQLENGEA PEENENEEASAGTDSQELGSEARGLSRGTYGDRTESKAYGSVH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLKPYGCEECGKSYRLISLLNLRKRHSGEARYRCED CGKLFTTSGNLKRHLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKNQVGNLKAHLKIHADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG EKPCQCVMCQKAPTQASSLIAHVQRHTGEKPYVCERCGRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLKHI IHTGEKPY LCDKCGRGFNRVDNLRSHVKT VHQKAGIKILEPEEGSEVSVVT VDDMVTLATEALAAATAVTQLTVPVGAATADETEVLKAEISKA VKQVQEEEDPNTHILYACDSCGDKFLDANS LAQHVR IHTAQALVM FQTDADFYQQYGGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAE |
| 5990 | 2 | 4700 | FGPGPDSGGGARGSGWGRSQAPYGTLCAGVSGGEQVLLHEEAGD SGFVSLSRSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR FRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSI PDPF MHLACPEBEDKATAEAMVPAAGDESISSLSLVAMHPYCLPN LTHLASLEDELQEQPDDLTPLEGCVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDSSLETSSALQLLMPLESETAAVPKVT L CSEKEGLSLNSEELDSACLLKPREVVEPVVPKEPQNPANAAF GSQRARKGRKKKSKQPAACVEGYARRLRSSSSRGQSTVGTETS QVDNLQKQPQEEELQKESGPLQKGPRAWARAWAAALENSSPFN LERSAGQSSPAKEGPLDLYPKLADTIQTNFIPTHLSLVDSQAS PMPVDSVEADPTAVGPVLGVPVDPGLVDLASTSSSELVEPLPA EPVLINPVLADSAAVDPAVVPISDNLPVDAVPSGPAPVDLALV |

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|------------|--|--|---|
| | | | DPVPNDLTPVDPVLVKSRTDPRRGAVSSALGGSAPQLLVESES LDPPKTI IPEVKEVVDLSKIESGTSATTHEARPRPLSLSEYRRR RQROAETEERSQPPTGKWPSPETPTGLADIPCLVIPPAPAK KTAQRSPETPLEICLVPGSPASPSPEPPVSKPVASSPTEQV PSQEMPLLARSPSPVQSVPAVPTPPSMSAALPPFAGGLGMPPS LPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP CLPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPSYSTCTY GPLGWGPGQHPFWSVTVPPLPPASIGRAVPQPKMESRGTPA GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKVPVPASPHPK HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETOETRPRE KPPLPATKAVPTPRQSTVPKLPVHPARLRKLSFLPTPRTQGSB DVVQAFISEIGIEASDLSLLEQFEKSEAKKECPPAPADSLAV GNSGGVDIPQEKRLDRLQAPELANVAGLTPPATPPHQLWKPLA AVSLLAKAKSPKSTAQEGTLKPEGVTEAKHPAAVRLQEGVHGGS RVHVGSGDHDYC\VRSTPPKK\MPALLIPEVGSRWNVKHKQDI TIKPVLSLGPAAPPPCIAASREPLDHRSTSEQADPSAPCLAPS SLLSPEASPCRNDMNTPTPEPSAKQSRMRCYRKACRSAPSSQ GWQGRGRNSRSVSSGNSRTSEASSSSSSSSSSSSSSSSSSSS HKRWRSSSCSSSGSRRCSSSSSSSSSSSSSSSSSSSSSSSSSS PSPRRSRDRRRYSYRSHDYQRQVQLKERAIEERRVFIGK IPGRMTRSELKQRFVSGEIEECTIHFVRVQGDNYGFVTTYRYABE AFAAIESGHLRQADEQPFDLCPGGRQFCRKSYSDLDSNREDF DPAPVSKPDSLDFTLLKQAQKNLRR |
| 5991 | 334 | 1379 | RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTLEYQELGLQAR DLRFPQVMSITVRNNRIIMRMEYLKAVITPBCILLIDYRNLNLK QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQWINTLQGGK SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI KIFKESILEILDEELLEELCVSKWSDPQVFEKSSAGIDHAEM ELLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM RLNLQLTMGTFSLSLFGMLGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGIVGELG |
| 5992 | 2 | 609 | AGPDFRLVCGVSGSGFPGGRQGGQATEWRPLRPWNGAMEKLRRVL SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFACFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKMFATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYLSYIPYARDAVIKCCSSLLS |
| 5993 | 1650 | 594 | AEGLSWAVWAGLWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMPQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPTAIREISLLKELKHFNIVRLLDVVHNRKLYLVFEFLSQ DLKYMSTPGSELPLHLIKSYLFQLLQGVSPCHSHRVIHRDLK PQNLLINELGAIKLADFLARAFGVPLRTYTHEVVTWLYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRMLGTPSEDTPWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLMLQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLRFRH |
| 5994 | 394 | 1934 | AGEVQLHVWIRGMRIQPO/KAAAIIDLDPDFEQSRPRSCWPL PRPEIANQFSKPEVEPDLGEKVHTEGRSEPIILLPSRLPEPAGG PQPGILGAVTGP RKGGSRNNAWGNQSYAELISQAIESAPEKRLT LAQIYEMVVRTVPYFKDKGDSNSSAGWKNSIRHNLHLHSKFIVK HNEATGKSSWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNRREADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEIIPASVSSYAGGVPTT LNEGLELLDGLNLTSSSHLSLSRGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTOVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPTTEAASQDRMPQDLDDMY MENLECDMDNIISDLMEGEGLDFNFEPDP |
| 5995 | 2 | 2437 | RPPGPGPAGAWLCTRARGSAFVFPPLPRPPSRGARRRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSSREERGAAAAA AEMMEELHSL\DP\RRQELLFAF\TGLGVSKGPLNSESNSQL CSVGSLSDKVETPEKKQNDQRNRKRKAEPYETSQKGTPRGHK |

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|------------|--|--|---|
| | | | ISDYFERRVEQPLVGLDGSAAKEATEEQSALPTLMSVMLAKPRL DTEQLAQRGAGLCFTFVSAQQNSPSSSTGSGNTEHSCSSQKQIS I QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLRANCCLR RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD KSMQDRRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQRINSQ REEIERQRKMLAKRKPAMGQAPPATNEQKQRKSKTNGAENETL TLAEYHEQEEIFKLRGLHLKKEAEIQAELERLERVRNLHIREL KRIHNEDNSQFKDHPTLNDRYLLHLHLGRGGSFSEVYKAPDLTEQ RVVAVKIHQLNKNWRDEKKNYHKKACREYRIHKELDHPRIVKL YDYFSLDTSDFCTVLEYCEGNDLDFYLLKQHLKMEKEARSIMQ IVNALKYLNEIKPPIIHVDLKPKNILLVNGTACGEIKITDFGLS KIMDDDSYNSVDGMELTSQAGAGTYWYLPPECFVVGKEPPKISNK VDVWSVGVIIFYQCLYGRKPPFGHNQSQDILQENTILKATEVQFP PKPVVTPEAKAFIRRCCLAYRKEDRIDVQQLACDPYLLPHIRKSV STSSPAGAAIASTSGASNNSSN |
| 5996 | 1612 | 981 | DQQAQLGLMLTLEFGILEFDPWSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDSCLY\ANQWQVSKPKDNPLNEGTASGRPSPPS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP |
| 5997 | 1612 | 981 | DQQAQLGLMLTLEFGILEFDPWSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDSCLY\ANQWQVSKPKDNPLNEGTASGRPSPPS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP |
| 5998 | 1612 | 981 | DQQAQLGLMLTLEFGILEFDPWSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDSCLY\ANQWQVSKPKDNPLNEGTASGRPSPPS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP |
| 5999 | 2 | 1790 | RPPMEKARRGGDGVPRGPVLHIVVGVFHHKKGCVFESYPLIP GDGHSHTLPEEWKYLPLFALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETQKSVCVLSKLPYLG LLOAKLQILITHAYFEEDKFSQISILKELYEHMNSSLGASLEGS QVYLGLSPRDLVLHFRHKGILILFKLILLEKKVLYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHNTLGTIRKVMAGNHGEDAAMKTEEPFQVEDSS KGEQPNDTNQYLKPPSRPSPDSESDWETLDPVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQHHLLSDVTVRGFVAGATNI LFRQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGEGGDEWIRAQFAVYIHALAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLETPPEDEKP |
| 6000 | 101 | 1561 | TEPCRTAENCTATMSENNKNLSLESSLRQLKCHFTWNLMGENSL DDPEDKVFYRTEFQNRFEKATMCNLLAYLKLKGQNEAALECLR KAEELIQEHAHQAEIRSLVTWGNAYVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPDLCEEGWTRLCGCGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNDP NQYLKVLALKLHKMREEGEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKATIELLKALEYIP\NNAYLHCQIGCCY RAKVPQVMNLRENGMYGKRKLELIGHAVHLKKADEANDNLFV VCSILASLHALADQYEDAEYFFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHFFIEGVKINQKSREKEKMKDKLQKIAKMR L SKNGADSEALHVLAFQLNEKMQQADEDSERGLESGSLIPAS SWNGE |
| 6001 | 176 | 1038 | AFASPSRGRHRTHTHTPRHTPRCTMAESHLQSSSLITASQFBEI WLHFDADGSGYLEGKELQNLIELQQAARKAGLEBSPMKTFVD QYQQRDDGKIGIVELAHVLPTEENFLLLFRQQLKSC\EFMKT WRKYDTHDSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM |

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|------------|--|--|---|
| | | | LKLFDSNNDGKLELTEMARLLPVQENFLKKFQGIKMGKEFNKA FELYDQDGNQYIDENELDALLKDLCEKNKQDLINNITTYKKNIM MALSDGGKLYRTDLALILCAGDN |
| 6002 | 977 | 81 | LAPPGGGLHIIPRTPPLSHSREPPSHHAPHSPPLPLPPADLHPHS SMAQRSDLELDCQLTRDRVVVSHDENLCROSGLNDRDVGSLDF EDLPLYKEKLEVFYFSPGHFAHGSDDRMVRLLEDLFQRFPRTPMSV EIKGKNEELIREQ/VLVRVYDRNBITIWASEKSSVMKKCKAANP EMPLSFTISRGFVWLLSYLLGLLPFIPIPEKFFFCFLPNIIINRT YFPFSCSCLNQLLAVSKWLMRKSLIRHLEERGQVVFVWCLNE ESDFEAAFSVGATGVTIDYPTALRHYLDNHGPAARTS |
| 6003 | 140 | 4098 | GKLAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP APKTSNPNANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIPTLFLNLPNSAKVMATSGCAAIRFII RHTHVPRLLIPLITSNCTSKSVPVRRRSFEFLDLLQEWQTHSLE RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKSSGVSASLPQSDRSSSSSQESLNRPFSS KNSTANPSTVAGRVSAAGSSKASSLPQSLQSRSDIDVNAAGAG AHHAAGQSVRSRGLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQVRVLVNSASAQKRSKIPRSQCSREASPSRLSV ARSSRI PRPSVSQGCSEASRESSRDTSPVRSFQPLASRHHRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSAC SERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVSFMLETLVDFI QVHKDDLQDWLFVLLTQLLKKMGADLLGSSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPLSKVKVAILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP RSPANWSSPLTSPNTSNTLSPSAFDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPLKRD SKKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTSHSSPRSRDYNPNYSDSIS PFNKSAKKEAMFDDDDAQFPDDLSDHSDLVABLLKELSNHNER VEERKIALYELMKLTQESFSVWDEHFKTILLLLETGLDKEPT IRALALKVLEIREILRHQPARFKNYAELTMKLTLEAKDPHEVVR SAEEAASV\LATSI\SPBQCIVLCP I IQTADYPINLAAIKMQT KVIERSVKETLNLNLLPEIMPLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTT DVS GQS |
| 6004 | 140 | 4098 | GKLAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP APKTSNPNANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIPTLFLNLPNSAKVMATSGCAAIRFII RHTHVPRLLIPLITSNCTSKSVPVRRRSFEFLDLLQEWQTHSLE RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKSSGVSASLPQSDRSSSSSQESLNRPFSS KNSTANPSTVAGRVSAAGSSKASSLPQSLQSRSDIDVNAAGAG AHHAAGQSVRSRGLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQVRVLVNSASAQKRSKIPRSQCSREASPSRLSV ARSSRI PRPSVSQGCSEASRESSRDTSPVRSFQPLASRHHRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSAC SERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVSFMLETLVDFI QVHKDDLQDWLFVLLTQLLKKMGADLLGSSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPLSKVKVAILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE |

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|------------|--|--|--|
| | | | FTMLLGALPKTFQDGATKLLHNLRLNTGNGTQSSMGSPLTRPTP RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTTHSSPRSRDYNPNYSDSIS PFNKSALEAMFDDDDAQFPDDLSDHSDLVAEALLKELSNHNER VEERKIALYELMKLTQEESFVSVDHFKTILLLETLGDKPEPT IRALALKVLRILRHQPARFKNYAELTVMKTLAHLKDPHKEVVR SAEEAASV\LATSISPEQCIKVLCPITQADYPINLAIAKMQT KVIERSKETLNLLEPEIMPGLIQGYDNSESVRKACVFCVLAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS |
| 6005 | 133 | 5955 | RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEDMDALL NNSLPPHPENEEDPEEDLSETETPKLKKKKPKKPRDPKIPKS KRQKKERMLLCRQLGDSSGEGPEFVEEBEEVALRSDSEGSYTP GKKKKKLGPKKEKKS KSKRKEEEEDDDDDSKPKSSAQLL EDWGMEDIDHVFSEEDYRTLTYKAFSQFVRPLIAKNPKIAVS KMMVLGAKWREFSTNNPFGSSGASVAAAAA AVVVESMVTA TEVAPPPPPVEVPIRAKTKEGKGNARRKPKGSPRVPDAKKPK PKKVAPLKIKLGGFGSKRRSSSEDDDLVDSEDFDASINSYSV SDGSTSRSSSRKKLRRTTKKKKKGEEVTAVDGYETHQDYCEV COQGGEIILCDTCPRAYHMCVCLDPMEKAPEGKWSCPHCEKEGI QWEAKENDSEGEIILREVGGDLEEDDHMEFCRVCKDGGELL CDTCPSSVHIHCLNPLPEIPNGEWLCPRCTCPALGKVKQKILI WKWGQPPSPPTPVPRPPDADPNTSPKPLEGRPERQFFVKWQMS YWHCSWVSELQLELHC\QVMFRNYQRKNDMEPPSGDFGGDEEK S\RKRKNKDPKFAEMBERFYRYGIKPEW\MMIHRILNHSVDKKG HVHYLIKWRDLFPYDQASWESEDVEIQDYDLFKQSYWNHREL MRGEEGRPGKLLKVKLRKLERPPETPTVDPVTKYERPEYLDATGG TLHPYQMEGLNWLRFSAWQGTDTILADEMGLKTVQTAFLYSL YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGD DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE LITIDMAILGSDWACLIVDEAHLKNNQSKFFRVNLNGYSLQHK LLLTGTPLQNNLEELFHLNFLTPERFHNLEGFLEEFADI QIKLHDMLG\PHMLRRLKADVFNMPKSTELIV\RVLSPM\Q KYYK\YILHSKFLKALN\ARGGGNQVSLNVMDLKCCNHPY LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSQMTKMLDLEDLEHEGYKYERIDGGITGNMRQEAID FNAPGAQQFCFLSTRAGGLGINLATADTVIYDSDNPHNDIQ AFSRAHRIGQNKVMYIRFVTRASVEERITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED SSVIHYDDKAIERLLDRNQDETETELQCMNEYLSSEFKVAQYVV REEEMGEEEEVEREIIKQESVDPDYWEKLLRHVYEQQEDLAR NLGKGKIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE DFDERSEAPRRPSRKLNDKDKPLPPLARVGGNIEVLGFNAR QRKAFLNAIMRYGMPQDAFTTQWLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGAETPADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFEHVNGRWSMPELAEEVENKMSQPGSPSPKTPPTSTPGDTQP NTPAPVPPAEDGIKIEENSLKEESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEKVEKAEVKERTTEPEMETEPKGGK AADVEKVEEKSAIDLTPIVEDKEEKEEKEEKEVMLQNGETPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT YEIWHRRHDYWLLAGIINHG YARWQDIQNDPRYAILNEPFGEM NRGNFLEIKNKFLLARRFKLLEQALVIEQLRRAAYLNMSDPSH PSMALNTRFAEVECLAESHQHLSESMAGNKPANAVLHKVLKQL EELLSDMKADVTRLPATIARI PPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ |
| 6006 | 1 | 965 | DNDFLRNTVHRHPPVTAEPILRLAENEDVVVVDKPSIPVHPC GRFRHNTVIFILGKEHQLKBLHLPLHRLDRLTSGVLMFAKTA AVS ERIHEQVRDRQLEKEYVCRVEGEFPTEVTCKEPILVVSYKGV CRVDPRGKPCETVFQRLSYNGQSSVVR CRPLTGRTHQIRVHLQF LGHPI LNDPIYNSVAVGPPSRGRGGYIPKTNEELLRLDLVAEHQAK |

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|------------|--|--|---|
| | | | QSLDVLDLCEGDLSPGLTDSTAPSSSELGKDDLEELAAA\QKME EVAAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG SLAPRPCDVPTCPTL |
| 6007 | 3 | 2351 | HELQVEYVFTDKTGLTENEMQFRECSINGMKYQEINGRLVPE GPTPDSSEGNLSYLSLNLNLSHLTSSSFRTSPENETELIK EHDLFKAVSLCHTVQINNVDCTGDGPWQSNLAPSQLEYVAS SPDEKALVEAAARIGIVFIGNSEETMEVKTGKLERYLHLILE FDSRRRMSVIVQAPSGEKLFLAKGAESSILPKCIGGIEKTRI HVDEFALKGLRTLCLAIYRKFTSKEYEIDKRIFEARTALQQR\B EKLAADVQFIEKDLILGATAVEDRLQDKVRETIEALRMAGIKV WVLTGDKHETAVSVLSGCHFHRTMNILELINQKSDSBCAEQLR QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV LCCRMAPLQKAKVIRLIKISPEKPI TLAVGDGANDVSMIQEAHV GIGIMGEGRQAARNSDYAIARFKLSKLLFVHGFFYYIRIATL VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLYNICFT SLPILYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT ILGFSAHIFFFGSLILIGKDTSLGNGQMFGNWTGTLVFTVM VITVTVMALETHFWTWINHLVTWGSIIFFVFSLFYGGILWPF LGSQNMVFFVFIQLSSGSFAFILLMVVTCFLFDI IKKVFDRLH HPTSTEKAQLTETNAGIKCLDSMCCFPGEAACASVGRMLERVI GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSC |
| 6008 | 4554 | 1089 | AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPAPEHAGPAR ASRPSQETMPQLPVNMLGSLRKARKTVKKILSDIGLEYCKEHIE DFKQFEPNDFYLNKTTWEDVGLWDPSTLKNQDYRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLEYIVRKHIYREHFQHVAAPIAKAGEKSLNGAVPLG SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG HTNVVVRPSKPLMLIAPKPDKKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPKPNLSTGVNMMSSVHLQNNYGVKSQVGGYSV GQSMRLGLGGNAPVSI PQQSQSVKOLLPSGNGRSYGLGSEQRSG APARYSLQSANASSLSSGQLKSPSLSQSASRVLGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFKEKHAEKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHLIHGLSCPYCRS TFNDVEKMAAHMRMVHIDEEMGPKDSTLSFDLTQQGSHTNIH LLVTYTNLRDAPAESVAYHAQNPPVPPKPKQKVEKADIFVKS SPQAAVYPYKDVGKTLCPCLFSLKGPISDALAHLRERHQVIQ TVHPVEKKLTYSKIHCLGVYTSNMTASTITLHLVHCRGVGKTNH GQDKTNAPSRNLQSPSLAPVKRTYEQMEFFLLKKRKLDDSDSP SFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPY TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVDRCEKYKPGVL LGFNMKELNKKVHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNESGSPFDPVFEVEPKISNDNPEBH VLKVIPEDASESEKLDQKEDGSKYETIHLTEPTKLMHNASDS EVDQDDVVVEWKDGASPSGPGSQVSDFEDNCEMKPGTWSDE SSQSEDARSSKPAKKKATMQGDREQLKWNSSYGVKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDEQFDNMTDGVAE MHGSLAGVKLSSQQA |
| 6009 | 4272 | 1534 | CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEEKSIC*GSPSC HLVLGVLPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNFPIQRPLVMKGRRIMCGKCEK*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEVVPFVEGQLVTVLGLVVPQSIRHTFVHTQLFLHP I*KLGA LDVAFLLHLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDMVMAGADVQVQW DPFVVGLAGIFHLIDDPHQIELSFQRRV*EQCQGVKPDSPVP RPLRVGLLQVGPLVRGGRRVAGRGKRCWRDLFPWRWGLSHRT RDLLRGGDRGHVVIVLCRLGSLVGGGTDELLWFGGR*LIIG |

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|------------|--|--|---|
| | | | I**RGRLSGEWGCGLGRGELFQVSIIGVSIHVIGQGDHEVLGG AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP GRVGQLPAEGLQVCITLVAQWRMHGRELGGAEWPWQALHGAAI CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR R*NGLTTHCFN*LI*GAVCCRLVILRWCGLLVHGVYGT*IHCL GSFPGRLLWP*PFISQERPNGHCQWELRALVPSWKCRWSRWRVGR TWRYGNPLNLL*GAWLGGAACGGQGGPLSTWQACTGPGQAAAF LPPFGAGACRPRTQRCRTWVCFIAWRQLLAYTRD |
| 6010 | 1 | 3533 | IMPCGSSRLRLGCVTHPNEPVSDDLSTYFDCIESVMENSKVLGESH AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDSEDNRNKCRITAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAASVQSLATRDDISVEALQEQLTSSVQIEIGHLIDP IATAARGEAAQLGHKGTQLASYFPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHIAFQGMMAATAEPPEEIGFQIRTRVQDLGHGCIPLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSILVLSALQAGNKGTOACI TAATAVSGIIADLDTTIFATAGTINAENSETFADHRENILKTA KALVEDTKLLVSGAASPDKLAQAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLKTKVKADEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSPEESIRMTKGITMATAKAVAAGNSCRQE DVIATANLSRKAVSDMLTACKQASFPDVSDEVTRALRFGTEC TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA EAMKGTENWDPEDPTVIAETELGAAASIEAAKKLEQLKPRK PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQK VGSIPANAADDGQWSQGLISAARMVAATSSLCEANASVQGH SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAGKADDDVVVKTKFVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREDEG |
| 6011 | 446 | 1835 | LLQFAMRKSPGLSDCLWAWILLSTLTGRSYGQPSLQDELKDNT TVFTRILDRLLDGYDNRRLRPLGLGERVTEVKTIDIFVTSFGPVS DMEYITIDVFFRQSWKDERLKFKGPMTVLRNLNLMASKIWPDTF FHNGKKSVAHNMTMPNKLRLITEDGTLTYMRLTVR\AECPMF GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWREPARSVVVAED GSRNLQYDLLGQTVDSGIVQSSSTGEYVVMTHFHLKRIKGYFVI QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMITLSIS ARNSLPKVAYATAMDWFLAVCYAFVFSALIEFATVNYFTKRGYA WDGKSVVPEKPKKVDPLIKKNNTYAPTATSYTPNLARGDPGLA TIAKSATIEPKEVKPETKPEPKKTFNSVSKIDRLSRIAPPLLF GIFNLVYWATVYLNREPQLKAPTPHQ |
| 6012 | 351 | 5013 | PAELFQSFATWHKELYDWRIGPWNQCQPVISKSLKPLECICKGE EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLI PCQD CIVSEFSAWSECSKTCGSLQHRTRHVAPPQFGSGGCPNLTEF QVCQSSPCEAEELRYSLHVGWSTCSMPHSRQVRQARRRGKNKE REKDRSKGVKDPARELIKKNRNRRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQKEKLPMTFQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVTRTIRQFPFIGSEKECFEKEPECLS QGDGVVPCATYGWRTTEWTECRVDPPLSQDKRRGNQALCGGG IQTRREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNNT QLCHIPCPTCEVSPWSANGPCTYENCNDQGGKGFKLKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPCYDVKAVRLGDCPEPDKG ECGPGTQVQEVVVCINSDDGEVDRQLCRDAIFP IPVACDAPCPK CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRS CNEHPCTVYHWQTGPWQGCIEDTSVSSFNNTTTW NGEASCSVMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL |

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|------------|--|--|--|
| | | | PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVITQLPAN GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS VQQDSP\GAQEGCGPGRQARAITCRKQDGGGAGIHECLQYAGPV PALTOACQIPQDDCQLTSWSKFSSCNGDCGAVRTRKRTLGVKS KKKECKKNSHLYPLIETQYCPCKYNAQPVGNWSDCILPEGKVE VLLGMKVQGGDIKECGQGYRYQAMACVDQNGRLVETSRCSNHGYI EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLEKPYN GGRPCPKLDHVNQAQVYEVVPCSDCNQYLWVTEPWSICKVTPV NMRENCGEVQTRKVRMCQNTADGPSEHVEDYLCDEEMPIGSR VCKLPCPEDCVISEWGPWTQCVLPQNSQSSFRQSRADPIRQPADE GRSCPNAVEKEPCNLNKNCHYDYNVTDWSTCQLSEKAVCGNGI KTRMLDCVRS DGKSVLDKYCEALGLEKNWQMNSTCMVECPVNCQ LSDWSPWSECSQTCGLTGKIMIRRTVTQPPQGDGRPCPSLMDQS KPCPVKPCYRWQYQWSPCQVQEAQCGEGTRTRNISCVSDGSA DDFSKVVD BEFCADIELIIDGNKNMVLBSCSQPCPGDCYLKDW SSWSLQCLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCEQML ETKSCYDGGQCYEYKWMASAWKSSRTVWCQRSDGINVTGGCLVM SQPDADRSCNPPCSQPHSYCSETKTCHCEGYTEVMSSNSTLEQ CTLIPVVLPMTEDKRGDVKTSRAVHPTQPSNPAGRGRTWFLQ PFGPDGRLKTWVYVGAAGAFVLLIFVSMIYLACKKKPKPQRRO NNRLKPLTLAYDGDADM |
| 6013 | 1161 | 710 | GAFIAGVPVQPVLIIRYPSNLDTTSAWARGPGVLKVLWLTASQPC SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE FVGSLPVIIVGRLKVALEPQL/WGTGKSASEGWA VRWL CGRWGR ARPESNDQPGRVCCQATAL |
| 6014 | 2857 | 613 | EAVAGGMEKSRMNLPGPDTLCPDKDEFMKEDFBDVDFVSDCRK RVQLEELRDDLELYKLLKTAMVELINKDYADF\VNLSNVLVGM DKALNQLSVPLGQLREEVLSLRSSVSEGI RAVDERMSKQEDIRK KKMCVLRILIQVIRSEKIEKILNSQSSKETSALAEASSPLLTGQI LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE GLLLEGLQTSDDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI DEVII EQFVESH?NGLQVMYNKLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLPISLFNPGNPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWD EMFLPLLVRHLWRLHSGRFWARYSVFV\N\ELSLRPISNESPK IKKPLVTGSKEPSITQGNTEQSGSPSETKPVVSISRTQLVYVV ADLDKLEQLPELLEIIPKLEMIGFKNFSSISAAEDSSQSSFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFLQLQSGHKDKLQAIQQWLBGTLESTHKYYET VSDVLNSVKMEESLKRKLQARKTTPANFVPGSGGMSDDDKIRL QLALDVEYLGEIQKLGLQASDIKSFALAEVLAAKQATAEQ P |
| 6015 | 13 | 2237 | AEGCAERRGTEPVVELSMSWESGAGPGLGSQGM DLVWSAWYGK VKGKGLPLSAHGIVVAWLSRAEWDQVTVYLP CDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGTDELRLLY GMALVRFVNLI SERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRCYFVLDWLQKTYWCROLENSLRETWELEEF EGIEEDQEEDKNIVDDITEQKFPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVS YEEEEQFTVLEKFRYLP KAIKAWNNSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVLDNDVLVPKPFQFWQFLRLGLHSQNFQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSFSGSEAKAQQEEQGSVNDVKEEKE EKEVLPDQVEEEEENDDQEEEEDEDEDDEEDRMEVGPFTSG QESPTAENARLLAQKRGALQGS AWQVSSSEDVRWDTFF\LGRMP SRPRTPAELMLENYDTHVIFWTKPVL\EQRLPESTCK\TDTLGL \SCGVGS\GNCSNSSSNFRGAFLLBARGSLH\GL\KTGLQLF |
| 6016 | 13 | 2237 | AEGCAERRGTEPVVELSMSWESGAGPGLGSQGM DLVWSAWYGK |

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|------------|--|--|---|
| | | | VKGKGSPLPSAHGIVVAWLSRAEWDQVTVYLFCDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRLQENSLRETWELEEF EGIEBEDQEEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAEKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVDLNDVLVFKPFSQFWQPLLRGLHSQNFQ ALLERMLSELPAIGISGIRPTYILRWTVELIVANTKTORNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASQQLRLI F\KAMGQGLQDE\BQEKLLRISYITQSGENSLVQEGSEASP KSPYTLDSLYWSVKPASSSSFGSEAKAQQEEQGSVNDVKEEEE EKEVLPDQVEEEENDDQEEBEEDEDEDEDEDEDEDEDEDEDE QESPTAENARLLAQKRGALQGSAAQVSSSEVVRWDTFF\LRMP SRFRTPAELMLENYDTHVIFWTKPVL\EQRLPESTCK\TDITGL \SCGVGS\GNCSSSSSNFRGAFLEARGSLH\GL\KTGLQLF |
| 6017 | 203 | 3469 | SHQETEQNSAMAPKRKGGGSGISFIFCCFRNNDHPEITYRLRND NFALQTMPEPALPMPVEELDVMSSELVDELDTDKHREAMFALP AEKKWQIYCSKKKQDEENKGSATSWPEFYIDQLNSMAARKSLAL EKEEEERSKTIESLKTALRTKPMRFVTRFIDLGLSCILNFK TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLHSESINVIAQ SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQAGVESL DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE DELEFAKRFELVHIDTKSATQMFELTRKRLTHSEAYPHFMSILH HCLQMPYKRSQNTVQYWLDDRIQQIVIQNDKGQDPDSTPLEN FNIKNVVRMLVNEVEVKQWKEQABKMRKEHNELOQKLEKKEREC DAKTQKEEMMQTLNKMKEKLEKETTEHKQVKQVADLTAQLHE LSRRACASIPGGSPGAPGGPFSSVPGSLPPPPPPPLPGGM LPPPPPLPFGGPPPPPPGPPPLGAIMPPPGAPMGLALKKSIQ PTNALKSFNWSKLPENKLEGTWVTEIDDTKVKILDLDELRTF SAYQROQDFVNSNSKQKEADAIDDTLSSKLVKELSVIDGRR QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFPVE KSDIDLLEEHKHELDMAKADRFLFEMSRINHYQRLQSLYFKK KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLEVVLAFGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNLNEELRDIQAAKVNMTLEDKELSTLRSGLKAVETELEYQ KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEAGKIQPDFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDL SKLRNRKRITNQMTDSSRERPIITKLN |
| 6018 | 13 | 2510 | TISQSGGIRRRREAVWFEVVMDFSRHLMYSPPQCVPTGTY ALSSSYSSDALDFETHEKLDPVFDSPRMSRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSASF INHVSQV TSSGVSYGGTVSLQDAVTRRPVLDSEWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAAATGHNGFFCSN CNMLSERKDVLT AHPAAGPVSrvysrdRnQKCDCKGKRHLDAHPGRAGTLWHI ACAGYFLLQILRRIGAVGQAVSRTANSALWAVAPGKAASGVF WWLGIGWYQPVTLISWLVFLTRCLRNICKFLVLLIPLFLLLG LSLRGGQ\NFFSFPLVNLWASMHRTQVRDDPDQVFKPTTSRLKQ PLQGDSEAFPHWMSGVEQQVASLSGQCHHGENLRELTTLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHV RMS HLEDILGKLEKSEAIQKELEQTQKTI SAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREVMKLLFSD QGGSLQELLQRFSSQFVSKGDLQTMRLDLQLQLRNVTHHVS TKQLPTSEAVVS AVSEAGASGIT EAQARAI VNSALKLYSQDKTG MVDFALES GGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIIYPCNCAFKSGQGYLVVRLSMMIHPAAFTLEHI PKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQGESLQMF QALKRPDDTAQFIVELRIFSNWGHPEYTCLYRFRVHGEPVK |
| 6019 | 2 | 1066 | TPNDREPPQRPSSRRASHLAQEITSAASLGQDTQILGSLTTA |

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|------------|--|--|--|
| | | | PVITSAIRSMFGISSQILTNAQQQVIGTLPWVNSASVAAPAPA QSLQVQAVTPQLLNNAQQQVIATLASSPLPPVAVRK\ PSTPES LLKSEVQPIKPTPTVPQPAVVIASPAAPAKPSASAPIPTCSET PTVSQLVSKPHTPSLDEEDGINLEEIREFAKNFKIRRLSLGLTQT QVGQALTATEGPAYSAICRFEKLDITPKSAQKLPVLEKWLN EAEARNQEGQQNLMEFVGGEPSSKKRRRTSFTPAIEALNAYFE KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLVNF QIP |
| 6020 | 4953 | 549 | EAIQFEVSIIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYLWP AHTKPVVTLTSYWEDISHRLDAVNILLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEGEWIIVDPERSLLTEADAGHTEFTDEVYQNESRYP CGDWKPAEDTYTDANGDKAASPSELTCPPGWEDDAWSYDINR AVDEKGWEYGITIPPDHKKPSWVAEKMVHTHRRRLVRKRKLD LTQTASSTAGAMELQDQEGWEYASLIGWKFWKQRSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHA TTVFGANTPIVSCNFRDRYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTEIIHSTLNPTWDQTIIFDEVEIYGEPTVLQ NPPKVMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAFNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTNPFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALS KMAS PATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAFEGLT DFDSTFKLYRGKSDENEDPSVVGFEFGKSFRIYPLPDDPSVPAPP RQFRELPSVQPECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPFVFRMYELSCYLQEKDLKISVYDWD TFRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQFILSEDSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYLRLVIWNTKDVILDEKSI TGEEMSDIYVKGWIPGNEW NKQKTDVHYRSLDGEKNFNWRVFPFDYLPAEQLCIVAKKEHFV SIDQTEFRIPPR\LIQIW\DNCKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIWRRFKWVIIGLLELLILL LFVAVLLYSLPNYLSMKIVKPNV |
| 6021 | 4953 | 549 | EAIQFEVSIIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYLWP AHTKPVVTLTSYWEDISHRLDAVNILLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEGEWIIVDPERSLLTEADAGHTEFTDEVYQNESRYP CGDWKPAEDTYTDANGDKAASPSELTCPPGWEDDAWSYDINR AVDEKGWEYGITIPPDHKKPSWVAEKMVHTHRRRLVRKRKLD LTQTASSTAGAMELQDQEGWEYASLIGWKFWKQRSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHA TTVFGANTPIVSCNFRDRYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTEIIHSTLNPTWDQTIIFDEVEIYGEPTVLQ NPPKVMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAFNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTNPFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR |

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|------------|--|--|---|
| | | | <p>DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDTFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD TFTREKVGETIIDLENPF\LSRFG\SHCG\IPBEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRLVLIWNTKDVLDEKSIITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEENFNWRVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIQIW\DNCKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMI PDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIWVRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV</p> |
| 6022 | 4953 | 549 | <p>EAIQFEVSIIGNYGNKFDITCKPLASTTQYSRAVFDGNYYYLFW AHTKPVVTLTYSWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKI PANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLARI EDWLDKLMQLTE EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTGENASGKYC GKTQTI FLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKPSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLEADAGHTEFTDEVYQNESRY GGDWKPAEDTDTDANGDKAASPELTCPGWEWEDDAWSYDINR AVDEKGWEGYITIPPDHKKPSWVAEKMVHTHRRRLVRKRKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFWKQSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLKQKHA TTVFGANTPIVSCNFDYDIYHLRCVYQARNLLALDKDSFSDP YAHICFLHRSKTTEI IHSTLNPTWDQTI IFDEVEIYGEPTVLQ NPPKVI MELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLTABEILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNPQMASITSPSLVVECGGERV ESVVIKNLKKTPNPFSSVLFMKVFLPKEELYMPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDTFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD TFTREKVGETIIDLENPF\LSRFG\SHCG\IPBEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRLVLIWNTKDVLDEKSIITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEENFNWRVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIQIW\DNCKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMI PDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIWVRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV</p> |
| 6023 | 102 | 916 | <p>SQELGMFVELNNLNTTPDRAEQGKLTLLCDAKTDGSLVHHFL SFYLANCKVCVVALIQSFSSHYSIVGQKLGVSILTMARERGQLV LEGL/IVCSGR/VFQAQKEPHPLQFLREANAGNLKPLFEFVREA LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT VCWELKGNMVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF AKGMSPAVL</p> |
| 6024 | 3 | 3260 | <p>FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEAB LPAELFQKKVVASFPRTVLSTGMDNRYLVAVNTVQNKEGCEK RLVITASQSLNKKELCILRNDWCSVPVEPGDIHLEGDCTSDTW IIDKDFGYLILYPDMLISGTSIASSIRCMRAVLSETFRSSDPA TRQMLIGTVLHEVQKAINNSFAPEKLQELAPQTIQEIIRHLKEM</p> |

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|------------|--|--|---|
| | | | YRLNLSQDEIKQEVEDYLPSCFKWAGDFMHKNTSTDFPQMQLSL PSDNSKDNSTCNIEVVKPMDIEESIWSRPFGLKGKIDVTGVVKI HRGYKTKYKIMPLELKTGKESNIEHRSQVVLTYLLSQERRADP EAGLLLYLKTGQMPVPANHLDKRELLKLRNQMAFSLFHRISKS ATRQKTQLASLPQIIIEEKTCKYCSQIGNCALYSRAVEQQMDCS SVPVIMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN HQNILWMPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH GAIPVTNLMAGDRVIVSGEERSLFALSRLGYVKEINMTTVTCLLD RNLVSVLPSTLFRDLQEEKNCDIDTPLGNLSKLMENFTVSKKLR DLIIDFRPQFISYLSVLPDADKDTVACILKGLNKPQRQAMKK VLLSKDYTLIVGMPGTGKTTTICTLVRLIYACGFSVLLTSYTHS AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI KS\LALLEELYTSQLIDATTCMGINHPISRKIFDFCIVDEASQ ISQPICLGPLFFSRFVVLVDHQQPLPLVLNREARALGMSSELF KRLEQNKSAAVQLTQYRMNSKIMSLSNKLTIEGKLECGSDKVA NAVINLRHFDVKLELEYFADYSDNPWLMGVFEPNPNVCFNLTD KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPDIGIAP YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN KDGTVGELLKDWRRNLNVAITRAKHKLILLGCVPSLNCYPPEKL LNHLNSEKLIIDLPSREHESLCHILGDFQRE |
| 6025 | 3977 | 89 | GGFPAQSDHLPVPFPLRSDLLITMSTLYVGFHPDAFFSLRALIA ARYGEAGEGPGWGAHPRIQLQPPPTSRTSFPPRLPALEQGGPG GLVWVGATAVLAQLLWPAAGLGGPGSRAAVLVQVWSYADTELIP AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA GEAPTADLAAVTALLLPFRYVLDPPARRIWNVTRWFVTCVRQ PEFRAVLGEVVLVSGARPLSHQPGPEAPALPKTAAQLKKEAKKR EKLEKFOQKQKIQQQPPPGKKPKPEKREKRDGVIYDLPPTP PGEKKDVSGMPDSSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLEEVW KWKEEGDRIYHQLKGLSSLDWDRACTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRLLSVPG YKEKVEFGVLVSFAKVKVQGSDESDEEVVATRIETMLGDVAVAV HPKDTRYQHLKGNVIHPFLSRSLPIVFDEFVMDDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPFGLGLPRFEAR KAVLVALKERGLFRGIEDNPMVPLCNRSKDVVEPLLRLPQWYVR CGEMAQAASAAVTRGDLRLPERHQRTWHAMMDNIRE\WCMFPFG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGGRYVWSGRNEABARE KAAKEFGVSPDKISLQQDEVDLDTWPFSSGLFPLSILGWPNQSED LSVFYPTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNLNLSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINDVN RILGYRHFNCNLWNATKFAIRGLGKGFVPSPTSQPGGHESLVDR WIRSRLEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAACARQTLTYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGGP QAQVVVAEAPWGLPAP\QCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVP\LE VQEADEAKLQOTEAEELRKVDEAIALFQKML |
| 6026 | 2674 | 514 | GPITFLKKKAKMKDMLRIHVLLGLAITTLVQAVDKKVDPCRLC TCEIRWFPTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTPEKCLSELSNLQELYINHNLLSTISPGAFIHLN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVLENLESISFYDNRLIKVPH VALQVVNLKFLDLNKNPINRIRRGDFSNNLHLKELGINNMP ISIDSLAVDNLPDLRKIEATNPNRLSYIHPNAFFRLPKLESML NSNALSALYHGTIESLPNLKEISHSNPIRCDCVIRWMNMNKT IRFMEPDSLFCDVPPFPQGGQNVQVHFRDMMELCLPIAPESFP SNLNVEAGSYVSFHCRTA\EPQPEIYWITPSGQKLLPNT\LTD |

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|------------|--|--|---|
| | | | KFYVHSEGLTDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG SFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVK TENSAAQASARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS CLSPMNCDGGHSYVRNVLQKPTFALGELYPPLINLWEAGKEKS TSLKVKATVIGLPTNMS |
| 6027 | 5254 | 4148 | GGRRAPGRGRSIRKDEEBETVFEVVSFSPDPLPVRYDKDITTK PISFYLSLEELLAWKPRLEDGFNVALEPLACRQPLSSQRPRT LLCHDMMGYLLDRFIQGSVVQTFYAFYHWQCIDVFVYFSHTV TIPFVGWNTAHRHGVCVLGTFITWNEGGRLCEAFLAGDERSY QAVADRLVQIT\RFRRFDGWLINIENSLSLAAVGNMPPFLRLYT TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRFVFDSCDGF FTNYNWRREEHLERMLGQAGERRADVVGVDVFARGNVVGGRFDT DKVGGGFRPRASGFPVPLGPHFLMDLFFPSAPQRNDSSCSSQSG DPVALNRNCPAPAKLCPH |
| 6028 | 120 | 3432 | NCLLLQAKGFHGETEDLQOWLTDTERRHLLASKPLGGLPETAKEQ LNVHMEVCAAFEAKEETYKSLMQKGQMLARCPKSAETNIDQDI NNLKEKWESEVETKLNER\KT\KLEELNLA\MEFHNSL\QDPIN WLTQAEQTLNVA SRPSLILDTVL FQIDEHKVFANEVNSHREQUI ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVQRLVERGR SLDDARKRAKQFHEAWSKMEWLEESKSLDSELEIANDPDKIK TQLAQHKFEQKSLGAKHSVYDTNRTGRSLKEKTSLADDNLKLD DMLSELDRKWDITCGKSVERQNKLEEA\LLFSGQFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ ALKRSARELIEGSRDDSSWVKVQMQLSTRWETVCALSISKQTR LEAALRQAEFEHVSVHALLLEWLAEAEQTLRFHGVLPDDEDALRT LIDQHKFEMKLEEKRAELNKATTMGDTVLAICHPDSTITIKHW ITIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ WAETTLTDKDEVIPOEIEEVKALIAEHQTFMEEMTRKQPDVDK VTKYKRRADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT QIETKNPRVNLVSKWQVWLLALERRRKLNDALDRLEELREFA NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKQDQGITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYEFVAAHPNKDA YKPI TDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ FGDSQQLRLVRI LRSTVMVRVGGGWMALDEFLVKNDPCRAKGR NMLREKFI LADGASQMAAFRPRRRSRPSSRGASPNRSTSVS SQAQAASQPVPATTPKILHPLTRNYGKPLWLTNSKMSPTCKAA ECSDFPVPSABGTPIQSKLRLPGYLSGKGPHSGEDSGLITTA ARVRTQFADSKKTPSRPGRSAGSKAGSRASSRSGSDASDFDISE IQSVCSDEVETVPQTHRPTPRAGSRPSTAKPSKIPTQRKSPASK LDKSSKR |
| 6029 | 1 | 3533 | IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECEVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDSEDRNKNKRIATAPLIEAVENLTAFASNPFFVS IPAQISSEGSQAQEPILVSAPKPMLESSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAQLMK EAVDDINVTLEAASEVGLVGGMVDAIAEAMSKLDEGTPEEPKG TFVDYQTTVVKYSAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGH LAFQGGMAAATAEP EEEIGFIQIRTRVQDLGHGCI FLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVS LVL SALQAGNKGTQACI TAATAVSGIIADLDTTIFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAAS TPDKLAQAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSD LISATKGAASKPVDDPSM YQLKGAQKVMVNTVTSLLKTVKAVEDEATRGTRALEATIECIKQ BLTVFQSKDVPKTSPEESIRMTKGITMATAKAVAAGNSCRQBE DVIATANLSRKAVSDMLTACKQAS FHPDVSDEVTRALRFGTEC |

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|------------|--|--|--|
| | | | TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAAEAMKGTEDVDPEDPTVIAETELLGAAASIEAAKKLEQLKPRAPKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGVGSIPANAADDGQWSQGLISAARMVAATSSSLCEANASVQGHASEEKLISAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAVKRASDNLVRAAQKAAFGKADDDVVVKTFFVGGIAQIIAAQEEMLKKERELEEARKKLAQIRQQQYKFLPTELREDEG |
| 6030 | 3 | 1777 | FPGRGSPALQLEVLICLGLMGLERLNLVLAIFVYRNTVNLLENAPWNSLAWTVTSYVFLKFLQGGGTGSGTFVSNLRTFLWIRVQQFTSRRVELLIFFSHLHELRLRHLGRRRTGEVLRIADRGTSSTVGLLSYLVFNVIPTLADIIIGIIYFSMPFNAWFLIVFLCMSLYLTLTIVVTWRTKFRAMNTQENATRARAVDSLNFETVKYNAESYBVERYREAI IKYQGLEWKSSASLVLLNQTNQLVIGLGLLAGSLLCAYFVTEQKLQVGDYVLFGTYYIIQLYMLNWFQTYRMIQTNFIDMENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGRBTLQDVSFTVMPGQTLALVGPAGKSTILRLFRFYDISSGCI RIDGDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVTAGNDEVEAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKORVAIARTILKAPGIIILLDEATSALDTSNERAIQASLAKVCANRTTIVVAHRLSTVNNADQILVIKDGCIVERGRHEALLSRGGVYADMWQLQQGQEETS EDTKQPOTMER |
| 6031 | 160 | 1694 | LRMSENLDKSNVNEAGKSKSNDSSEGLEDAVEGADEALQKATKSDSSSPQRVQRPHSSPPRFVTVBELLETARGVTNMLAHEIIVNGDFQIKPVELPENSLLKRVKEIVHKAFWDCLSVQLSEDPDPAYDHA IKLVGEIKETLLSFLLPGHTRLRNQITEVLDDLQKQEAENGALDISKLAEFIIGMMGTLCAPARDEEVKLLKDIKEIVPLFREIFSVLDLMKVDMANFAISSIRPHLMQSSVEYERKKFQEIILERQPNSLDFVTQWLEEASEDLMTQYKHALPVGGMAAGSGDMPRLSPVAVQNYAYLKLLKWDHLQRFPETVLMQSRFHELQLQ\REQTLILGAVLLVTFMSMAAPGISSQADFAEKLKMIKILLTMDHLPFHLKDVLTIGEKVCLVSSCLSGSSPFTTDKETVLKGQIQAVASPPDDPIRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAIKFARLVNKNMVFPCPYDAILSKILVRS |
| 6032 | 39 | 2415 | AARLCRAQPTKSAWMIRDLSKMPQTRHPAPHQPAQPFKFTISESCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMSYGLNIEMHKQAEIVKRLNAICAVIPFLSQEHQQQVVQAVERAKQVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIPIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQDRDSIKSSSVSPSASFRGAEKHRNSADYSSSEKKQKTEEKEIAARYDSGGEKSDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISPASIASSSSSTPSSKSKLSLNEKSTTPVSKSNTPTPRTDAPTGPSNSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAGMNGELTSPGAAYAGLHNISPQMSAAAAAAYGRSPVVGFDPHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMOPVFPFPDALIGPGIPRHARQINTLNHGEVVCATISNPTRHVYTGKGCVKVWDISHPGNKSPVSQLDCLNRDNYIRSCRLPDGRTLIVGGEASTLSIWDLAAPTPIKAELTSSAPACYALAI SPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHDTGASCIDISNDGTLWTGGLDNTVRSW\DLREGRQLQHD/FFTSPVFSLGYP\TEEWLAVGMENS\N\VEVLHVTKPDQYQLHLHESCVLSLKFACGKWF\VSTGKDNLLNAW\RTYPY\ASIF\QSKESS\VLSCDI\SVDDKYIVTGS\GDK\RATVYEVY |
| 6033 | 39 | 2415 | AARLCRAQPTKSAWMIRDLSKMPQTRHPAPHQPAQPFKFTISESCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMSYGLNIEMHKQAEIVKRLNAICAVIPFLSQEHQQQVVQAVERAKQVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIPIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQDRDSIKSSSVSPSASFRGAEKHRNSADYSSSEKKQKTEEKEIAARYDSGGEKSDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISPASIASSSSSTPSSKSKLSLNEKSTTPVSKSNTPTPRTDAPTGPSNSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG |

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|------------|--|--|---|
| | | | MNGELTSPGAAYAGLHNISPQMSAAAAAAYGRSPVVGFD PHHMRVPAIPPNLTGIPGGKPAYSPHVSADGQMOPVFPFDAL IGPGIPRHARQINTLNHGEVVCVATISNPTRHVYTGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLPDGRTLIVGGEASTL SIWDLAAPTPIKAELTSSAPACYALAI SPDSKVCFCSSDGN AVWDLHNQTLVRQFQHTDGASCIDISNDGTLKWTGGLDNTVRS W\DLREGRLQQHD/FTSPVFSGLGYCP\TEEWLAVGMENSN/V EVLHVTKPKDYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESS\VLSCDI\SVDDKYITGS\GDK\ RATVVEVY |
| 6034 | 2683 | 714 | ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAA EIAQAEAPPVPGADGDIIEAPAEAGSPSPASPPADGRLKAAAKR VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLN RQIPKLLRQLQEFDTLGHRLDCLDLKGEKLDYKTCEALEEVFKR LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT RGWQAAAHMMRKTSLQYL\DARNTPLDHSAPFVARALRIRSS LAVLHLENASLSGRPLMLLATALKMNMLRELYL\ADNKLNGLO DSAQGLNLLKFNCSLQILDLRNNHVLD SGLAYICEGLKEQKQGL VTL\VLWNNQLTHTGMAFLGMLTLPHTQSLLETNLGHNPIGNEGV RHLKNGLISNRSVLRGLASTKLTCGAVAVAEFIAESPRLLRL DLRENEIKTGGLMALSLALKVNHSLRLDLDREPKKEAVKSFI TQKALLAEIQNGCKRNLVLAREREKEQPPQLSASMPETTATEP QPDDEPAAGVQNGAPSPAPSPDSDSDSDSGEEEEEEGERDET PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP PPGPEVKGSGCGLEHLSCKNEKELEELLEASQESQETL |
| 6035 | 19 | 404 | SVTYLGIILHKNITGALPADPVQLISQTPPTKQQLLSFLGMVG YFYLWIPGFAITKPLCKLTENLADAI DPKSFSSHFRSLKTA LENASTLALPDSSQPF\SLHTAIVQGCVEILTQGLGPLPV |
| 6036 | 1745 | 356 | LPDVEKLRGRGRKMSVEKGAATSVSNFRGRPSRGRPPKLRN SRGGQGRGVEKPPHLAALILARGSGKGIPLKNI KHLAGVPLIG VLRALDSGAFQSVWVSTDHDEIENVAQFGAQVHRRSSEVSKD SSTSLDAIIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRHQFRWSEIQKGVREVTEPINLNPAPRRQD WDGELYENGSGFYFAKRHLIEMGYLQGGKMAYEMRAEHSVDIDV DIDWPIAEQRLRYGYFGKEKLEIKLLVCNIDGCLTNHGIYVS GDQKEIISYDVKDAIGISLLKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSKLAVVDEWRKEMGLCWKEVAYLGNEVSDDEECLK RVGLSGAPADACSTAQKAVGYICKNGGRGA\IREFAEHIC\LL MEKGLINFMKRNRLAVNIGKK |
| 6037 | 2936 | 1919 | WTSWWMSSVLTILLFSLQGNKMLNYSAPSGAGYLLPRKPVGTPA GGGFPRRHSVTLPPSSKFRQNLSSSLKGEPAALSSRDSRFRDR SFSEGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHLRLSLTRHPKYKTEL CRTFTHTIGFCPYGPRCHFI HNAEBERRALAGARDLSADRPRQLQHSFSFAGFSAATAAATGLL DSPTSITPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSES PHMFDSPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD |
| 6038 | 1450 | 426 | SSALQEFGRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQSVTAKDSAKTFTSITTNTINTS SDKTDGTAGTAPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRL\YCSLCKVAVNSASQLEAHNSGTKHK TMLERNSGGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCICD VHVNSETQLKQHISRRHKDRAAGKPPKPKYSPYNKLOKTAHPL GVKLVSKEPSKPLAPRILPNLAAAAAAAVAVSSPFSRLTAP AATLFQTSALPPALLRPAPGPRTAHTPVLPVFPY |
| 6039 | 4073 | 1000 | LDEYEARLTLANLDDFEEDNEDDENRVNQEEKAKITELINKL NFLDEAEKDLATVNSNPFDDPDAELNPFDPDSEEPITETASP RKTEDSFYNNSYNPFKEVQTPQYLNPPDEPEAFVTIKDSPPQST KKKNIRPVDMSKYLADSSKTEEEELDESNNFFYEPKSTPPPNL VNPVQBLETERRVKRPAPPVLSPKTGVLNENTVSAGKDLSTS |

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|------------|--|--|--|
| | | | PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW RNGLSFCAILHHFRPDLIDYKSLNPQDI KENNKKAYDGFASIGI SRLLPESDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA VDFLSQDDSVFVNDSSGVGESESEHQTPDDHLSPTASPYCRRTK SDTEPQKSQQSSGRTSGSDDPGICSNSTDSTQAQVLLGKRLKKA ETLELSDLYVSDKKKDMSPFFICEETDEQKLQTLDIGSNLEKEK LENSRSLSECRSDPESPIKKTSLSPSTKLGYSSRDLDLAKKHA SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQELKERARVL LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER ARQLIAEARSGGKMSLPSYGERAAEKLKERSKASGDENDNIEI DTNEEIPGFGVGGDELNTLENDLDTPEQNSKLVDLKLKLL VQPQVANSPPSSAAQKAVTESSEQDMKSGTDLRTERLQKTERF RNPVVFVKDSTVRKTQLQSFQSYIENRPEMKRQSIQEDTKKGN EKAATITETQRKPSSEVLNKGFKDS\SQYVVGELAALENEQKQ IDTRAALVEKRLRYLMDTGRNTEEEAMQEWFLVNKKNALIR RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE QLLLDELVALVNKRDAVRLDLAQEKQAEEDDEHLERTLEQKNG KMAKKEKCVLQ |
| 6040 | 475 | 1052 | PTALMTAPSCAFFVQFRQPSVSGLSQITKSLYISNGVAANNKLM LSSNQITMVINVSVEVNTLYEDIQYMQVPVADSPNSRLCDFFD PIADHHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL |
| 6041 | 2 | 3886 | TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS NLLQVLQPKGSLKSSKKKNGKVRPADEILESNEKENEKCVSSEG EKIECWELTTEPSLTHNSSGLSPLRKKPLEDLVCKLADISINY VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIQAKPLE IAKLQKQNPVQFLYQKLIGWLNEDQKDFGFLVDILYSALRCC DNDMERKKVLDLTKVDLKNWLLKIEKACPSDDKHALVTPWL KGDILGEKLVNLADCLCNEDLESRVSSSESHFSEWTLSSVLVSQ HVKNLYLIGDVYVERIIVRLHETLFPKTKKLSEASSDSSVSFIC DVAYNYFSSAKGCLMPSSBDLLLTFLQCAQSKEKTHLPDFLI CKLNTWLSGVNLVHQTDSYKESTFLHLSALWLNQVQASSL DINSQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK MRQSLPMQWLHRLPLEGRSLNLYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP IFLIGFCEILQKMNITYDNLRVLGNMGLLQLLFNRSREHGTW SLIIAKLILSRSSSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFCNLSEASPEVLGV NIEIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTLTDTIGNLPVNLISEWK EFFSQGHSLLLPILVTVTGENKDVSETS FQNAMLKPMCELTLY ISKEQLLSHKLPARLVADQKTNLPEYLQTLNLTAPLLLFRRAP VQIAVYHMLYKLMPELPQYDQDNLSYGDDEEPEALSPPAALMS LLSIQEDLLENVLGCPVPGQIVTIKPLSEDFCYVLGYLLTWKLI LTFKFAASSOLRALYSMYLRKTKSLNKLHYHLFRMPENPTYAB TAVEVPNKDPKTFTEELQLSIRETTMLPYHILPHLACSVYHMTL KDLPAVRLWWSSEKRVFNI VDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIQPLSNYPGFS IIVESGKRVGVAVQQWRNWLQSTYLTQNGSIMEGLALWKN VDRKFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSALCLY KWTSSNKTCSLCRETFF |
| 6042 | 1306 | 253 | MAELAPASPSDIKASVSNNGDTTLLCSRRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNNMAMAYGSSSLAAQKKE LVDKNIDRFIPITKLKYYFAVDYTMVGRKLGLLFPYPLHQDWVE QYQDDTPVAPREDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAF GYKYVGMIGGVLMGLLFGKIGYLVVLGWCCVAIFVMIRTLRLK |

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|------------|--|--|---|
| 6043 | 403 | 599 | ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMMLMYWLTFLHVR LCLFFFPFCATPVLPLPSLISAL/CLSHLSVSSWFPCQPPLPC PLPPLQNKTAAGSLSTEQSERG |
| 6044 | 793 | 412 | KLEMNFTLISKVKISREVTMIASKFGIGQQVRHSLGVLGVV LIDPVSLSSESPDELAVNDELRAAPWYHVVMEDDNLFPVHTYL AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAFRLRN |
| 6045 | 155 | 2299 | SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRQPFPFPPPG AHSFGATPGPGTATAERSSGVAPASPAAPSPGSSGGGGFFSSSL SNAVQTTTAAATFSEQVGGSGGAGRGGAASRVLLVIDEPHT DWAKYFKGKKIHGEIDIKVEQAEFSDNLVAHANGGFSVDMVL RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS VNSLHVSYNFCDKPWVFAQMVRLLHKKLGTEEFPLIDQTFYPNHK EMLSS\TTYPVVVMGHGTLWGKGKVKVDNQHDFOIASVVALT KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKNTGSA MLEQIAMS DRYKLWVDTCEIFGGLDICAVEALHGKDGDRDHIIE VVGSSMPLIGDHQDEDKQLIVELVNKMAQALPRQRDASPGR GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPGGGPPQPGPGP QRQGPPLQQRPPPGQQLSLGLPGAGSPLPQLPSPTSAPQQP ASQAAPPTQGGQRQSRPVAGGPGAPPAARPPASPSPPRQAGPPQ ATRQTSVSGPAPPKASGAPPGGQQRQGPQKPPGPGAPTQASQ AGPVPRTPPTTQQPRPSGPGAGRPKPQLAQKPSQDVPPPATA AAGGPPHPQLNKSSQLTNAFNLPEPAPPSPSLQDEVKAETIRS LRKSFASLPDS |
| 6046 | 212 | 1075 | EGLTGPCERVFFLLGRGPPHAGTRAGHRRRAVRWAGPESLPPLPR SLIMDS PRAGTHQGPLDAETEVGADRCTSTAYQEQRQVEQVGK QAPLSPLGAPMGPGPGPCEDPAGAGGAGAGGSEPLVTVTQGA FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH SYSAQGPEDLGFQGDITVDVLCEVDQAWLEGHCDGRIGIFPKCF VVPAGPRMSGAPGRLPRSQGDQP |
| 6047 | 49 | 1405 | PVLVTSLRMREADTLRFPQLMEVSADIISTVEFNHTGELLATGD KGRVVFVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLSLE IEEKINKIKWLQQNAHSLSTNDKTIKLWKITERDKRPEGYN LKDEGKLDLSTVTSLQVPVLKPMDLMEVSPRRIFANGHTYH INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA NMDLTEVITASEFPHHCNLFVYSSSKGSLRLCDMRAALCDK HSKLFEEPEDPSNRSFSEIIS\SVSDVKFSHSDRYMLTR\DYLT TVKVDL\NMBARPIETQVHDYLRSLCSLYENDCIFYDKFECA WNGSDSVIMTGA\YNNPFRMFDRNTKRDVTL\EASRESSKPRAV LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA TNNLYIFQDKVNSDMH |
| 6048 | 1 | 3194 | GIRTPKFCDSPTSLEMRNGRGRGKMRPNSNTPVNETATASDS KGTSSSKTRAGANSKGRRGSSQNSSEHRPPASSTSEDVKASPSS ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV EPTVLDNRNCPSPVLIDCPHPNCNKYKHINGLYHQAHATDDD SKPEADGDSEYGEPIHLHADLGSCNG\ASVSQK\GSLSPARSAT PKVRLVEPHSPSPSSKFSTKGLCKKLSGEGDIDLGALSNDGSD DGPSVMDETSNDADFSLERKCKMEKCKKPSLKEKIPSKSLK SARPI/APLAIPPQIYTFQTATFTAASPGSSSGLTATVAQAMP NSPQLKPIQPKPTVMGEFFTVNPALTPAKDKKKDKKKKESKE LESPLTPGKVCRAEKGSPFRESSNGMKMEGLLNGSSDPHQSR LASIKAEADKIYSTDNAPSISIGSSRLNTPTQPLTPLHV TQNGAEASSVKTNPSAYSDISDAGEDGEGKVDVSKSDAEQLVK EGAKTLFPPQPSKDSPIYQGFESYYSPSYAQSSPGALNPSSQ AGVESQALKTKRDEEPESIEGKVNNDICEKKPELSSSSSQPSV IQORPNMYQSLYNNQYAYVPPYGYSDQSYHTLLSTNTAYRQQ YEEQKQKQSLQEQQRGVDKKAEMGLKEREALKEEWKQKPSIPP TLTKAPSLTDLVKS GPGKAKEPGADPAKSVIIPKLDSSSKLPGQ APEGLKVKLS DASHLSKEASEAKTGAECGRQAEMDPI LWYRQEA EPRMWTYVYPAYSDIKSEDERWKEERDRKLKEERSRSKDSVPK |

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|------------|--|--|---|
| | | | EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSYPYMHGYSYSQSYDPNHPSYRSMMPAVMMQNYPGSYLPSSYSFSPYGSKVSGGEDADKARASPSVTCKSSSES KALDILQHASHYKSKSPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRTSPSQRLMSTHHHHHLLGYSLLPAYNLPYAAGLSSTAIVASQOGSTPSLYPPRR |
| 6049 | 215 | 1089 | AMTGVFDRRVPSIRSGDFQAPFQTSAAHHHPSQESPTLPES SATDSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGSYPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMVNGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELASLGLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSPQSPAVWEPQGSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS AASSINSHLPPPGSLQHPLALASGTTY |
| 6050 | 566 | 1718 | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWLPNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILDRIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHYQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRD LIFKEREEDLRRLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRNFAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQFKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSIPSAATLINIRNARKHFEKLERVDGPKQCCLLMR |
| 6051 | 566 | 1718 | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWLPNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILDRIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHYQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRD LIFKEREEDLRRLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRNFAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQFKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSIPSAATLINIRNARKHFEKLERVDGPKQCCLLMR |
| 6052 | 566 | 1718 | KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWLPNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILDRIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLWDGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHYQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRD LIFKEREEDLRRLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRNFAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQFKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSIPSAATLINIRNARKHFEKLERVDGPKQCCLLMR |
| 6053 | 201 | 1704 | KGTEMNKSRRWQSRRRHGRSHQONPWFRLRDSEDRSDSRAAQP AHDSGHGDDESPSTSSGTAGTSSVPELPGFYFDEPKKRYFRLLPGHNNCNPLTKESIRQKEMESKRLRLQEEEDRRKKIARMGFNASMLRKSQGLFLNVNTYCHLAHELRLSCMERKKVQIRSM DP SALASDRENILADTNSDRFLTVDVTVGSKYGIINLQSLKTPTLKVFMHENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLLPASL FVN SHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSPGTNSDVLAAQFALMAPLLFNGCRSGEIFAIDLRCGNQKGWKATRLFHDSAVTSVRILQDEQYLMASDMAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVGQDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRGAPGLMAVGQDLYCYSYS |
| 6054 | 1 | 1054 | PPIARLQEFGTSSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIY LHKQSSSQRRNFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDYVTGTGVPDWGDSIEVKNEQIQGLHQACQLARHVLLLAGKSLKVDMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCHGIPDSRPLQDGDIIINIDVTVYNGYHGDTSSETFLVGNVDECKKLVEVARRCRDEAIAACRAGAPFSVIGNTISHITHONGFQVCPHFVGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPFKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQIILTKLPHEA |

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|------------|--|--|--|
| 6055 | 421 | 2364 | PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHHD GCANCSRFCRDCSPACQCHTHVFPGNALNGVQPPELSRTLALI SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELOHGLAGICM TLLITGDSIVSAEAVWDHVTMANRELAFAKGDVIKVLDAKNDW WWGQIDDEEGWFPASFVRLWVNHEDVEEGPSDVQNGHLDPNSD CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKIDCEGYLKQC RKRDMFSDEQLKVI FGNIEDIYRFQMGFVRDLEKQYNNDDPHL SEIGPCFLEHQDGFVIYSEYCNHLDACMELSKLMKDSRYQHFF EACRLLQQMIDIA\IDGFLTPVQKICKYPLQLAELLKYTAQDH SDYRYVAAALAVMRNVTTQINERKRRLNIDKIAQWQASVLDW GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK KDLIRDLILYKGRIDMDKYEVDIEDGRDDDFNVSMKNAFKHL NKETEELHFFAKKLEEKIRWLRAFREERKMVQDEKIGFEISE NQKRAAMTVRKVPKQKGVNSARSVPSPYPPPPQDPLNHGQYLVP \DGIASQVFEFTEPKRSQSPPWQNFSLRTPFFKK |
| 6056 | 43 | 3358 | SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRLSSLPFPPPSRA LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK YLAYMESKGAHRAGLAKVIPPKWKPRQCYDDIDNLLIPAPIQQ MVTGQSGFLTQYNIQKKAMTVKEFRQLANSKYCTPRYLDYEDL ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP KSWYAIPEHGRRLERLAQGGFFPSSSQGCDALRHKMTLISPSV LKKYGIPIFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFT VRWIDYGVAKLCTCRKDMVKISMDIFVRKFPQPDYQLWKQGD IYITIDHTKPTASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP KADEEEVSDEVDGAEVNPNDSVTDDLKVSEKSEAAVKLRNTEA SSEESSASRMQVEQNLSDHILKSGNSCLTSVTEDIKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS SVAESNGVLTEGEESDVESHNGLEPGEIPAVPSGERNSFKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQAPSDEELFEVLISI EEVEETESWAKPLIHLWQTKPPNFAAEQSYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLEVVVTSEGKTKPLIPEMCF IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPI EICDGLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMA VAVPEVRFTNVPERTQIDVGRIPLQRLKLCIFCRHRVXRVSGA CIQCSYGRCPASFHTCAHAAGVL\MEPDDWPYVNIITCFRHKV NPNVSKACEKVISVGQTVITKHNTRYYSRCVMAVTSQTIFYEV MFDGSGFSRDTFPEDIVSRDCLKLGPPAAGEVVQVWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTQVNSLSPPHVSQAQQETYLGFWINSKKSQCNI LSGTY |
| 6057 | 1 | 853 | FVARLKEQEGEGGLQPRKEKGRARGRERRRMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS RPMANSTLLGLLAPGAEWGIQPPNPNHSPPPSAKVKKIFG WGDYFSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMWEKVE\RGRR TSLFTHTDPAKICSRDHAQSSATWSQSPPFKVVCVYIAFYSTDYR LVQKVCDDYNHSDTPYYPG |
| 6058 | 1 | 986 | HPLPSASLGLPSVSLGVSCLVRSALLEAVVPMPLPKRRRARVGS SGDAASSTPPSTRFPGVAIYLVPRMGRSRAFLTGLARSKGFR VLDACSEATHVMEETSAAEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPPVECRHRLLEVAGPSKGPLSPAWMPAYACQR PTPLTHNTGLSEALEILAEAAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSLQGLPHFGEHSSRVVQELLEHGVCCEEVERVRSE/ RLFTQIFGVGKTAADRWYREGLRTLDDLRBQPKLTQQKAGBP SREAGPWASLNCITLDPASATP |
| 6059 | 2 | 3650 | QQDFESLADLTDRHARCPGDDDDPQLSWVASSFSSKDVASPT QMIGDGCGLGEGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SKLFPKCTYCSRLFKHRSRDRHIKLHTGDKKYHCECEAAFS RSDHLKIHKLTHSSSKPFKCTVCKRGFSSTSSLSQSHMQAHKKNK EHLAKSEKRAKKDDFMCDYCEDTFSQTEBLEKHVLTTRHPQLSEK |

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|------------|--|--|---|
| | | | ADLQCIHCPEVFDENTLLAHIQAHANQKHKCPMCFE\QFSSV EGVYCHLDNRQPDSSNHSVSPDPVLGSSVAMSSATPDSSASV ERGSTPDSTLKPLRGQKMRDDGQGWTKVVYSCPYCKRDFNSL AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRLKHN HAYPVMQFGNISAFHCNYCPMFADINSLQEHIRVSHCGPNANP SDGNNAFFCNQCSMGFLTSSSLTEHIQ\Q\AHCSVGSAKLESFV VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHKENHKNIPLAHS KKSKEQSPVSSDDEVSSPKRQRLSASANSISNGEYPCNQCDLK PSNFESFQTHLKLHLELLRLKQACPOCKEDFDSQESLLQHLTVH YMTTSTHYVCECDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L CQEVFDS\KVISI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ VHVKSHLGNPAKAKHCFI CGETFSFEVELQCHITTHSKKYNCK FCSKAFHAIILLEKHLREKHCVFDAATENG TANGVPPMATKKAE PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCIDCGAAYTME VLLQNHRLRDHNI RPDGDDGSRKKAFTIKGSHKCNVCSRTFFSE NGLREHLQTHRGPAKHVMCPICGERFPSLLTLTEHKVTHSKSLD TGTCRICKMPLQSEEEPIEHQCMHPDLRNSLTGPRCVCMQTVT STLELKIHGTFHMQKLAGSSAASSPNGQLQKLYKCALCLKEFR SKQDLVKLDVNGLPYGLCAGCMARSANGQVGLAPPEPADRPCA GLRCEPCSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSFV PRKKTYYQCIKQMTFENEREIQIHVANHMI BEGINHECKLCNQM FDSPAKLLCHLIEHSFBGMMGTFFKCPVCFVTVFQANKLQQHIFA VHQEDKIYDCSQCPQKFFQFQTELQNHMTSQHAQ |
| 6060 | 2145 | 202 | SYEIVGKKNLEVNHSQKALCKSLPSRLPLGENLPLLDGRFR KEPRSRGSRERDNMLHLHSHCLCFRSLPAMLAVLLSLAPSASS DISASRPNILLMADDLGIGDICYGNNTMRTPNIDRLAEDGVK LTQHISAASLCTPSRAAFLTGRIYFVRSGMVSSIGYRVLQWTGAS GGLPTNETTFAKILEEKGYATGLIGKWHGLNCESASDHCHHPL HHGFDHFYGMFPSLMGDCARWELSEKRVNLEQKLNFLFQVLLALV ALTLVAGKLTHLIPVSWMPVWSALSAVLLASSYFVGLALVHA DCFLMRNHTITEQPMCFQRTTPTLILQEVASFLLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLNQLGNTQYGGWNGIYKGGKMGWG EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDFELMHY CERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVHHDPPLLFD LSRDPSETHILTASEPVFYQVMER\VOQAVWEHQRTLSVPVPLQ LDRLGNIWRPWLQPCCGFFPLCWCLREDDPQ |
| 6061 | 110 | 1330 | MNIHMKRKTIKNTFENRMLMDGMPAVRVKTELLESEQGSFN VHNPDM EAVPLLLNNVKGEPEDSLSDHVFQTEPVDLSINK ARTSPTAVSSSPVSMASASSPSTSTSSSSSRLASSPTVITS VSSASSSSTVLTGPPLVASASGVGGQQLHIIHPVPSSPMNLQ SNKLSHVHRIPVVVQSVFVYTAVRSPGNVNNTIIVVPLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLNVTLDVNETGSTALSIA RAVQEVHPSVSRVRGNRMNNQKFPCSI SPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQLYTKSSSPGRVHRRTHTEKPY KCTWEGCTWKPARSDELTRHYRKHTGVKPKCADCDRSPSRSDH LALHRRRRLV |
| 6062 | 71 | 1079 | ETMAKNGPENCEDCHILNAAEFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR TEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP BFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKI LEICDNVTMYW\INPTL\ISGTFKQLHHNFAPILVSELQDPE REGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYP YPICYQGGRVICRVIMPCNWWVARMLGRV |
| 6063 | 71 | 1079 | ETMAKNGPENCEDCHILNAAEFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR TEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKI LEICDNVTMYW\INPTL\ISGTFKQLHHNFAPILVSELQDPE |

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|------------|--|--|--|
| | | | EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLEDERGYCCYICRRGNRYCRRVCEPLLGYYP YFYCYQGGRVICRVIMPCNWWVARMGLGRV |
| 6064 | 913 | 311 | NLPQSLPRPTEHSPFYSLEKMTDLVAVWDVALSDGVHKEIEFEHG TTSGRKRVVYVDGKEEIRKEWMFKLVGKETFFVGAAKTKATINID AISGFAYEYTLLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\ SSG\KRKEGIHTLIVDNREIPEIAS |
| 6065 | 1153 | 641 | MSVRVARVAVVRGLGASYRRGASSFPVFPFGAQQVAELLRDATG AEEEAAPWAATERMPPGQCSVLLFPQGQSQVVMGRGLLNYPVR ELYAAARRVLGYDLLELSLHGPPQETLDRTVHCQPAIFVASLA EKLHLHQPSVIENCVAAGFVSVEFAALVFAGAMEFAEG |
| 6066 | 68 | 3470 | VKENMPATRKPMRYGHTEGHTEVCFFDSGSIIVTCGSDGDVRIW EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG VPDGIILTRFTTNANHVVFNQDGTIAAGSSD\FLVKIVDVMDS QOKTFRGHDAVPLSLSDPKDI FLASACDGSVRVWQISDQTC ISWPLQKCNVDINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR ESWQHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV ETKDCMERVKHEKGAYICGLAWHPTCGRISYTDAGNGLLENV CDPSGKTSKSVSRVEKDYNLDFGDDMSNAGDFLNDNAVEIP SFSKGIINDEDEDLMMASGRPRQRSHILEDDENSVDISMLKT GSSLLKEEEDGQEGS IHNLPVTSQRPFYDGPMPTRQKPFQS GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK EWIIDLQONEDIEAICLGQGWAAATSAALLRLFTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRGTGFDGQCLGVQLLELGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSBGIVRMLNRLG NTWTPICNTRHCKGKSDHYWVVG IHENPQQLRCIPCKGSRFP TLPRPAVAILSKLPYCQIATEKGMEEQFWRSVIFHNHLDYLA KNGYEYESTKNQATKEQQLLMKMLALSCKLEFRFCVELADL MTQNAVNLAIKYASRSRKLILAQKLSLAVEKAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFFKVAS SKEPAMSMNSARSTNILDNMGSSKSTALSRTTNNEKSPI IKP LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSPTAI CPPQNTENQRPKTGFQMWLEENRNLSDNPDFSDEADI IKEGM IRFRVLSTEERKVVANKAKGETASEGTEAKRRKRVVDESDTEN QEBKAKENLNLSSKKQKPLDFSTNQKLSAFQKE |
| 6067 | 858 | 321 | LPWQRLGVLLSRGKMAVTGWLESRLTAQKTALLQDGRKRVHYLF PDGKEMAEYDEKTSSELLVRKWRVKSALGAMQWQLEVGDPAPL GAGNLGPGLIKESNANPIFMRKDTKMSFQWRIRNLPYKDVYSV SVDQKERCIIVRTTNKKYKFKFSIPDLDRHQLPLDDALLSFA\T PTAP |
| 6068 | 13 | 1730 | GSKMADLANEEKPAIAPPVVFQKDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELGRSAGGSSPEGGEDSDREDGNYCPCPKRETTSSLTQ FPPSQSEERSGFRLPKPTLIHQAPSAGLPSQKPKQQRSVLR PAVLQAPQPKALSQTVPSGNTGVSLPADCTGAVPAASPDAAW RSPSEAADEVCALEEKEPKNESSNASEEEACEKDPATQQA FGQNLDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKVFGQNMSESVLSPKLENVSSDANRENA AESGSESSSQEATPEKESLAESAAYTKATARKCLLEKVEVIT GEEAESNVLMQCKLFVFDKTSQSWVERGRGLRLNDMASTDDG TLQSRISDAGPRGSLR\LI LNTKLWQM QIDKASEK\SRITAM DNEDQGVKVF LISASSKDTQGVYALHHRILALRSRVEQEQA MPAPEPGAAPSNEEDSDDDVLAPSGATAAGAGDEGDGQTTS T |
| 6069 | 583 | 27 | PTRPGQAGSSSMAAQR LGKRVLSKLQSPSRARGPGGSFGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN IDELLESEEEERSRKIQGLLSCGKPVEDFIQELLAKLQGLHR |

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|------------|--|--|---|
| | | | QVPLRQPSPP\DGQPSAPFQGPARTASPLTLLALPPGPPER RPALLCVLSCI |
| 6070 | 478 | 858 | IRVTVDEGEFLHYIFPLQFLDSPW/RFTETHRGRHF\QVTLTAE TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND RVYIGKRYHYDIRLNFYQMSTPEIRRSPLTQHFQNSRRYW |
| 6071 | 2 | 1654 | HEARTKGNMALARP\VRFLSVLTRLALLAPRRGLTVRSPDEPLPV VRIPVVALQRQLEQRQSRRRNLPRPVLRPGPLLVSARRPELNQF ARLTLGRWERAPLASQGWKSRRRARDHFSIERAQEAPAVRKLS SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSSTIPSLLR GRHVVCAAETGSGKTLSYLLPLLQRLG\HPSLDSLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLGLLVRDLBGGHGMRRIRLQLS RQPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLDES FLRLVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ LLNKVASPDVTTITSSKLHCIMPHVKQTFRLKLGADKVAELVH ILKHRDRAERTGPSGTVLVFCNSSTVNWLGYILDHDKIQHLRL QGQMPALMRVGIQFSQFKSSRDILLCTDIASRGDSTGVELVN YDFPPTLQDYIHRAGRVRGVSEVPGTVISFVTHPVDVSLVQKI ELAARRRRSLPGLASSVKEPLQAT |
| 6072 | 1 | 742 | KMERTEMMPTINSQLEFKSKPFLVSSSRWLVRKGELTAYVEDT VLFSRRTSKQVYFFLPNDVLIITKKKSEESYNVNDYSLRDQLL VESCDNEELNSSPGKNSSTMLYSRQSSASHLFTLVLSNHANKE VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT AKQPELSLQVADVLI\YQVSDGWYEGE\LRDGERGWFPME CAKEITQATIDKNVERMGRLLGLETNV |
| 6073 | 620 | 860 | PCRRGLARPLSRPG/SILVHCAGVSRSATLVLAYLMLYHHLT LVBAIKKVKDHGRIIPNRGFLRQLLALDRRLRQGLEA |
| 6074 | 168 | 1110 | PGARCMATELQCPDSMPCHNQVNSASTPSPEQLRPGDLILDHA GGNRASRAKVIILLTGYAHSSLPABELDSGACGSSLNSENGSGG DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNGCVS IMRSGEAMEQGLRDCRSIRIGKILIQSDEET QRAKVYYAKFPDIIYRRKVLMPILQGT\NTVIEAVKVLIEHG VQPSVILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD |
| 6075 | 320 | 1091 | PPTCQPQVEVHH\YGYVPILGNKTLPSRCHQCIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTFPTVFIWGPSPKMQKPGQSLVRVIRAGLVFP NMEAYAVSPGRMRQFDDLFRGETGKDKREKSHSWLSTGWFTMVA VELCDHVHVGMVPPNYCSQRPLQRMPIHYEYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT |
| 6076 | 1721 | 107 | HPSPTAEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV KKPASVSVKSCVSGYTLTELSMHWVRQAPKGLEWMAFDPED GETIYAKQFQGRVTMTEDTSTDTAYMELSSLRSEDATVYYCATD HGDIYAFDIWGQGTMTVTVSSAPTAPDVFPPIISGCRHPKONSPPV LACITGYHPTSV\TVTWYMGTSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQRQGEYKCVVQHTASKSKEIFRWPESPKAQASSV PTAQPOAEGSLAKATTAPATTRNTGRGGEKKKEKEEQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHNSGSQSQHSRLTLPRSLWNA GTSVTCTLNHPSLPQRLMALREPAQAPVKLSLNLASSDPPE A\ASWLLCEVSGFPPNILLMWLEDHGEVNTSGFAPARPLPKF\ RSTTFWA\WSVLRVPAPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMPK |
| 6077 | 3687 | 1268 | LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSRCDLLEALKKKGCPDDIENPR GSKDIKKNKNTNRSGTAEKLPEDITQIQPQLVLRSLRSGEP QTFTLKFKRAEDYPIDLYLM\DLSSYMKDDLNVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFYSYNVLSLTKNGEVFNELVGKQIRISGNLDSPEGGDAIMQVA VCGSLIGWRNVTRLLVFSTDAGFHAGDGKLGIVLPNDGQCHL |

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|------------|--|--|--|
| | | | ENMYTMSHYDYDPSIAHLVQKLSNNIQTIFAVTEEFQPVYKE LKNLIPKSAVGTLSANSSNVLIIDAYNSLSSEVILENGKLS GVTISYQSY\CKNGVNGTGNGRKCSNISIGDEVQFEISITSNK CPKDSDSFKIRPLGFTEEEVILQYICECECQSEGIPESPKCH EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCTARKENQ FQKSASNHGRVPSAGQCVCRRKRDNTNEIYSGKFCECDNFNCDRS NGLICGGNGVCKCRVCECNPNYTGSAACDCGLDSTCEASNGQIC NGRGICECGVCKCTDPKFGGQTCCEMCQTCLGVCAEHKECVQCR FNKGEKDTCTQECSEYFNITKVESRDKLPQVPQDPVSHCKEKD VDDCWFFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVG IVLIGLALLLIWKLMI IHDRREFAKFEKEKMNKWDGTGENPIY KSAVTTVVNPKEYGK |
| 6078 | 1425 | 180 | ETEDVMELLEEDLTCTPICCSLFDDPRVLPCHSHNFKCKLEGILE GSVRNSLWRPVFPKCPCTCRKKTFSYWELIPLQVNYSLKGIKEY NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL\CGIC\ATR GEHTKHVFCSEIDAYAQRDAFESLPQS FETWRRGDALSRDLTL ETSKRKSLLTKDSDKVKEFFEKLQHTLQKKNEILSDFTMK LAVMAYDPEINKLNTILOEQRMFNIABAFKDVSEPIVFLQCM QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVVK LSLPQDTGTFISKIPWSFYKFLLLILLGLVIVFGPTMFLEWSL FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEFVCKYKLL |
| 6079 | 1586 | 141 | ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFGLGLSP GVLDRLYGHAPATCLAVFRELPSLAKNWVMRMLFLEQLPQAABA LWVKKEFSKAQEEESTGLSGLRIWHTQLLPGLQGLIILNPIFRQ NLRIALLGGGKAWSDTSQGLPDKHARDVPSLDKYAERWEVVL HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQL LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSPSTLGKD YSVEGMSDSSLNLFQHLREFGLVPQRKRKSRYYPT/RALAINL SSGVSAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE MLYPPF\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP VMLKQTPVLPPTITDQIRLWELERDLRFTGVLNQLFSLQVDF ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWRQK HSS |
| 6080 | 1 | 1199 | IETIDHVGFEFAMAAAGVSRQRAATQGLGSNQNALKYLQDQFK TLRQCLDSGLVFKDPRFPACPSALGYKDLGPGSPQTQGIWKR PTELCPSPQFIVGGATRTDICOGLGDCWLLAAIASLTLNEELL YRVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR LPTKNGQLLFLHSEQGNFWSALLEKAYAKLNGCYEALAGGSTV EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLGCSIDVY SAAEAEAITSQKLVKSHAYSVTGVEBNFQGHPEKILRLRNPWG EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR QFSRLEICNLSPDSLSSSEEVHKWNLVLFNGHWTRGSTAGGCQNY PGSS |
| 6081 | 3 | 865 | EMLPDLLPLPLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC SVFYLEYGKWDSTPAYGHWFRGVSVDOETPVATNNSQKVQKE TQGRFHLGDPFRNNCSLSIRDARRRDNNGSYFFWVARGRTKFSY KYSPLSVYVTALTHRPDILIPFLKSGHPSNLTCSPVWVCEQGT PPIFSWMSAAPTSLGPRTLHSSVLTIIIPRQDHGTNLICQVTFP GAGVTERTIQLSVSWKSGTVEEVVVLAVGVAVKILLCLCLI ILSFHKKKAVRAVEVEENVYAVMG |
| 6082 | 283 | 1288 | EARSFGPTQTRTAPGLAAPGLAQPAALRLLSRPPSAAMDGDGD PESVGQPEEASPEEQPEEASAEERPEDQEEEA\Y\LDL LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL LKCCQEGLVPEGGVEEERDHWQFYFLSKRRRNLRLNPGCEEDL EGWCDVEHGGDGWRVEELPGDSGVFEFTHDESVKYFASSFEWC KAQVIDLQAEGYWEEELDTTQPAIVVKDWYSGRSDAGCLYELTV KLLSEHENVLAEFSSGQVAVPQDSGGGWMEISHTFTDYGPGVR FVRFEHGGQDSVYWKGFGARVTNSSVWVEP |
| 6083 | 1865 | 309 | KQWCAERRGLGMSLADELLADLEEAABEEEGGSYGEEEPAIE |

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|------------|--|--|--|
| | | | DVQEEETQLDLSGDSVKTI AKLWDSKMF AEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELES LVPNALDYIRT VKELGNSLDKCKNNENLQQILT NATIM VVSVTASTTQGGQLSEEEELERLEEACDMALELNASKHRIY EYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPFFSVAP\DL RRKAARLVA AKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEP PPVKQVKPLPAPLDGQRKKRGGRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGKSGLMST |
| 6084 | 1865 | 309 | KQWCAERRGLGMSLADELLADLEAAEEEEEGSGYEEEEEPATE DVQEEETQLDLSGDSVKTI AKLWDSKMF AEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELES LVPNALDYIRT VKELGNSLDKCKNNENLQQILT NATIM VVSVTASTTQGGQLSEEEELERLEEACDMALELNASKHRIY EYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPFFSVAP\DL RRKAARLVA AKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEP PPVKQVKPLPAPLDGQRKKRGGRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGKSGLMST |
| 6085 | 2 | 1456 | SGPRSFQGNRAVGRISLGGKRNFEVTL LPGVSSERVRWRARV GVARVKGPNPWPSPATQVPR/VPAQVYLPGRGPPLREGEELVM DEEAYVLYHRAQTGAPCLSFDIRDHLGDNRTTELPLTLYLCAGT QAESAQSNRLMMLRMHNLHGTPPPSEGSDEEEEEDEDEEER KPQLELAMVPHYGGINRVRVSWLGEPPVAGVWSEKQVEVFALR RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR VTGRLLTGDCQKNIHLWTPTDGGSWHVDQREFFVGHTRSVEDLQW SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAVPT SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG LADLPQQLLFVHQGETELKELHWHPCPGLLVSTALSGTIFRT ISV |
| 6086 | 2419 | 1357 | GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGF RV YNTDPLKEKEKEQFLEGGVGHVEMLFRCNYLALVGGGKPKPYP NKVMIWDDLKKTIVIEIEFSTEVKAVKLRR\DKIVVLD SMIKV FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGHTG HVQLVDLASTEKPPVDIPAHEGVLSIALNLQGTRIATASEKGT LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLIVSSDHG TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFKQVPSGSP CICAFTGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT DDKL |
| 6087 | 476 | 1877 | QNSQRTGLPITIFSRSPFLLTGSDLCENMPCTCTWRNWRQWIRP LVAVIYLVSI VVAVPLCVWELQKLEVG IHTKAWFIAGIFLLTI PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVILEAKD QQKHFPPLCCPPWAMGEVLLFRCKLGVLYTTVVRPFTTIVALI CELLG IYDEGNFSPSNAWTYLVIINMNSQLFAMYCLLLFYKVLK EELSPIQPVGKFLCVKL VVFSFWQAVVIALLVKGVISEKHTW EWQTV EAVATGLQDFIICIEMLAAIA\HHYTF SYKPYVQEAEE GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKLPEDQ DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP TTAKISDEILSDTIGEEKEPSDKSVDS |
| 6088 | 1684 | 689 | GASGLVRLLOQGHRCCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCP PPPVRRSEKPNWDYHAEIQAFGHR LQENFSLDLL KTA FVNSCYIKSEAKRQQLGIEKAVLNLKSNQELSEQGT SF SQTCLTQFLEDEYPMPTGINKLVDFLTGEEVVCHVARNLAVE QLTLSSEFPVPPAVLQQTFFAVIGALLQSSGPRTALFIRDFLI QTMTGKELFEMWKIINPMGLLVBELKKRNVSAPE SRLTRQSG\A |

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|------------|--|--|--|
| | | | PTALPLFYVGLYCDKKLIAEGPGETVLVAEEAARVALRKLYGF TENRRPWNYSKPKETLRAEKSITAS |
| 6089 | 3 | 3054 | TRLGIPGSTISSRRLCALAEGHFLGHSWTGSRAGAHTGAPAW PSRRLRLDPAGGMWRLRRRAVACEVCQSLVKHSSGIGKSLPLQK LHLVSRSIYHSHHPTLKLQRPQLRTSQQFSSLTNLPLRLKFS PIKYGYQPRRNFWRPARLATRLKLRLYLILGSAVGGGYTAKKTFD QWKDMIPDLSEYKWIVPDIWEIDYIDFEKIRKALPSSSEDLVK LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDEKHFKE VSDKEKIDQLQEELLHTQLKYQRIERLEKENKELRKLVLQKDD KGIPFIESLRKSLIDMYSEVLVLSYDASINTQDHLPRVVVVG DQSAGKTSVLEMAIQAIRIFPRSGGEMMTRSPVKVTLSEGPHEVA LFXDSSREFDLTKEEDLAALRHEIELMRKNVKEGCTVSPETIS LNVKGPGLQRMVLVDLPVINTVTSGMADPTKETIFSISKAYMQ DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTQVDL AEKNVASPSRIQQIIIEGKLFPKALGYFAVVTGKGNSSIESIAI REYEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES VEQQADSFKATRFNLETEWKNNYPRLELDRLNELFEKAKNEILD EVISLSQVTPKHWEIILQQSLWERVSTHVIENIYLPAAQTMNSG TFNTTVDIKLKQWTDKQLPNKAVEVAMETLQEEFSRFMTPEPKK EHDDIFDKLKEAVKERSIKRHKWDFAEDSLRLVIQHNALEDRI SDKQQWDAAIYFMEALQARLKDTENAIENMVGPD\WKRWLYW KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE SRGVEVDPSLIKDTWQVYRRHFLKTALNHCNLCRRGFYYYQRH FVDSLELCNDVVLFWRIQRLAITANTLRQQLTNTVEVRLKENV KEVLEDAEDGEEKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK |
| 6090 | 194 | 1560 | PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELFPQASTL FELQLFFCQIALFVHYINIYKTVWWYPPSHPSHTSLNFHLID FNLLMVTITVLGRRFIGSIVKEASQGRKVSLSRILFLTRFTV LTATGWSLCSRLIHLFRTYSFLNLL/PPLLSVWDVHVSFAAELR P\RKTSLFNHHMAMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSML SAYYVAFVPVWFVNTHYYDKRWSCLEFLLVSISTSILMQHLL PASYCDLLHKAHAHLGCWQKVDPALCSNVLOHPWTEECMWQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHHFSSKPLRLILNILL LEGAVIVYQLYSLSMSSEKWHQTI SLALILFSNYAFAFKLLRDL VLGKAYSYSASQPRDLDRHS |
| 6091 | 3279 | 412 | SSRTREMEKEIILRRQIRLLQGLIDDYKTLHGNAAPAGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHGSPSWRKYSLVNRPFG PSDFPADHAVRPLHGARGGQPPVPQGHVLERQVLSQGNVVK VKPPSKSGSASASGAQRGSLEEFEDTPWSDORPREGEGERPGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVMGSDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQVPVSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNKYKWAASSKSPRVARRALS PRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPVAGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTTHRLCRLPPSRAHLPKTA SSLHAVRTAPTSTKVIKTRYRIVKKTTPASPLSAPFFPLSLPSWRA RRLSLSRSLVNLRLRPVASGGGKAQPGSPWWSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLRTGRLDPAGSCSRSLASRAVQ RSLAIRQARQRREKRKEYCMYNNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTGCPFSHHVSKEMPVCSYFLKGICNSN CPYSHVYVSRKAECSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRAATSPAPGPSDATARSRVASHG PRKPSASQRPTRQTPSSAALTAATAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL |
| 6092 | 143 | 3190 | AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKYYVE |

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|------------|--|--|---|
| | | | VIQLIKTNKKHIHSRSTLECYRTHLVAGIGFYQHLLLYIQSHY QLELQCCIDWTHVTDPLIGCKKPVASAGKEMDWAQMACHRCLVY LGDLSRYQNELAGVDTELLAERFYYQALSVAPOIGMPFNQLGTL AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLQPKSSSVDSHEL TSLCQSVLEDFNLCLFYLPSNPNSLASEDEEYESGYAFPLPDL LIFQMVIICLMCVHSLERAGSKQYSAATAFTLALFSLHVNHNVI RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEDPEPPPVPT PQVGEGRSRKRFSRLSCLRRRHPPKVGDDSDLSEGFESDSSH SARASEGSDSGDKSLEGGGTAFDAETDSEMNSQESRSDLEDME EEEGTRSPPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ MFQTKRCFRLAPTFNSNLLQPTTNPHTSASHRPCVNGDVDPKSE PASEGSESESGESSGRSCRNERSIQEKLQVLMAGELLPAVKVF LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA LCPEVQDLEGCLEPDLPSLLLPEDMALRNLPPLRAAHRFRNF DTRPPLLSTLEESVVRICIRSFHF IARLQGSILQFNPEVGIF VSIQSEQESLLQQAQAQFRMAQEAEARRNRLMRDMAQLRLQLEV SQLEGSLLQPKAQSA MSPYLVPDTQALCHHLPVIRQLATSGRFI VIIPRTVIDGLDLLKKEHGPARGDGI RYLEAEFKKGNRYIRCKQE VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG MVTIITGLPLDNPSLLSGPMQALQAAAHASVDIKNVLDIFYKQW KEIG |
| 6093 | 76 | 1002 | ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\ PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP VLGYLIEEDFNIALGVFALAGLTDLDDGFIARNWANQRSALGS ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDMVLI AAVF YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV IKD |
| 6094 | 23 | 1010 | PFLRCLRGDQKAKMSERKVLNKKYPPDFDPSKIPKLLPKDRQY VVRLMAPFNMCRCKTCGEYIYKGGKFNARKETVQNEVYLGLPFR FYIKTRCLAEITFKTDPENTDYMTEHGATRNFQAEKLEEEEEK RVQKEREDEELNPMKVLENRTKDSKLEMEVLENLQELKDLNQR QAHVDFEAMLRQHRLSEBERRRQQQEEDQETAALLEARKRRL LEDSDSEDAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV GSLGSRPPLSRLVVVKAKADPDSCNSNGQPQA/APHPRSPAEGEG GQPYTPDAWRVLPPTGCI PGQ |
| 6095 | 1 | 1599 | TRGAAERSRGRGHGFLGGGFA\SVVDYFPSED FYRCGYCKNES GSRSGMWAHSMTVQDYQDLIDRWRRSGKYVYKPMNQTCPCQ YTIRCRPLQFQPSKSHKKVLKMLKFLAKGEVPKGSCE\DEPMD STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGNKSKKE EPQELLQSQDFVGEKLGSGEP SHS |

TRADCS:1416257.1(%CSH01.DOC)

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|------------|--|--|--|
| | | | VKVHTVPKPGKADLSKPPCRKAKETRKRRRLKLMQQNPAGEL EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR FLCSSPLEAETPPNGPDCGYGSFHHQQYWLGDGKIIAVGVIDILPN CVSSVLYLDPDYSFSLGVSALREIAFTRQLHEKTSQLSYY MGFYIHSCPKMKYKQYRPSDLLCPETYVWVPIEQCLPSLENSK YCRFNQDPEAVDEDRSTEPDRLQVFHKAIMPYGVYKKQKQKPS EEAVALQYASLVGQKCSERMMLFRN |
| 6096 | 2277 | 575 | QRVRAALLSSAMEDSEALGFEHMGDLPRLLQAVTDLGWSRPTLI QEKAIPALLEGKDLLARARTGSGKTAAYAI PMLQLLLHRKATGP VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA EDSVSQRAVLMEKPDVVVGTPSRILSHLQDQSLKLRDSLELLVV DEADLLFSFGFEEELKSLCHLPRIYQAFILMSATFNEDVQALKE LILHNPVTLKLQESQLPGPDQOQFQVVCETEEDKFLLYALLK LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGBLPLRSR CHII SQFNQGFYDCVIATDAEVLGAPVKGKRGRGPKGDKASDP EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV LTFVLPTQFHLGKIEBLLSGENRGPILLPYQFRMEETIEGFRYR CRDAMRSVTQAIREARLKEIKELHSEKLTTFEDNPR\DLQ LLRHDLPHPAVVKPHLGHVDPDYLVPPALRGLVRPHKK\GRSCL PLVGRPREQSPRTHCAASSTKERNSDPQSPPEVVGPLWS |
| 6097 | 1673 | 192 | APGTMSGGKKKSSSQITSVTTDYEGPGSPGASDPPTPQPTGPP RLPNGEPSDPDGGKGTFRNGSPPPGAPSSRFVRVVKLPHGLGEP YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ LVVPSKAKAEKPPLSASSPQRPPEPETGESAGTSRAATPLPSL RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPLDS RPSSPALYFTHDASLVHKSPPDFGAVAAQKFSLAHSMIAISGHL DSDDDSGSGSLVGIDNKIEQAMDVLKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLRALA\ SPEGQLGSAGPPRGVPR\LGPPA PNGPFVLSLPSLTIVPLGLPLASAAWPPPLMPALIVPVFPVG VQALSNGPWSPGFLPHLLIIPSLDGGGEGFRGTGRQQGAFFGEET QPPPSLPGTPQQ |
| 6098 | 168 | 1074 | NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETS DTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETS VNASRSPEKCAQQRQK RLNASQRSSSLPSPNRKSSPTKREIMLTPVTVAYS PKRSPKE NLSPGFSHLLSKNESSPIRFDILDDLDTPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVNGVKVSVR TAWKKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALS RMPSPGGRITLQTRLNQEAFGRSFGKD |
| 6099 | 168 | 1074 | NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETS DTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETS VNASRSPEKCAQQRQK RLNASQRSSSLPSPNRKSSPTKREIMLTPVTVAYS PKRSPKE NLSPGFSHLLSKNESSPIRFDILDDLDTPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVNGVKVSVR TAWKKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALS RMPSPGGRITLQTRLNQEAFGRSFGKD |
| 6100 | 2 | 713 | FVEVSGYRSRADPEPRGRD TMTYALFKYIIIGDTGVGKSCLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDI TRRET FNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREGEAFARE\HGLIFMETS AKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC |
| 6101 | 1 | 1399 | FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLA FKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY AELWMGTHPRGDAKILDNRISQKTL SQWIAENQDSLGSKVKDTF |

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|------------|--|--|---|
| | | | NGNLPFLFKVLSVETPLSTIQAHPNKELAEKHLQAPQHYPDANH KPEMAIALTPFQGLCGFRPVVEIIVTFLKKVPEFQFLIGDEAATH LKQTMSHDSQAVASSLQSCFSLMKSEKKVVVEQLNLLVKRISQ QAAAGNNMEDIFGELLQLHQQYPGDIGCFAYFLNLLTLKPGE AMFLEANVPHAYLKGDCECMACSDNTVRAGLTPKFIDVPTLCE MLSYPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\BVP G\SVTEYKDLALDSASILMVQGTVIASPTPTTQTPIPLQGGVL FIGANESVSLKTEPKDLLIFRACCLL |
| 6102 | 70 | 2415 | QTPQATLAANGAEDSRGGEMPLPAGEIGASPAAPCCSESGDERKN LEEKSDINVTVLIGSKQVSEGTDNQDLPYSYSAFIEKEVGNLKL SLKKLDKLEIQRVTSKMQLEEQLTISSEIPKRIRSALKNAEES KQFLNQFLEQETHLFSAINSHLLTAQPMDDLGTMSQIEIER HLAYLKWISQIEELSDNIQQYLMNNVPEAAS TLVSMALDIKL QESSCTHLLGFMRA TVKFWHKILKDKLTSDFEILAQHLWPFIA PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\ HSQKNTLFLPPLLSS/WPIQVMLTPLOKRFYHFRGNRQTNVLS KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG LMMVLLEKLATDIPCLLYDDNLFCHLVDEVLPERELHSVHGYP GTFASCMHILSEETCFQRWLTVERKFALQKMDMSLSSEA WVSQ YKIDITDVDEM KVPDCAETFM TLLVITDRYKNLPTASRKLFLE LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNIYSTVLA DWADNVFFLQQAALVFAENNTLSKLQGLQASMESSVFDDM INLLERLKHDMLTRQVDHVREVKDAKLYKKERWLSLPSQSEQ AVMSLSSSACPLLLTLRDHLLQLEQQCFSLFKIFWQMLVEKLD VYIYQEIILANHFNEGGAQLQFDMTRNLFPFLSHYCKRPNFY KHIKEACTIVLNLNVGSALTAGKDVLPVQLQGSFPAT |
| 6103 | 207 | 2523 | ESNSTMTTYLEFIQNEERDGVFRFSWNVWPSSRLEATRMVVPVA ALFTPLKERPDLPPIQYEPVLCSTRTTCRAVLNPLCQVDYRAKLW ACNFCYQRNQFPSPSYAGISELNQPAELLPPQFSSIEYVVLGRGP PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR MVQVHELGCBGISKSYVFRGT KDLSAKQLQEMGLSKVPVTQAT RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRPWPVPQGRK PLRSSGVALSIAVGLECTFPNTGARIMMFIGGPATQGPGMVVG DELKTPIRSWHIDDKDNAYVKKGTKHFEALANRAATTGHVIDI YACALDQGTGLEMKCCPNLTGGYVMVMDSFNTSLFKQTFQRVFT KDMHGQFKMGFGGTLEIKTPR\BIKISGAIGPCVSLNSKGPCVS ENEIGTGGTCQWKICGLSPTTTLAIYFEVNVQHNAPIPQGG\RG A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD QEAAILMARLAIYRAETEGPDVLRWLDRQLIRLCQKFGEYHK DDPSSFRFSETFSLYPQFMFLRRSSFLQVFNNSPDESSYRHH FMRQDLTQSLIMIPIYAYSFGPPPEPVLLDSSSILADRILLM DTFFQILYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE ILHSRFMPRIYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES GAPILTDDVSLQVFMHLKLLAVSSAA |
| 6104 | 124 | 732 | KVSEYIILSKDKILFHALAMLVLVSPWSAARGVLRNYWERLLR KLQPSRPGFPPSPWGPALAVQ\AQPCLOSQQMIPVEVKRI/RS LDSIFWMAAPKNRRTIEVNRERRRNPQKLKVKNNIDVCPEGH LKQKHVLCAYCYEKVKETAERRRQIGKQEGGPFKAPTITVVL YTGETPSEQDQGRKRIERDRKRPSWFTQN |
| 6105 | 3 | 989 | PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAPVLLLLLFC GSQRKAATAACGRPRMLNRMVGGQDTQEGEWPOQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYQGTASSADVALVEAPVPFTNYILPVCLPD PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR CNLLYSKDTEFGYQPKTIKNMCLCAGFEKGKDACGDSAGPLV CLVQGSWLQAGVISWGECCARQNRPGVYIRVTAHNNIHRIPK |

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|------------|--|--|--|
| 6106 | 3 | 1302 | LQVQPSSEVGRPEVTPPGPGAP GRPPTAPHTGRPPTANRGDPRDLKRGCARLLTSIESRGRPAAS AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPG WSRARHQPGGLCLLLLLLQCFMEDRSAQAGNCWLRQAQNGRCQV LYKTELSKEECCSTGRLLSTSWTEEDVNDNTLFKWMIFNGGAPNC IPCKETCENVDCGPGKKCRMKNKPRCVCAPDCSNITWKGVPVC GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPS STCV\VDQTNNAVCVTCNRICPEPASSEYOYLCGNDGVTYS\SAC HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV GRGRCSLDELCPDSKSDPEVCASDNATYASECAMKEAACSSGV LLEVKHSGSCNSISEDTEEEEEDEDDQYSFPISILEW |
| 6107 | 623 | 168 | SRCSFPRPEPGRGRGK/LSPSEHRRKWVEVFKACDEHKGYSRE DFKTAVVMFLFGYKPSKIEVDVSMSSINPNTSGILLLEGFLNIVRK KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFFKAQRQVAPKLPE RTVLEVFREV\DRDS\DGHVSF |
| 6108 | 3 | 1348 | GGSLRFSPFPRVPCSRVFCPVFPGGCGLPSPMSASRPQSPTTPW CLPRRYMKHKRDGPEKQDEAVDVTVMTCVFFVMCCSMLVLL YYFYDLLVYVYVIGIFCLASATGLYCLAPCVRRLP\SASAGESA LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ WAWVLQDALGIAFCLYMLKTI RLPTFKACTLLLLVLFYDIFFFV FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL ALCDRPFSLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI AYGVGLLVTFVALALMQRGQPALLYLPCTLVTS CAVALWRREL GVFWTGSFGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE PATSPWPAEQSPKSRSTSEEMGAGAPMREPGSPAESSEGRDQAQPS PVTQPGASA |
| 6109 | 1 | 1381 | CRSRAGAASGGAILLEGTKLRRQRVDTNKPLDPLVPSALRAAMLY LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNDQLEQRVSEFF MNAKKNKPWEERQMASIKKDYKALEDADEKVQLANQIYDLVD RHLRLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN HHAHSHTPVEKKRYNPTSHHTTTDHIPEKKFKSEALSTLTSDA SKENTLGCRRNNNSTASSNNAYNVNSSQPLGSYNIGLSSTGTGAG GI\TMAAAQAVQATAQMKEGRTSSSLKASYEAFKNNDQQLGKEF SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSNNNKSSS QQSSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT YDPNEPRYICINQVSYGEMVGCDDTQDCPIEFHYGCVGLTEAPK GKWYCPQCT\AAMKRRGSRHK |
| 6110 | 77 | 2464 | ACPSAATMSDQDHSMDMTAVVKIEKGVGGNNGGNGGGGAFSQ ARSSSTGSSSSSTGGGGQESQPSPLALLAATCSRIESPENENSNS QGPGSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG SSTNGSNGSESSKNRTVSGGQYVVAAPNLQNNQVLTGLPGVMP NIQYQVIPPQFQTVGQQLQFAATGAQVQDQSGQIQIIPGANQQ ITNRGSGGNIIAAMPNLLQQAQVPLQGLANNVLSGQTQYVTNVP VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGMNFTTSG SSGINSQGTQPRVSGLQGS DALNIQQNQTSGGSLQAGQQKBE Q\NQQTQAAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA ISQETLQNLQQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQQLNLQ VQNPQAQTITLAPMQGVSLGQTSSTNTTLTPIASAASI PAGTVT VNAAQLSSMPGLQITINLSALGTSGIQVHPIQGLPLAIANAPGDH GAQLGLHGAGGDIHDDTAGGEEGENSPDAQPQAGRRTREACT CPYCKDSEGRSGDPGKKKQHI CHIQGCGKVYKTSHLRAHLRW HTGERPFMCTWSYCGKRFTSRDELQRHKTHTGEEKKFACPECCK RFMRSDHLSKHIKTHQNKKGGPGVALSVGTLPDLSGAGSESGT ATPSALITTNMVAMEAICPEGIARLANSINGINVEGGQFCSPINT SANGF |

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|------------|--|--|--|
| 6111 | 1637 | 797 | RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG SVEAVARLKRSRLKVRFCNTESQKSRAELVGQLQRLGFDISEQE VTAPAPAAQCILKERGLRPYLLIHGCV\ASEFDQIDTS/STPNC VVIADAGESFSYQNMNNAFQVLMELKPVILSLGKGRYYKETSQ LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG YVDNLAEAVDLLQHADK |
| 6112 | 77 | 196 | MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK |
| 6113 | 1779 | 567 | WEGRSWAACGVNLQGAWERSGVRASEAESPGKRAVSVWWSRQL ETMVDHLANTEINSQRIAAVESCFGASGQFLALPGRVLLGEGVL TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEV TLELLPETLQAKNRMIKTAKKSFVVSAAATERQEWISHIECV RRQLRATGRPA\STEHAAPWIPDKATDICTMCTQTRFSALTTRH HCRKCRVVVCAECRQRFLPRLSPKPVVRVCSLCYRELAQQRK EEAEQAGVPRAAASHLARPICGRPVEMTMTPTTRRAAGTATG PAAWSSTPRGWPLPSTADPRPAEHLSPSLHCPGPGQEGSSRSC PGLRDPPIPWQVQRWGVALSGLPVFFCWTLCPIYGFTAGNAFFPR KPQNTHRSW |
| 6114 | 818 | 246 | PTSRPRPSPGSPAMSWACVSAAPSSSWPASSWPCGPRRCCTR RRRCSPRCGLAAGSMCSCSPSWRCTPVPAWSPPPP\PAEQVQC GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCLLAATEPTPSRPHQRWTRDRMLGRGSQVT GRPQWFLRGLVLFSL |
| 6115 | 324 | 71 | DVCGRVCAPHLYTHIHMHCAC\IHTHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTPHPTAVHKEHRADVLRLTTLPLR |
| 6116 | 595 | 1430 | TGVMPPGRWHA/ISSSGPVFEGARA\LTQVKKEEEDSYTFVQ AARQTLNRPGQELFRQLFRQLRYHESGPLETSLRLRELCRW LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\ L WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL ASPLRSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSDQEWGLDSAQRN LYRDVMLENYRNMAISLGK |
| 6117 | 1433 | 222 | VGVPSFAPPCSWEVGPGGWTGPIIKEGQGGRRTPLLLLATRTR GLLSLFPPAAMHPAFLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLOGLVEAHPDNACSPIAPPPAPV NGSVFIALLRRFDCNFDLVLNAQKAGYGAAVVHVNNSNELLNM VWNSEBIQQIWIPIPSVFIGERSSEYLRALFVYKGARVLLVDPD TPLGYLIIPFTGIVGLLVAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQVDVCAICLDEYEDGDKLRVLPCHAY HSRCDPWLQTQRTKTCPICKQPVHRGPGDEDEQEETQCGEGDE GEPRDHPASERTPLLGSSTPLPTSFGSLAPAPLVFFGPSTDPPL SPPSSPVILV |
| 6118 | 1044 | 247 | STISCRACSTGATPGAQSHRSARGHAAGGKETAALGMRGKVKK KEKETQKEKIGEGREEKVKRKEVEQKI KQEKQEKQERRK GK EKEEKRTQKGKETNKEKEQFKGQEEKGENKDSLTTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYSN/ADSLARSFVSGFKQDSQP ITWAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II |
| 6119 | 1217 | 462 | DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLNGVLTIVLEEDGTAVDSBDFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSDIARFTFDVYKQNPRL FGLSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ GLGHMLLGISSTLRHAVEGAEQWQKGRLSHY |

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|------------|--|--|--|
| 6120 | 785 | 179 | LERAGGGGLSSRALVGSAGCLSLVARANGKGLPRGRKEFVRAVR VRYVAPRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR SSRAGLQFPVGRVHRLLRKGNVAERVGAGAPVYLAHVLEYLTAE ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTIAQG G\VLNPIQAVLLPKKTESQKDEGANDP |
| 6121 | 1612 | 107 | FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE KLMRCSQCRVAKYCSAKCQKAWPDHKRECKLKSCKPRYPDS VRLLRVVFKLMDGAPSESEKLYSYFDLESNINKLTEDKKEGLR QLVMTFQHFMRREEIQDASQLPPAFDLPEAFKVICNSFTICNAE MQEVGVGLYPSISLNLHSCDPNCSIVFNGPHLLRAVRDIEVGE ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAISSNSERL PDINIYQLKVLDCAMDACINLGLLEALFYGTRTMEPYRIFFPG SHPVRGVQVMKVGKLQLHQGMFPOAMKNLRLAFDIMRVTHGREH SLIEDLILLE/AMRRQHQSIILRERSQREIRRVSLNALLRSHT LCFVSCVNLVSYWKFCVSVFV |
| 6122 | 2 | 2324 | RFRKMDGGAASQDESSAAAAAADSRMNNPSETSKPSMESGDG NTGTQTNGLDFOKQFVPVGGAISTAQAQAFGLHGHQVQLAGTSL QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA GGQITGLTLTPAQOQLLQQAQAQALLAAVQQHSASQQHSAA GATISASAAATPMTQIPLSQPIQIAQDLQQLQQLQQLNMLQQFV LVHPTNLQPA\QFIISQTPQGGQGLLQA\QNLLTQLPRQSQA NLLQSQPRI\TLTSQPATPTCTIAATPIQTLPSQSTPKRIDTSL LEEP\SDLEELQFAKTFKQRRIKLGF\QGDAGLAMVKLYGND FSPTTIFRFBALNLSFKNMCKLKLPLEKWLNDENLSSDSSLS PSALNSPGIEGLSRRRKRRTSIEA\NIRVALEKSFLN\QKPTS BEITMIADQLNMEKGVIRVWFENRRQKEKRINPPSSGG\TSSSP IKAIFPSPTSLVATTPSLVTSAAATTLTVSPVPLPLTSAAVTNLS VTGTSDDTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA SSASESTTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTSL GALSPALMSNSTLATIQALASGGLPITSLDATGNLVFANAGGA PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA TSTSAESIQNLSLFTVASASGAASSTTTTASKAQ |
| 6123 | 3 | 2944 | HLLHRWFQTDQMNFMTTGEFQLTEACPYLGTHSEESRFGILHL HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPAGGSLRFKVPESTLMDCCRQLKDSKQILSIT KNFKVENIGPLPITVSSSLKINGYNCQGYGFVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLGVILIAFQQAQYIIM EFMKTRQRQNASSSSQONNGPMDVISPHSYKSNCKNFLTDTYGPS DKGRGKNCLPVNTPQSRIQNAKRSPATYGHSSQKHKKSVMYYSK HKTSTAAASSTSTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQDLPETSRKNGNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGLN QNLNWSKSRTCRKNKKRGVAPVSRPPQSCLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREABGYQKPEK KCVDFKCSDDSSDCGSSSGSVRASRGWSGWSSTSSSDGDKPM VDAQHFLPAGDSVSQNDFFSEAPISLNLSHNCNPMGTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVQIESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAPP EENMNYANGFPADVQTDIFIDHNSQSTWNTPP\NMPAS\WGNA QFPSSSRPYLKSTPKACLPMGSLFGPI\WAP\QSDVYENCCPIN |

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|------------|--|--|--|
| | | | PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAVMNLDIWT\A NRNANFPLSRDSSYCGNV |
| 6124 | 1573 | 236 | SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL GAPLPFFRAIRVTCIGSCGVSNKANDTAWVEEGYFNSSLSLADK GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF SKDHKCSLVFYILSPLNLSIPDIEQPNVASATKKFSYKLVKTG SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV SYKAKRWIHDVRTIAEVEGAGVKAWRRRAQWHEQILVLPALPQSAL PGCSLIHIDYYLQVSLKAPEATVTLVPVFIGNIAV/NPCPSBPPA RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS HSQRQPLLATLSSVPGAPEPCPDGSPASHPLHPPLCISTGATV PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAAPPSEYQSCGGVE PSLTPE |
| 6125 | 1 | 904 | KTCPKLTCAFTVSVDPSCCRVCRGDGELSWEHSDGDI FRQFANR EARHSYHRSHYDPPPSROAGLSRFPGARSHRGALMDSQQASGT IVQIVINNKHKGQVCVSNKGYSHGESWHPNLRAPGIVECVLC TCNVTKECKKIHCNRYPCYPQKIDGCKCKVCPG/KKAKEEL PGQSFDNKGYFCGEEETMPVYESVFMEDGETTRKIALETERPPQV EVHVWTIRKGIHQHFIKISKRMFEELPHFKLVTRTTLTSLQWKI FTEGEAQISQMCSSRVCRTLEDLVKVLRLERSEKGGHC |
| 6126 | 1224 | 389 | RLLEAPCPRSRRRFQMNPEWQAFVHVAVAGGLCAVAVFTGIF DSVSQVGYEHYAEAPVAGLPAFLAMPFNSLVNMAVTLGLSLW HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRRLWTQWRAAVLDQ WLTLPFAWPAWCLYLDGRWRP\WLFSLCVCVSLASVGLALLH PQGFVALGAHVVPVAVGQALRT\HRHYG/SATPSATYALGVLS CLGFVVLKLCQHQLARWRLFQCLTGHFNSKVCVLDLQFHFAFLFL THFNTHPRFHPSGGKTR |
| 6127 | 1335 | 463 | VLPRCLVFFVNTMDSSREPTLGRDLAAGFWQVQWRFDADEKGY IEEKELDAFFLHMLMKLGDDTVMKANLHKVKQFMTTQDASKD GRIRMKELAGMFLSEDENFLLLFRENPLDSSVEFMQIWRKYDA DSSGFI SAELRNFLRDLFLHKKAI SEAKLEEYTGTMKIFDR NKDGRDLNLDLARI LALQENFLQFKMDACSTEKRGDFEKFIFA YYDVSKTGALEGP\EVDGFKMMELVQPSISGVLDLDFKFEILL RHCDVNDKGKIQKSELALCLGLKINP |
| 6128 | 2511 | 843 | TCRMSRRQLERWVWSSQVQARGNRVAPRLGKIAMGLEMSKSD SPGSLDGRAWEDAQKPSAWCGGRKTRVYATSSRRAPPSEGTTR GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTS MSSQVVGIEPLYIKAEPA SPDPKGSSETETEPVALAPG\ PAP TRCLPGHKEEDGEGAGPGEQGGKLVLSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSI EYSCPASNECEITKRRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLFPFGP FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDEAGPD GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS VWMEVLVLGVAQRSLLTQDELAFAYLVLDDEEGARPAGLGELG\ AALLQLVRRQLALRLEREYVLLKALALANSDSVHI EDEPRLWS SCEKLLHEALLEY EAGRAGPGGAERRRAGRLLLTPLLRQTAG KVLAFYGVKLEGVPMHKLFLMLEAMMD |
| 6129 | 1764 | 771 | ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK HPCNASMECDKQRRQKNRAFCYFCNSVQKLPICACQCGKTKCMM KSSDCVIKHAGVYSTGLAMVGAICDPCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDHGGRI FSCSFCHNFLCEDDQFEHQAS CQVLEAETFKVSCNRLGQHSCLRCACFCDHTRSKVFKQKAG KQPPCPKCGHETQETKDLMSSTRSLKFGRTGGEEGDGASGYDA YWNLSDDKYGDTSYHDEEDEYEAEDEDEDEDEGRKDSSTESS DLFTNLNLGRTYASGYAHYEEQEN |
| 6130 | 3 | 577 | GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE |

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|------------|--|--|--|
| | | | DFYRKEIEV\DSSPSVAGISWTQQTQEQF\ASMRDLYIKKGQGC ILVYSLVNQQSFQ\DIKPMRDQIRVKVSEKVPVI\LVGN\SVD LESEREVSSEGRALAEWGC PFMETSAKSKTMVDELFAEIVRQ MNVAAQPKDDPCCSACNIQ |
| 6131 | 3 | 1811 | SSPREKTSDDSHRPSRHGFLFLRLVGLSPFSYLCVPPSRFPVPGS PRSLSAMRLLPLAPGRLLRGRSPRHLFSCSPALLLLVLGGCLGVF GVAAGTRRPNNVLLLTDDQDEVLGGMTPKKTALIGEMGMTFS SAYVPSALCCPSRASILTGYPHNHVNNNTLEGNCSSKSWQKI QEPNTFPAILRSMCGYQTF\AGKYLNEYGAPDAGGLEHVPLGW SYWYALEKNSKYNYTSLINGKARKKHGENYSVDYLTDLANVSL DFLDYKSNFEPFFMMTATP\APHSPTAAPQYQKAFQNVFAPRN KNFNIHGTNKHWRQAKTPMTNSSIQFLDNAFRKRWQTLTSSVD DLVEKLVKRLFTGELNNTYI FYTSDNGYHTGQFSLPIDKRQLY BFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPITLDIAGYDLNK TQMDGMSLLPILRGASNLTRSDVLVEYQGEGRNVDPDTCPSLS PGVSQCFPDVCEDAYNNTYACVRTMSALWNLQYCEFDQEVFV EYVNLTAQPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT PGVFDPGYRFPRLMFSNRGSRVTRRFSKHL |
| 6132 | 96 | 1241 | AAGLLPGLVPEDPRRTNLLPFGIQGPPFALSRLPFCVESGW AWEAMEPEFLYDQLPKGVEPPAEELS KGGKKKYLPTSRKD PKFEELQKPA\VLMEWINATLLPEHIVVRSL EEDMFDGLILHHL FORLAALKLEAEDIALTATSQKHKLTVLEAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI ESTKSGLKSEKLVQLTEYSTDKDEPPKDVDFELFKLAPEKVNA VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLTNPSPAEMLHNVTLALELL/IGRGPALQPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN |
| 6133 | 2 | 4256 | FVHGSMADTDLFMECEEELEFPWQKISDVIEDSVVEDYNSVDKT TIVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTPVLR PVQVMQNAHVTSPPVASQPIFITTQGFVVRNVRPVQAMQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTFVRPG STMPVRPTNTFTTVIPATLTIRSTVPQSQSQTKSTPSTSTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPFPSPPAVSIASFT VKRPVGTGENSNEVAKLVNTLNTIFSLGQSPGPVVVSNNSAH\ GSQRTSGPSSMKVTSSI PVFDLQDGGRIKCPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHKMDTHKPGEMPYVCQVCQYRSSLYSEVD VHFMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTRKPKQLEGLKPGTKVTIRA SRGQPRTPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPSPSPPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHQALALPPLATEGAECNLVDDQDEGSPVTQEP E LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIIRRLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQLP VNEETLFQKATKIGRSLEGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIIDEISLFL DTEVLSSDDRKENALQTVGTGBPCDVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVQKHATACQ RSKGMLVMDCHRTLHSEVLAMLSASSTLPVVPAGCSSKIQPL |

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|------------|--|--|---|
| | | | DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPDPGNINSPTRNADMQEELIAS LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI |
| 6134 | 2 | 4256 | FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAAPVPIAAHASVAGHLSTSTTVSSSGAQNDSSTK KTLVTLIANNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQANANHTSSPVASQPIFITTQGFPPVRNVRPVQANMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPOVFSQMTFVRPG STMPVRPTTNTFTTVPATLTIRSTVPQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSAH\ GSQRTSGPESSMKVTSSI PVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPVVCQVCYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNAGNAQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTPVPSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFNFHFTTYVHCSLCRYST CCSRAYANHMNNHVPKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPSPSPPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHQALALPPLATEGAELNVDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPLVIFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMVMDCHRTLSSEVLAMLSASSTLPVVPAGCSSKIQPL DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPDPGNINSPTRNADMQEELIAS LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI |
| 6135 | 2 | 4256 | FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAAPVPIAAHASVAGHLSTSTTVSSSGAQNDSSTK KTLVTLIANNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQANANHTSSPVASQPIFITTQGFPPVRNVRPVQANMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPOVFSQMTFVRPG STMPVRPTTNTFTTVPATLTIRSTVPQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSAH\ GSQRTSGPESSMKVTSSI PVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPVVCQVCYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNAGNAQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTPVPSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFNFHFTTYVHCSLCRYST CCSRAYANHMNNHVPKSPKYLALFKNSVSGIKLACTSCTFVT |

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|------------|--|--|---|
| | | | SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPSPSPFNKAATVKSAGATPAEPEELLTPALAPALPSPA STATPPPTPTHPQALALPPLATEGAECNLVDDQDEGSFVTQEP E LASGGGSGGGVGGKKEQLSVKKLRVVLFCNCNTEQAAEHFRNPQ RRIIRWLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMLVMDCHRTLSSEVLAMLSASSTLPAVVPAGCSSKIQPL DVCIKRTVKNFLLHKKWKEQAREMADTACDSDVLLQLVLVWLGVE LGVIGDCPELVQRSFLVASVLPDPGNINSPTRNADMQEELIAS LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI |
| 6136 | 1704 | 539 | FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEYRLGQVAS SLFRGEHHSRGGTGRLASLFSLEPQIQPVYVPVK\ESALASA DLEEEIHQKQGOKRKNSQPGVKVADRKILDDTETVVSQRKKIQ INQEEERLKNERTVFGNLPVTCNKKLKSFFKEYGQIESVRFR SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK RGAQIADGFRIRVDLASETSSRDKRSVFGNLPYKVEESAIEK HFLDCGSI MAVRIVRDKMTGIGKGGFYVLPENTDSVHLAKLNN SELMGRKLRVMSVSNKEKFKQNSNPRLNKNSKPKQGLNFTSKT AEGHPKSLFIGEKAVLLKTKKGQKKSGRPKKQKQK |
| 6137 | 141 | 2656 | RALRKRRCPGRRGALGSGGPGPQRRPGRVPEERPAPEERKHG MWNLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGD LAKK YLWQ\LFQLYLDEAGRGHSFSGHGAALTAPKQGOELMAKALLES LSCPKDMAPSHCAEHKQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIIFYFSVPFAYEDIARNINSSCRPGGAWLRVV LEKPPFGHDHPSAQQLATELGTFQBEEMYRVDHYLKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYBEYGV IRDLQNLHTEVLTIVAMELPHNVSSAEAVLRHKLQVFOALRGL QRGSVAVGQYQSYSEQVRRELQKPDSPHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCQSEKHMAAQS QCLPRQLVFHIGHDLGSPAVLVSRNLFPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLSELAHKAPRLYPGAENGRLLDFEPSSGRLFPS QQQPEQLVPGPGPGMPSPDFQVLRKYRESSLVSAWSEELISKL ANDIEATAVRVRRFGQFHLALSGGSSPVALFQQLATAHYGF PW AHTHLWLVDERCVP LSPDFESNFOGLQAHLLQHVRIPIYNIH\AM PVHLQORLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPGTGLDGEQLVVLTTPSPSQPHRRMSLSLPLINRAK V AVLVMGMRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFIG |
| 6138 | 4587 | 934 | EFSKLTDRWQNAVQGVQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKQGERFSLYQTRSLIHELKKNKEIHFQRRRTTCAL TLEAGEKLLLTDLKTESVGRRIISQLQDSWKMEPQLAEMI KQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHROWEDLCRLVAIRKQEIIDLRLNTWVVFNEKNKELCAWLQVM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKILQLKQMGDQL IKASNKSRAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFIFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLHSDACANETECDSIQQTTRS LDRWRNICAMSMERRMKIETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRLRHFT |

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|------------|--|--|---|
| | | | NQREEFEGTRESILVNLTEMDLQLTNVEHFSESDADDKMRQLNG FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDVLIIEDELELHR YCOEVFGRVSRFHRRLTSCPTGLEDEKEASENETDMEDPREIQT DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETFPVSDS\IPLE WDHTGRRGGPSSSH\EEDEBAQYY\SALSGKSISDGHSHWHPDS PSCPEHHYKQMEGDRNVPPVPPASSTPYKPPYKLLLPPTDGG KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIAQEL\HNK LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQIE LRVKRLQEILKAFDITYKALVSVNVSSKEFLQTESPESTELQSR LRQLSLLWEAAQGAVDSWRGGRLRQSLMQCQDFHQLSQNLLLWLA SAKNRRQKAHVTDPKADPRALLECRRELMOLEKELVERQPDVDM LQETSNLSLLIKGHGEDCIEAEKVVHI\EKKLKQLREQVSDLM ALQQTQNPASPLPSFDEVDSDGQPPATSVPAAPRAKQFRAVRTTE GEEETESRVPQGSTRPQRSFLSRVRAALPLQLLLLLLLLAACLL PSSSEEDYSCTQANNF\ARSFYPMRLRYTNGPPPT |
| 6139 | 52 | 1131 | LGDVWVSRTCGVLETPTSVLRRARARGPCPTDSKWLPRLEGE TERRPWEASSWKT/LAGWIGGAASVIVGHPLDTVTRLQAGVG YGNLSCIRVVYRRESMFGEFKGMSFPLASIAVYNSVVFVFSN TQRFSLQHRCEPEASPPRTLSDLLASLVAGVSVGLGGPVDL IKIRLQMOTPPVSGRQPRFEVQSGSGCG\EPAYQGVHCITITIV RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACT PSPCAVWLAGGMAGAIISWGTATPMDVVKSRLQADGVYLNKYKGV LDCISQSYQKEGLKVFFRGITVNAVGRGFMSAAMFLGYELSLQA IRGDHAVTSP |
| 6140 | 694 | 136 | RPELEMLRLRSRWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALEPLGPAPV SVAPQAEAEARSTFGPAGSRLGPETFRQRFRQFRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRRTDVIRITG |
| 6141 | 2 | 984 | AQVGPRSRPCKMPLKLRGKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAGHSATGRVEGFSSIQELYAQLAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKITCVGDHIESI NGENIVGWRHYDAKKLKEKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTNFEAGKDKVNPDEFAVALDETLDGFAPF DEFVFDVVGVIIDAKRRGL |
| 6142 | 116 | 602 | EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEVRQLMEKL REKQLSHSLRAVSTDPHHDHDEFC\LMP |
| 6143 | 2802 | 270 | FRMRIFLHCPWNQMWKIWNLLSLESCKAHLISIQKLLKER/Q QLPVFKHRDSIVETLKRHRVVVAGET\GSGKSTQVPHFLLED LLNEWEASKCNIVCTQPRRISAVSLANRVCDLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLRLKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLILKEILQKRSOLHLILMSATVDSE KFSTYFTHCPILRISGRSYVPEVFHLEDIEETGFVLEKDSYC QKLEEEEEVTINVTSKAGGIKKYQEIYIPVQTGAHADLNPYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLSNDRRFYSERYKVALHSILSTQDQAAAF TLPPPVGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSIVETFVSKASALQROGRAGRVRDGFRCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSBDFLSKALDPPQLQVINS AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTESPFPTTIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVQKE |

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|------------|--|--|---|
| | | | LIKLVKAAGFSSSTTSTSWEGNRASQTLSFOEIALLKAVLVAGL YDNVKGKIIYTKSVDTVTEKLACIVETAQGKAQVHPSSVNRDLQTH GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIQVQHRERLLS IDGWIYFQAPVKIIVFKQLRVLIDSVLRRKKLENPKMSLENDKI LQIITELIKTENN |
| 6144 | 1289 | 568 | SGPGSMGQQRVDVKVVMGKEYVGKTSLSVERYVHDRFLVGPYQN VSASGGARHGGRSGGVPVICTYGPDLFPLVA\TIGAAFVAKVMS VGRDRTVTLGIWDTAGSEREYAMSRIYYRGAKAAIVCYDLTSSS FERAKFWVKELRSLSEEGCQIYLCGTKSDLEEEDRRRRRVDFHDV QDYADNIKAQLFETSSKTQSVDLFPQKVAEDVVSAAAFQVMT E DKGVDLGQKPNPYFYSCCHH |
| 6145 | 1109 | 196 | GGMDLSELERDNTGRCLSSPVPVAVCRKEPCVLGVDEAGRGPVL GPMVYAIYCPLPRLADLEALKVADSKTLESERERLFAKMETD DFGWALDVLSPNLISTSMGLRVKYNLNSLSDTATGLIYALD QGVNVTVQFVDTVGMPEYQARLQSSFPGIEVTVKAKADALYPV \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD /TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSHYFLERGLESTTS L |
| 6146 | 428 | 781 | LKKKGKEKAEAAQQVEALPGPSLDQWHSAGEEEDGPVLTDEQKS R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE EIVTKERHREINKQATRGDCCLAFQMRAGLLP |
| 6147 | 1 | 2304 | GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMKLKLYYGLSE GEAAGRPAGPDPLDPTDLNGAHFDEPVYLDKLRRECPLAQLMDS ETDVMVRQIRALDSMQTLVYENYNKFISATDTIRKMKNDFRKME DEMDRLATNMMAVITDPSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEP A EELCEEFLAHARGRLEKELRNLEAELGSPPPADVLEFTDHG\ S SGFVGGLCQVAAAYQELFAAQGPAGAELKLAFAARQLGSRYFALV ERRLAQEQGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYPFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHTYVKVQGLVISQMLRKSVEITRDNLSTLEPRNVRAVMKRV VEDTATIDVQVLPRLAGVALTQAGGTVP SRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTVQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK |
| 6148 | 3056 | 353 | VPAVGGTTFADGAMGEAEKFHYIYSCDLIDINVQLKIGSLEGKREQ KSYKAVLEDEPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNNEWLKLVPKYPDLP RNAQVALTIWDVYGP GKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDMQSRILAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRVCVKDDKEYGIVYEEKDGEDESSPILTSFE LVKVPDPQMSLENLVESKHNLPRLSRSGPSDHDLPKYPSPRPDQ LKNIVSYPPSKPPTYEEQDLVWFEFRYLTNQDKALTILTSVIW DLPQGAQALALGKWKPMVDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLMLYLLQVLQALKYENFDDIKNGLEPTKKDSSQSSVS ENVNSNGINSAEIDSSQIIT/SAPFSPVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANLYLYWYVIVECEDQDTQQRDPK THEMYLNVMRFRSQALLKGDKSVRVMRSLAAQQT FVDRVLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDELIPLEPQVK IRGII PETATL FKSALMPAQLFFKTEDGGKYPVIFKHGDDL RQD QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV |

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|------------|--|--|--|
| | | | PVAEVLDTGEGSIQNFRRKYAPSENGPENGISAEMVMTYVVKSCAGY CVITYILGVGDRHLDNLLTKTKGLFHIDFGYILGRDPKPLPPP MKNLKMVEGMMGTQSEYQYQFRKQCYTAFHLRLRYSNLILNLF SLMVDANIPDIALEPDKTVKKVQDKFRDLSDDEAVHYMQSLID ESVHALFAAVVEQIHKFAQYWRK |
| 6149 | 1 | 1413 | RVDPVRRENGTANPIKNGKTSFASKDQRTGKKTSSVQGVQKQND ESESDFESDPPSPKSEEEEEQDDEEVLDQEQGDFNDDTPEPNL GHRPLLMDSDEEEEEKHSSDSYEQAKAKYSDMSSVYRDRSGS GPTQDLNTILLTSAQLSSDVAVETPKQEFDFVGAVPFFFAVRAQQ PQKEKNEKNLPQHRFPAAGLEQEEFDFVTKAPFSKKVNVQECH VGPEAHTIPGYPKSVDFVGSSTPFQPFLLTSTSKSESNEFLPLG FDEITGSQQQKVKQSLQKLSSRQRRTKQDMKSNKGRHGTPT STKTKLTPTYRTPERARRHKKVGRDRSQSSNEFLTISDSKENIS VALTDGKDRGNVLQPEESLDDPFGAKPFHSPD\LSWHPP\HQGL S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F LTELVVQSITPHQSQQSQPV\BLDPFGAAPPFSKQ |
| 6150 | 372 | 37 | MSNKKYIIDYDWKASITETIDHDMTEBKLHQINNFWSSEYR LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG QEGWPPMDGSEGIPTDIDTSGIF |
| 6151 | 1555 | 521 | DSNQSVSGTAASTLLHSFKATIIYQGTGHVQQFYGVTS PYSQT TPPIVQSYAQPSLQYIQGQIIFTAHPQGVVQPAAAVTTIVAPG QPQLQPSSEMVTNNLLDPPSPPKPTIVLPPNWKATARDPEG KIYYHYVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPPYDEN PMK\ASKKPKTAEADTSELAKKSKVFRKEMSQFIVQCLNPYR KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DL NENVKHKTKEYIKKYMOKFGAVYKPKEDTEFRVTGPGWEDGWS GKTDSSRERKSCGPPCSTPVSIVLLMIHHPGBFNPADVN |
| 6152 | 1366 | 648 | NRTWSTPSTWGMVALPFLCSTGFWPVTQTARTTCGAVPAKCP PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRC KCEHHCPDCKTGNCSVSRVKQCLQPPEATLRAGELSFPTRTAW LALTLALAFLLLIISTAANLSLLSRAERNRRLHGDYAYHPLQEM NGEPLAAEKEQPGGAHNPFKD |
| 6153 | 2 | 3368 | GRVGARSPGRAYALLLLLCFNVGSGLHLQVLSTRNENKLLPKH PHLVQRKRAWITAPVALLEGEDLSKKNP IAKIHSDLAEERGLKI TYKYTGKGITPPFGIFVFNKDTGELNVTSILDRBETPPFLLTG YALDARGNNVEKPLELR I KVL DINDNEPVFTQDVFGSVEELSA AHTLVMKINATDAEPNTLNSKISYRIVSLEPAYPPVFLNKDT GEIYTTSVTL DREHSSYTLTVEARDNGEVTDKPVKQAQVQIR ILDVNDNI PVVENKVLEGMVEENQVNVETRIKVFDADEIGSDN WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKND FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI SIYVSSEMDRSSKQIIIGNFQAFDEDTGLPAHARYVKLEDRDNW ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDPYRKT TGTVLINVEDINDNCPTLIEPVQTI CHDAEYVNVTAEDLDGHPN SGPFSFVIDKPPGMAEKWKIARQESTSVLLQOSEKKLGRSEIQ FLISDNQGFSCPEKQVLTITVCEVLHGS\GCREAQHDSYVGLGP AAIALMILAFLLLLLVPLLLLMCHCGKAGKFTPIPGTIEMLHP WNNEGAPPEDKVVPFLPVDQGGSLVGRNGVGGMAKEATMKGSS SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE TTITARATGASRDVAGAQAVALNEEFKNYFTDKAASYTEED ENHTAKDCLLVYSQEETESLNASIGCCSPIEGELDDRLDGL KFKTAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM VNSENTYSSGSSFPVPSLQEAANAQKVTQEVTERSVSRRQAK VATPLPDPMASRNVATETSYVTGSTMPPTTVILGPSQPSLIV TERVYAPASTLVDPQPYANEGTVVVTERTVIQPHGGGSPLEGTQH |

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|------------|--|--|---|
| | | | LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL APASTLQSSYQIPTENSMTARNITVSGAGVPGPLPDFGLEESGH SNSTITTSSTRTVKHSTVQHSYS |
| 6154 | 3660 | 2146 | KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKDLDTDAKN SDTAHIKSIETISILNGLQASESSAEDSEQDERGAQDMNDNGK EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDITDKSSKPQIK RGKRRYCNTEELKTGSPGKKEEKAKNKESELCMENSSNSSSDED EETKAKMTPTKKYNGLEEKRSRLRTTGfYSGFSEVAEKRIKLL NNSDERLQNSRAKDRKDVWSSIQQGWPKKTLKELFSDSDTEAAA SPHPAPEEGVAEESLQTVAEESCSPSVELEKPPPVNVDSKPI EETKTEVNDRAEFPSSSGSNFSA*IPLPYLHLNRLHQSL*QKGS RQSSSVTVSEPLAPNQEEVRSIKSETDSTIEVDVAGELQDLQS ERE*LASRF*QCELEQ**SARTRTS*KSLYRSEKSERCSGRRK FIKKAEEKP*SNSGKQKEGK |
| 6155 | 869 | 121 | HLLPELRGKSWITMKYVFLGLVLAGTFFADSSVQKEDPAPYLV YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMGNFKSRVRDG TEQTNPIQIVRYWNYSHSAPQDDMLIKLAKPAMLNPKVQALN P/PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLAPVMSDRE CQKTEQKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGTIE VGHEMGDVGIIYTNVYKYVSWIENTAKDK |
| 6156 | 5725 | 3984 | GTSTVTMATKKHFSIILNLLGMLKKDNQDTRKLLMTWALEVAV VMKKSETYAPLFLCPSFHKFCCKGLLADTLVEDVNICLQACSSHL ALSSSLPDDLLQRCVDVCRVQLVHRGTICIRQAFGKLLKSIPLGV FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFIFY GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDVWLQW AIWEAAQFTVLSKLRTPLGRAQDTFQTEGIIIRSLAGHTLNPDQ DVSQWTTADNDEGHGNNQLRLVLLQYLENLEKLMYNAYEGCAN ALTSPPKIVRTFLYTNRQTCQDWLIRLSIMRVGLLAGQPAVT VRHGFDDLTEMKTTLSQGNELVSIIMMVVEALCELHCPEAIOG IAVWSSSIYVGHLLWINSVAQQAEGRFKASVEYQEHLCAMTGV DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSPKPTDSS PEVINYLGNKACECYISTADWAAVQEWQNAIHDLLKSTSTSLN LKADFNYIKSLSSPESGKFVECTEQLELLPGENINLLAGGSKEK IDMKLLLRNM |
| 6157 | 946 | 329 | MANRGPSTYGLSREVQEKEIEQKYDADLENKLDVWIIILQCAEDIEH PPGGRAHFQKWLMDGTVLCKLINSLYPPGQEPPIPKISESKMAFK QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL GSVAVTKDDGCVRGEPSPFHRKAQONRRGFSEBQLRQGNVIGL QMGSNKGASQAGMTGYGMPRQIM*DAASCP |
| 6158 | 441 | 1482 | LGSILVLSLHCKVIFSSQSLEAMKEKAVDLVPILAQNPGLAQN PILEGKDHQNTGVDPIDHVDQRKTD/SRSKSPHKRSKSRER RKSRSRSHSRDKRDKTREKIKERKERVKEKREKEREREKEKE KERGNKDRDKEREKREKDKEREREREKEHEKDRDKEKEKE QDKEKEREKDRSKEIDEKRRKDKKSRTPPRSYNASRRSRSSRE RRRRSRSSSRSPRTSKTIKRKSSRSPSPSRNKKDKREKERD HISERRERERSTMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD SSVSKEVDDKAPRTEENKIQHNGNCQLNEENLSTKTEAV |
| 6159 | 53 | 84 | AVIAPLHISLGDRAAPYLKNTKSSSTTCRRRNQSFPPVMSLTH RLHLCKYWGCAVSNVCRFWEGRPPLPLMIVVPYTLVPSLPGSCV IITGTPILTfVKDPQLEVNFYTGMDSDSDIAFQFRHLHFGHPAIM NSCVFGIWRYEKCYLLPFEDGKPFELCIYVRHKEYKVMVNGQR IYNFAHRFPASVKMLQVFRDISLTRLVLISD*GRCVRITAVQEF DVSVSCDCTTAYQPG |
| 6160 | 1626 | 1790 | AGAKFFP*F*KVADAQPTSEKEIYNQVNVVLKDAEGILEDLQS YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGLKPKFYFSQR |

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|------------|--|--|--|
| | | | LEAALRGLLGALTSTPYSPTOHLEREQALAKQFAEILHFTLRFDELKMTNPAIQNDFSYYRRTLSRMRINNVPAGEGENEVNNELANRMSLFYAEATPMLKTLSDATTKFVSENKNLPIENTDCLSTMASVC RVMLETPEYRSRFTNEETVSPCLRVVMGVII LYDHVHPVGAFATSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQIKSMLQ*QLLTLVNKG |
| 6161 | 455 | 1569 | PVSGSESLRRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*KSHVLEPLSSSLALEBQCLALSLDWSGTGKTRAGDQPLKI ISSDSTGQLHLLMVNETRPRLOKVASWOAHQFEAWIAAFNYWHPPIVYS GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT GSYDEHILLWDTRNMKQPLADTPVQGGVRIKWHPFHILLLLAA CMHSGFKILNCKAMEERQEATVLTSHLTPDSLVIYADWSWLLP RSLQRAPSWSPFNLTGKTADLKGASELPTPCHECREDNDEGBGH ARPQSGMKPLTEGMRKNGTTLQATAATTRDCGVNPEEADSAFSL LATCSFYDHALHLWEWEGN |
| 6162 | 1 | 586 | RTIHATGRAGASPMHRLTVWRLAEANKQHVRCQKCLEFGHWTYE CTGKRKYLHRPSRTAELKKALKEKENRLLQLQSIGETNVERKAK KKRKSVTSSSSSSSDSSASDSSSEETSTSSSSSDSDTDESS SSSSSASSTSSSSSDSDSSSSSKQ*HQHR*QL*R*TTKEE EKEIELLHSYWTGDLKTLM |
| 6163 | 1081 | 785 | RIRSTTEGCAVRLHPTONTGKARIMILLSVSLGRHWAFTYKFFL TPVVFVFFFFFHRKE*VMQKNPMKSREDEWMEKLNHLHVQRAD MNRLLMNVLTGEGFKEAAEKFRMESGIEPSVDLETDERIKIRE MILKGQIQEAIALINSLHPELDTNRYLYFHLQQQHLELIRQR ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF GDLHHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLWQON ELDQKKVKYPKMTDLSKGVIEEPK |
| 6164 | 90 | 406 | PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKRR SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALK A VARLSTGIPKEWRRKVWLTADHYLHSAIDWDKTMRTFNERS NPDDDSMGIIQIVKDLHRTGCSSYCGQEAQDRVVLKRVLLAYAR WNKTVGYCQGFNLAALILEVMEGNEGDAKIMIIYLDKVLPE S YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAFPFPQLAELREKYTYNITPFPATVKPTS SVSGRHS KARDSDEENDPDEDAVVNAVGLGPFSGFLAPLQKYQKQIKE PNEEQSLRSNNIAELSPGAINS CRSEYHAAFNSMMERM TTDIN ALKRQYSRIKKKQQQVHVYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISVPYEDLKTCLNS PWRTHIRVHKKNMPTKSHPGCGDTVGLIDEQNEASKTNGLGAA EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT SKAPQGSNSKTPIFSPPFSVKPLRKSATARNLGLYGP TERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEQYQRN GGERFG |
| 6165 | 90 | 406 | PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKRR SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALK A VARLSTGIPKEWRRKVWLTADHYLHSAIDWDKTMRTFNERS NPDDDSMGIIQIVKDLHRTGCSSYCGQEAQDRVVLKRVLLAYAR WNKTVGYCQGFNLAALILEVMEGNEGDAKIMIIYLDKVLPE S YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAFPFPQLAELREKYTYNITPFPATVKPTS SVSGRHS KARDSDEENDPDEDAVVNAVGLGPFSGFLAPLQKYQKQIKE |

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|------------|--|--|---|
| | | | PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTDIN ALKRQYSRIKKKQQQVHVQYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVYEDLTKLNS PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDBQNEASKTNGLGAA EAPPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA VQAKLGALELNQRDAAAE TELRVHPPCQRHCPEPPSAPBENKAT SKAPQGSNSKTPIFSPPFSVKFLRKSATARNLGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEQYQRN GGERFG |
| 6166 | 2 | 1206 | HKLWRTVAMAGA EWKSLEECLEKHLPLPDLQEVKRVLYGKELRK LDLPREAFEAASREDFELQYAFRAAEQLRRPRIVHVLQVNR IPLPANAPVAEQVSALHRRRIKAIVEVAMCGVNIICFQEAWTMP FAPCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDVVVSPILE RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYTM EGNLGHPVFQTFGRIVAVNICYGRHHPNLWLMYSINGAEIIFNP SATIGALSESLEWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS GDGKKAHQDFGYFYGSSVVAAPDSSRTPGLSRSRDGLLVAKLDL NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS VPALG |
| 6167 | 1220 | 1844 | YGI V T G P S L C A G D K Q P K K Q E K N P V L S P E F V D E A L C A C E E Y L S N L A H M D I D K D L E A P L Y L T P E G W S L F L Q R Y Y Q V V H E G A E L R H L D T Q V Q R C E D I L Q Q L Q A V V P Q I D M E G D R N I W I V K P G A K S R G R G I M C M D H L E E M L K L V N G N P V V M K D G K W V V Q K Y I E R P L L I F G T K F D L R Q W F L V T D W N P L T V W F Y R D S Y I R F S T Q P P S L K N L D K * A P L Y L T P E G W S L F L Q R Y Y Q V V H E G A E L R H L D T Q V Q R C E D I L Q Q L Q A V V P Q I D M E G D R N I W I V K P G A K S R G R G I M C M D H L E E M L K L V N G N P V V M K D G K W V V Q K Y I E R P L L I F G T K F D L R Q W F L V T D W N P L T V W F Y R D S Y I R F S T Q P P S L K N L D K |
| 6168 | 84 | 1392 | VWPVPSVSAMPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK GAKQQKFIKAVTHQVKFGQONPRQVAQSEAEKKLKKDDKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCQTKGDKCKFSH DLTLERKCEKRSVYIDARDEELEKDTMDNWEKKLEEVVNNKKG EAEKKKPKTQIVCKHFLEAIENNKYGFVWVCPGGGDCMYRHAL PPGFVLKKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFAGKALVISGREVFEFRP ELVNDDEEADDDTRYTQGTGGDEVDDSVSVNDIDLSLYIFRDVD ETGITVASLERFSTYTSKDKENKLSBASGGRAENGERSDLEEDN EREGTENGADAVPVDENLFTGEDLDELEELNTLDLEE |
| 6169 | 112 | 662 | APAAAMAERPEDLNLNPAVITRII KEALPDGVNISKARSATSR AASVFVLYATSCANNFAMKGRKTLNASDVL SAMEEMEFQRFVT PLKEALEAYRRBQKGKKEASEQKKDKDKKTDSBEQDKSRDBDN DEDEBRLEEEBQNEEEVDN*KGRETVAPWKVPLEMRRATCFCE AFPCWAE |
| 6170 | 62 | 667 | STKVMLEPNTGRLAGCTVFITGASRGIGKAIKAAKDGANIVIA AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA VEKAIKFGGIDILVNNASAI SLTNTLDTPTKRLDLMNVNTRG TYLASKACIPYLKSKVAHIPNISPPNLNLPVWFQKHCGRW*VV G*GDGLCLICFELNLCMSDVITICT |
| 6171 | 382 | 941 | HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQK*GLRGSRRRHHAN SGGDI PGDSFAAYFPRVLKQVHQALSLSQEA VSMDSMVRDILD RIATEAGHLAHYSKCVTTISRDIRMAVCLLPKMGKLAESQGT NATLRYTKSK |
| 6172 | 651 | 54 | GLCRAGGAHRFSRTHVEAALKMLRREALRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFALBLKLVFPGA |

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|------------|--|--|---|
| | | | QRMNRRGHEVGALVRACKANGVTDLLVVEHRTGPVGLIVSHLP FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV SDILRYLFFVPKDDSHRVITFANQDDYISFRHHVYKKTDRHNVE LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYNTARKRVF LSTE*AAPRPLGQLL |
| 6173 | 3 | 288 | SVDRHEVQVLSQSMPLTPHQAVALRGERPYMCVECGKCFGRSSHL LQHQRIHTGEKPYVCSVCGKAFSSQSSVLSKHRTIHTGEKPYECN ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAPTQLSHLIQHQ RIHTGERPYVCLCGKAFNHSTVLRSHQVRHTGEKPHRCNECGK TFSVKRTLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHNNVHT GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ HSHLIHQHKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP MCAVVVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE |
| 6174 | 1060 | 959 | PRPPGKRMMVAGLGNPGLPGTRHSVGMVGLQLARRLGVAESWT RDRHCAADLALAPLGDALVLRPRRLMNANGRSVARAAELFGL TAEVYLVDDELDPGLRLALKLGGSARGHNGVRSCISCLNSNA MPRLRVGIGRPAHPEAVQAHVLCGCFSPAEQELLPLLLDRATDLI LDHIRERSQGPSLGP*H*WFSKKA |
| 6175 | 2204 | 334 | RYFRADPRSRSGQFRAEGLGAFAGPLRAMAAPVKGNRKQSTEG DALDPPASPKPAGKQNGIQNPISLEDSPGAGGEREEBQEREEBQ AFLVLSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE LVTGRRLWKNVYNELGGSFPGSTSGATCTRRHY*RLVL PYVRHLK GEDDKPLFTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM MPGKTADAADPAPLPSQEPNRNSTEQQGLASGSSVSFVGASGC PEAYKRLLSFYCKGTHGIMSPPLAKKKLLAQVSKVEALQCQEEG CRHGAEPQASPAVHLPESPQSPKGLTENSRRHLTPQEGLOAPGG SLREEAQAGPCPAAPIFKGCIFYTHPTVLKPVSQHPRDFFSRLLK DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGRKGLIYP KPKACWVSPMAKVPAESPPLPPTFPSSPGLGSKRSLEEBGAHS GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPEA YRGTMHLHCLNFTGTGPGPLKGQAALPFSPLVIPAFPAHFLATAG PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF FHLNTKL |
| 6176 | 1040 | 402 | PLSALRAMAEVHVIGQIIQASGFSESSLFCWKGIHTGAAWKLLS GVREGQTQVDTPOIGDMAYWSPIDLHFATKGLQGWPRLHFQVW SQDSFGRCQLAGYGFCHVPSPTGTHQLACTWRPLGWSRBLAR AFVGGGPQLLHGDIIYSGADRYRLHTAAGGTVHLEIGLLLRNFD RYGVEC*GTLPTSPSTPRTPSDGGGWHSGQEHRL |
| 6177 | 1400 | 992 | VPIESLVGKVHNFPLIAFYCCEKGRQPHKSLHRCFCGEALDPN CSHCYLDQIKRSDPLGFGSGYSPHFVAISTNSEHKMQPSSMQQAL PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPLPGTSGCSDRPP VCFI |
| 6178 | 1027 | 254 | STQRGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL HCHSNFSKKFSFYRHHVNFKSWWVDIPVSGALLTDWSDDTMKE LHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELR NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNCTDSHVA CFGYNCESSAQWKS AVQGLLNYINNWHKQDTSMPRSSAFSWPG THRAAPAFVLVLPALRCLEPPHLANLSLEDA*CLKQH |
| 6179 | 806 | 276 | RGETREMAGNLLSGAGRRLWDVPLACRSFSLGVPRLIGIRLTL PPPKVVDWRNEKRAMFGVYDNIIGLGNFEKHPKELIRGPIWLRG WKNELQRCIRKRMVGSRMFADDLHNLNKRIRYLYKHFNHRK FR*KRKLRTSEKAHLSPPWRRETVLFPVRKRLCIFSVIKWGFPGI |
| 6180 | 156 | 1833 | DHHILKAASTTHVCARGNIFATPNTRCLEC*ATATPSSLEQCN* SHLSLCLPLATTSGLT PNSMIPEKERQNIARLLRVMCADLGA SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR MYNQVKVKTCAIGSNACLGIGVTCHS QSVGPDSCYILTAYQAE |

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|------------|--|--|---|
| | | | GNHIKSYVLGVKGADIRDSGLVHHVQNVLSBFVMSEIRTVYV TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE VIELNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDLSLLV HERYEQICEFYSSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE LSNESQPTLQLVLPITYRLEKLF TAKANDAGTVSKLCHLFLEAL KENFKVHPAHKVMILDPQQLRPVPPYQHEEIIIGKVCELINEV KESWAEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN MCEQALLIKRRRLSPEDMNKLMFLKSNML |
| 6181 | 169 | 1032 | TRTLSPVLLPGPRWKPRRRPMGLALPAWLQPRYRNAYLFI YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVISQEEVQE KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP IYPLCVLAEAFIYQSLPYFESFGTYSTKLFPDLSIYFPYVLKI YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKM*STAFQCDTR KDRLWQCSK*NTGSILVEKFLVF |
| 6182 | 1769 | 1224 | AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI VRPFGSSVNTFGKLGCDLDMFLDDETRNLNSAHKISGNFLMEFQ VKNVPSEIATQKILSVLGECLDHFGPGCVGVQKILNARCPILVR FSHQASGFQCDLTNNRIALTSSSELLIYGALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMMVIFPLQRRSPPIPTLDLSL KTLADAEDKCVIEGNNCTFVRDLRSRIKPSQNTETLELLLEKFFE YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFTSLNISKNV SQSQQLQKFDLARESAILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKQLLESCLKGNRTENFTKTSKRTI STQT |
| 6183 | 1118 | 452 | HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRMTGCCGCSRG GSGCGCGSSCGCGCGSGCGGCGSGRGGCGSGCGGSSCGGCGS RCYVPVCCCKPVCWVPACSTSCGSCGSGKGGCGSGCGSKGC GSCGCSQSSCCKPCCSSGCGSSCCQSSCCKPCCQSSCCVPVC CQSSCCKPCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP |
| 6184 | 1 | 2191 | IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGSGGGGARGAE EPPPPQLQAVLVADSFDRRFFFIISKDQPRVLLPLANVALIDYTL FLTATGVQETFFVCCWKAQIKEHLLKSKWCRPTSLNVRIITS ELYSRSGDVLVDKALVRSDFLLVYGDVISNINITRALEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTNRL HFQKTQGLRRFAFPLSLFQGSDDGVEVRYDLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRAAGAIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGNITLPEGSVISLHPPDAEDEDDEGFEFSDSGADQEK DKVKMGYNPAEVGAAGKGYLWKAAGMNMEEEELQQLNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEPPLQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAEID FFLEHEALGISMALVMAFYQLEILAEETILSWFSQRDITDKGQ QLRKNQQLQRFIQWLKEABEESDD |
| 6185 | 791 | 44 | PCTSCVLWATLHLPASTRKAPQAECEMISITEWQKIGVIGITGF IFFILFGTLLYFDSVLLAFGNLLPLTGLSLIIGLRKTFWFFQR HKLKGTSLGGLGVVIVLLRWPLLMGFLETYGFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTESSSLNDHWLKGAK REEWEPPQSPALTHSPTYPGPPQVQKERNGAEQLTSPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK |
| 6186 | 569 | 238 | VYGDSSNTNTHGAERNRKLKKHWKLCHAQSRDLVNGLALKMA |

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|------------|--|--|---|
| | | | KERKVKNKVRNKADTEEVFNNSPTNQEKMPSTAILPDFSGSVIS NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQOI PNRETSEANKERRKMTSKSSESNIYSPITSFITADSELHDIKD LEDCLMVGLHTCGDLAPNLTIRIFTSNSEIKGVCSVGCYHLLSE EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV AAGQGLPTESLFYRAVLQDIKDCCYGITKCDRHVGKIYSKSSP LDYVRRSLKKGLEDKSLPKIIMNYYEKYKPRMNELEAFNMLK VVLAPCIETLILLDRCLCYLBQEDIAWSALVKLDFPVKSPRCYA VIALKKQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP PSGRVGSRYD |
| 6187 | 1701 | 771 | DAWGPETRLARILNPDSFIEPRPGRLLPELEATRPHMEPKASCPA AAPLMERKFHVLVGVGTGSVAALKPLLVSKLLDIPGLEVAVVTT ERAKHFYSPQIDIPVTLYSDADEWEMWKSRSDDPVLHIDLRRAWDL LLVAPLDANTLGKVASGICDNLCTCVMRAWDRSKPLLFCEPAMNT AMWEHPITAAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG TIVDKVKEVLFOHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV GKIGGYPHLLNGGPALS LPRGQACSRLNWTGPGLSFFQPGEEAA A |
| 6188 | 238 | 1534 | KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV PSPSSSGSRKVVGSMPTAGSAGSVPENLNFPEPGSKSEBIGKK QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG VPNGMMTTQQAGYAGMAAMPQT VYGVPQAQQLQWNLTQMTQQM AGMNFYGGANGMMNYGQSMGSGNBQANQTLSPQMWK |
| 6189 | 1297 | 793 | LGEPLGDLCELI PGDQQQLQMGVEHPGTGAQGSAAQSVAGEVQL TQLSHARQRPSCQGSQILALDLQHMDISRQPRWQHVPVARQVQ RAQQQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR RVRAFMIHNLQITGIGREDFATTYFLEELNLSYNRITSPOVHRD AFRLRLRLSLDLSGNRLHMLPPGLPRNVHVLKVKRNLAAALR GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN KLAVGSVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE EEEEDEVEEBETR |
| 6190 | 66 | 1309 | ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTGQCECRPGYQ GLHCETCKEGFYLNYSGLCQPCDCSPHGALSIPCNSSGKQCK VGVIGSICDRCDGYGFGSKNGCLPCQCNRSASCDALTGACLN CQENSKGNHCCECKEGFYQSPDATKECLRPCSAVTSTGSCSIK SSELEPECDQCKDGYIGPNCNKCEGYYNFDSICRKCQCHGHVY PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLBGNCIK KVILPTPEGSTILVSNASLTTSVPTVINSTFTPTTLQTFVSVS TSENSTALADVSWTQFNIIILTVIIIVVLLMGFVGAVMYRE YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLEDDGNE VAPNGQLTLTTPIHNYKA |
| 6191 | 1212 | 1511 | VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQPKCPS MIDWIKKIWIYITMEYYATIKRNEIMFFAGTWEMEAIIILSKLM QDYMFSLISGS |
| 6192 | 3 | 950 | TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAEE KGGLVSDAYGEDDFSRLGGDEGDGYEEEDENSQSEDDDSFETK PEADDPKDNTEAKRDPQLVASFSERVNMSFDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYEEALAKAQKIEMDKLEK |

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|------------|--|--|--|
| | | | AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ |
| 6193 | 3 | 950 | TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAE KGGLVSDAYGEDDFSRLLGGDEEDGYEEEDENSQRQSEDDSET PEADDPKDNTEAEKRPQELVASFSEVRNMSPPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ |
| 6194 | 3 | 950 | TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAE KGGLVSDAYGEDDFSRLLGGDEEDGYEEEDENSQRQSEDDSET PEADDPKDNTEAEKRPQELVASFSEVRNMSPPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ |
| 6195 | 736 | 235 | VANGLQSNMPPKFCYCDYTLTHDSPSVRKTHCSGRKHKENVKD YYQKWMEECAQSLIDKTTAAFOQGGKIPPTFFSAPPAGAMIPPP PSLPGPPRPGMMPAPHMGGPPMMPMMPGPPGMPMPVGPAPGMRP PMGGHMPMMPGPPMMPRPPARPMMPVTRPGMTTRPDR |
| 6196 | 1512 | 623 | KTGKRSSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEDSH QRLMLGLMVSELKDHFLRHLLQGVEKKIEQMVLDIYISKLDLIC HIVETNWRKHNLSWVLFHNSRGSAAEFVAFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLHCIDSGVLLLTETAVIRL MKDLNTEKNEKLKFSIIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL |
| 6197 | 3 | 819 | ADPEGTEEAVMSRYTRPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQPEDVDAEDALYNLRKWCVC RQIEIQFAQGRDKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSWGRNRRRSDSLKESRHRFRSFSQSKSRKSLPRRSTARSQ SRTPRNFGSRGRSRKSLQKRKSKSIGKSQSSSPQKQTSSTGTS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSR YRHKNSW |
| 6198 | 111 | 1912 | SEAAALSPSFISPAFLRLKLPALDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAGLQDSQ REMPPPPPSPSDPAQKPPPRGAGSHSLTVRSLSLCLFAASQFL LACGVLFWSGYGHIWSQATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLTTLVWHLRLTPPEPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLPVPBTPVFDVCMVDIKPEADP TSLTVKSMGLQERRGSNVSLTDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDLSSYINANYIRG YGEEKVYIATQGPVISTVADFWRMVWQEHPIIVMITNIEEMN EKCTEYWPEEQVAYDGEITVQKVIHTEDYRLRLISLKSCTEER GLKHYWFTSWPDQKTPDRAPLLHLVREVEEAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE |
| 6199 | 144 | 1211 | MARENGESSSWKKAEDIKKIFEKETLGTGAFSEVVLAEKA TGKLPVAVKCIKKALKGKESSIEIEIAVLRIKHENIVALEDIY BSPNHLVLMQLVSGGELFDRIVEKGFYTEKASTLIROVLDAV YVLRHMGIVHRDLKPNLLYSQDEESKIMISDFGLSKMEGKD VMSTACGTPGYVAPEVLAQKPYSAVDCWSIGVIAYILLCGYPP |

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|------------|--|--|---|
| | | | FYDENDSKLFEQILKAEYFDFSPYWDIDSDSAKDFIRNLMKDP NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ AFNATAVVRHMRKLHLGSSSLDSSNASVSSLSLASQKDCASGTF HAL* |
| 6200 | 702 | 96 | LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAFFDLDTLWPF WVDTHVDPFPHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL QOKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTL S QGLETFAKAQTGPLRSSLEESPFEA |
| 6201 | 2809 | 2383 | GQTPRVVRWMMRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA GPPQIRILKRPTSNVSSPNSTSRPTLPVKSQAQREAEYAEA RKRLGSSASPBEQEKPILDRPTRISQPEDSRQPNVIRQPLGP DGSQGFQRR |
| 6202 | 2 | 426 | INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE DGI FDSGNFEQFLREKVNGKGTGNLGNVHIERFKNKITVVSE KQFSKRYLKYLTKKYLKNNLRDWRVVASDKETYLRYFQISQ DEDESESED |
| 6203 | 419 | 2550 | RCPRPPATAGAAASRPDRSPFSGISGSEAAAGAGAAAPASQHPA TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDYQERMNKG ER LNQDQLDAVSKYQEVNTNNLEFAKELQRSFMALSQDIQKTIKKT A RREQLMREAEQKRLKTVLELQYVLDKLGDDDEVRTDLKQGLNGV P ILSEELSLDDEFYKLVDPERDMSLRLEQYEHASIHLDLLE GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNGHQLCEEEEA S APAVEDQVPEAEPEPAEEYTEQSEVESTRYVNRQFMAETQFTS GEKEQVDEWTVETVEVNSLQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM NPTQNMMPQLVCPVHSESRLAQPNQVQVPEATQVPLVSSTS EGYTASQPLYQPSHATEQRQKEPIDQIQTATISLNTDQTASS S LPAASQPVQFQAGTSKPLHSSGINVNAAPFQSMQTVFNMAFVP PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQEQELQTVVG TYHGPSDQSHQVTGNHQPPQONTGFPRSNQPYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFNTPNSGYTQSQFSAP RDSGYQRDGYQQNFKRGSQSGPRGAPRGRGPPRPNRGMPQM NTQQVN |
| 6204 | 2933 | 787 | CTHNLISLGGRALIHFNRLNLKIQGEAHNIFCPAYDCFQLV PGDI I KSVVSKEMDKRYLQFDI KAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTSLFPPLRAPAVDCGKGLFCWECLGEAHEP CDCQTKWNWQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCNMHMQCAKCKYDFCWICLEEWKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHFRQELDRFMHYITRFK NHEHSYQLEQRLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFLEPKSTKKEIFELMQTDLEMTEDL AQKVNRPYLRTPRIHKI IKAACLQVQKRQEFASVARGVAFADSP EAPRRSFAGGTWDWEYLGFPASPEEYAEFQYRRRRRQRRRGDVHS LLSNPDPDEPSESTLDIPEGGSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSNQDSLQALSSLEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAFHDMNPQSIALIPATTEISADSQLP CIKDGSEGVKDELVLPEDSMFEDASVSEGRGTQIEENPLEBNI PGGGKQHPQAW |
| 6205 | 1 | 1200 | RAHRGKMALEVGDMDGQLSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDSDSCLWKR KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLKESQEHKTD LDKELDEYMHGKKMGSKKEENGQGHLLKRPVKDRLLGNRPEMN |

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|------------|--|--|--|
| | | | YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA IELLMETAEEVQNGGLFIMNGSRRTPGGVFLNLLKNTPSISEE QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAISLNFQED DDTSRETFASDTNEALASLDESQEGHAEAKLEAEAEIEVDHSHD LDIF |
| 6206 | 10 | 1442 | IIISERRERSCLHLVCIRCSCDVVEMGSLGLCSMASWIPCLCGS APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ LNKIPGFCENEKGVVPCNVLVGKAVYRLCFGLAMPYLLLSLLM IKVKSSSDPRAAVHNGFWFFKPAIAAIIIGAFFIPEGTFTTW FYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYA ALLSATALNYLLSLVAIVLFFVYYTHPASCENKAFISVNMLLC VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPE TNCNPSLLSIIGYNTTSTVPKEGQSVQWHAQGIIGLILFLLCV FYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLDGDVH RAVDNERDGVTSYSFFHFMFLASLYIMMTLTNWYREPSREM KSQWIAVWVKISSWIGIVLVVTLVAPLVLTNRDFF |
| 6207 | 2924 | 1471 | TVMAEAAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDFY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEWVNAIEFVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGDS CDMCGQLVHHPMDAAQORSQHIKSCIEA HEKDMELSAVQSRKDMVCGICMEVVYEKANPSERRFGILSN CN HTYCLKCIRKWSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKLILKYKEAMSNKACRYFDEGRGSCPPFGGNCIFYKHAYPD GRREBPQRQKVGTSRYRAQRNRHFWELIEERENSFPDNDDEE VVTFFELGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL |
| 6208 | 2924 | 1471 | TVMAEAAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDFY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEWVNAIEFVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGDS CDMCGQLVHHPMDAAQORSQHIKSCIEA HEKDMELSAVQSRKDMVCGICMEVVYEKANPSERRFGILSN CN HTYCLKCIRKWSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKLILKYKEAMSNKACRYFDEGRGSCPPFGGNCIFYKHAYPD GRREBPQRQKVGTSRYRAQRNRHFWELIEERENSFPDNDDEE VVTFFELGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL |
| 6209 | 1758 | 829 | ERLCFPCMQSKIYSYMSPNKCSGMRFPQLQERNSVTHHEVKCQK PLAGIYRKREKRNAGNAVRSAKSEEQIKIDARKGPLVFPFNQ KSEAAEPPKTPSSCDSTNAIAKQALKKPIKQKQAPRKAQKQ TQNRKLTDFYPVRRSSRSKAEQLQSEERKRIDELIESGKEEGM KIDLIDGKGRGVIATKQFSRGDFVVEYHGLDIEITDAKKREALY AQDPSTGCMYFYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH |
| 6210 | 3761 | 387 | IFGMSKLRMLLEDGSGSADFRRHFVNLSPTTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEWGTVCNNGWSMEAV SVICNQLGCPATAKAPGWANSSAGSGRIWMDHVS CRGNESALWD CKHDGWSKHSNCTHQDAGVTCSDGSLNEMRLTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFEGE SGPIWFDLIDCNGNESALWNCKHQGWGKHNCDAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAVACK QLGCPTAVTAIGRVNASKGFGHIWLDVSVCQGHFAVWQCKHHE WGKHYCNHNEAGVTCSDGSDLELRLRGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRLGCGSALKTSYQVYSKIQTANTWL |

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|------------|--|--|---|
| | | | FLSSCNGNETSLWDCKNWQWGGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGD TWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFGEGNGQIWAEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVCSSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGTETQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRACAGRVEIYHEGSGWTICD DSWDLSDAHVVCRLGCGEAINATGSAHFGEGTGPIWLDKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCADKKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSGWTVCDSDWLDLDAQV VCQQLGCGPALKAFKEAFGQGTGPIWLNVEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSSFI VGILGVVLLAIFVALFLLTKRRRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDMNSSGGHSEPH |
| 6211 | 3761 | 387 | IFGMSKLRMLVEDSGSADFRHFVNLSPTITVVLILLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEBWGTVCNNGWSMEAV SVICNQLGCPATAIKAPGWANSSAGSGRIWMDHVS CRGNESALWD CKHDGWGKHSNCTHQDAGVTCSDGSNLEMLRTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFEGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDAEDAGVICSKG ADLSRLRLVDGVTECSGRLEVRFGQEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFHILWLDVSVCQGHEPAVWQCKHHE WGKHYCNHNEADAGVTCSDGSLELRRLRGGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRLGCGSALKTSYQVYSKIQTATNWL FLSSCNGNETSLWDCKNWQWGGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGD TWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFGEGNGQIWAEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVCSSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGTETQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRACAGRVEIYHEGSGWTICD DSWDLSDAHVVCRLGCGEAINATGSAHFGEGTGPIWLDKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCADKKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSGWTVCDSDWLDLDAQV VCQQLGCGPALKAFKEAFGQGTGPIWLNVEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSSFI VGILGVVLLAIFVALFLLTKRRRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDMNSSGGHSEPH |
| 6212 | 1 | 1134 | LKWE LRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFR RELPPACHEIGLGAEGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTGLITRILESSPGVTEVTIIIEKPPAERHMISSE QKNNCVMPEVDKNFYLMINGFHMNTSVKLDHEIIPLGSMAINS SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSNGSGKVCLVYKSGKPALAEDTEIWFDRALYWHFLT DTFTAYYRLLITHLGLPOWQYAFTSYGISPOAKQRVSMYKPTTY NTNLLTEETDSPVNKLDPSKVFKSKNKIVIPKKKGVPVQAGGQK GPSGSGPSTSTSKSSSGGNPTRK |
| 6213 | 1 | 1134 | LKWE LRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFR RELPPACHEIGLGAEGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTGLITRILESSPGVTEVTIIIEKPPAERHMISSE QKNNCVMPEVDKNFYLMINGFHMNTSVKLDHEIIPLGSMAINS SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS |

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|------------|--|--|--|
| | | | VIFELDCSCNGSGKVCIVYKSGKPALAEDTEIWFLDRLALYWHFLTDTFTAYYRLLITHLGLPQWQYAFSTSYGISPAQQRVSMYKPITYNTNLLTEETDSFVNKLDPKSVFKSKNKIVIPKKKGFPVQAGGQKGPSPGSPSTSTSSSSSGSNPTRK |
| 6214 | 2 | 460 | HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRGTGWSFVGWVVLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRRESKRFSAYNYRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVHIGQLYSTDKLIIENRDMPT |
| 6215 | 2 | 1849 | FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRCILVSIAGKNVMLDCGMHMGFNDRRFPDFSYITQNGRLTDFLDCVISHFHLDCGALPYFSEMVGVDGFIYMTHTPTQAICPILLEDYRKIAVDKKGANFFTSQMIKDCMKKVAVHLHCTVQVDELEIKAYYAGHVLGAAMFQIKVGSSEVVYTGDMNTDPDRHLGAAWIDKCRPNLLITESTYATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELCILLETFWERNMLKVPIYFSTGLTEKANHYKLPFPWTNQKIRKTFVQRNMFEFKHIKAFDRAFDNPGPMVVFATPGMLHAGQSLQIFRKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVMQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKMEFLKQLPEAKKPRLLHGTLMKDSNFRVLSSEQALKELGLAEHQLRFTCRVHLHDTRKQETALRVYSHLKSVLKDHCVQHLDPGSVTVESVLLQAAAPSEDPGTKVLVSWTYQDEELGSLTSLKKGLPQAPS |
| 6216 | 11 | 393 | QTTREPEPRNSALRQSRKMAVVGVSRSRLGRSRPQLGRPMSSGAHGEEGSARMWKTTLTFFVALPGVAVSMLNVYLKSHHGEHERPEFIAYPHLRIRTKFPFPGDGNHTLFHNPHVNPLPTGYEDE |
| 6217 | 9 | 1178 | TRVGRGESGLKMEVKPPFGRFPQDSGRRRRRRGEHDPKEPEQLRKLFIGGLSFETDDSLREHFEKWTLTDCVVMRDPQTKRSRPGFVTYSCVEEVDAAACARPHKVDGRVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRDYFEKYKIEETIEVMEDRQSGKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCVKKALSQEMQSGSQRGRGGSGNFMGRGNGFGGGGNGFGRGNGFGGSGGGGGGSGRGSYGGGDDGNGFGGDDGNGYGGGPGYSSRGGYGGGPGYGNQGGGYGGGGYDGYNEGGNFGGNGYGGGNYNDFGNYSQQQS NYGPMKGSFSGRSSGSPYGGGYGGGGSGGYGSRFP |
| 6218 | 1305 | 906 | SCERRGFIMADDLKRFLYKLLPSVEGLHAIVVSDRDGVFVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIIICYNTYQVQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS |
| 6219 | 2 | 890 | AGPGEAGAGAGTRCAGAEAMASAGGEDCESPAPEADRPHQRPFLLIGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVILSQDRFYKVLTAEQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVEPVTYDFVTHSRLLPETTVVPADVLFEGILVFYSQEIRDMFHLRLFVDTSDVRLSRRVLRDVRGRDLQILTQYTFVVKPAFEEFCLPTKKYADVIIIPRGVDNMVAIHLIVQHIQDILNGDICKWHRRGSGNSRSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH |
| 6220 | 227 | 764 | EQNISLEMSCTIEKALADAKALVERLRDHDAAESLIEQTALNKRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQENKELRTSLEEHQSALELIMSKYREQMFRLLMASKDDPGIIMKLKEQHSKIDMVHRNKSEGFPLDASRHILEAPQHGLERRHLEANQNVH |
| 6221 | 98 | 916 | RNIWDLNPFVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTPNIWAGLSWGLYFVFNKISYKTEGRAERLEATEYLVSAAEAGAMTLCITNPLWVTKTRLMQLYDAVNSPHRQYKGMFDTLVKIYKYEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPEAQLSTVEYISVAALS KIFAVAATYPYQVVRARLQDQHM FYSGVIDVITKTWRKEGVGGFYKGIAPNLI RVT PACCTFVVYENVSHFLDLREKRK |

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|------------|--|--|--|
| 6222 | 2 | 2116 | MARELRALLLWGRRLRPLLRAPALAAVPGGKPLCPRRRTTAQLG PRRNPAWSLQAGRLFTQTAEDEKPEPLHSIISSSTESVQGSTSKH EFQAEKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLVS SDGQALPEMEIHLQTNAEKGTITITQDTGIGMTQEELVSNLGTIA RSGSKAFLDALQNAEASSKIIGQFGVGFYSAFMVADRVVEVYSR SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIHLKSDCKEF SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMDPKDVR WQHEEFYRYVAQAHDKPRYTLHYKTDAFLNIRSIFYVPMKPSM FVDSRELGSVALYSRKVLITKATDILPKWLRIRGVVDSEDI PLNLSRELLQESALIRKLRDVLQQRLLIKFFIDQSKKDAEKYAKF FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSL EYASRMRASTRNIYYLCAPNRHLAEHSPPYEAMKKDTEVLFCE EQFDELTLHLREFDKKKLISVETDIVVDHYKEEFEDRSFAAE CLSEKETEEELMAWMNRNLGSRVTNVKVTLRDLTHPAMVTVLEMG AARHFLRMQQLAKTQEBRAQLLQPTLEINPRHALIKKLNQLRAS EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRRLNELLVKALERH |
| 6223 | 3 | 715 | DAWARTMAGMVDVFDDEEQVKSFLNEMVEVCNHYCEKDPDGCY RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDCYKLGAYVVTGK GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVND GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQAGPGFPKMDL ACKYSMKACDLGHIWACANASRMVYKLGDGVDKVEAKAEVLKNRA QQVHKEQQKGVQPLTFG |
| 6224 | 1 | 133 | LRTISSMAWGPIILLTLAHCTGSAQSVLTQPPSVSGARIPHEK |
| 6225 | 3259 | 938 | LLSCHRLAICKLPFSVESRKTVMGPGQARRQAFLEFGDVTVDFT QKEWRLLSPAQRALYREVLTENYSHLVSLGLHLSKPELIRLEQ GEVWPGEERRRRRPGPCAGIYAEHVLRPKNLGLAHQROQQLQFSD QSPQSDTAEGQEKEKSTKPMASFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTIDKVLKGIENSRWGAFCABRGQDFSRKMMVIH KKAHSRQKLFTCREHQGFDESAALLHQNTHTEKSYVCSVC RGFSLKANLLRHQRTSHGEKPFCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFPNDKSSYNKHLKAHSGEKPFVCKECCGRGYT NKSYFVHVHRIHSGEKPYRCQECGRGFNSKSHLITHQRTSHGEK PFACRQCKQSFVKGSLLRHQRTSHGEKPFVCKDCERSFSQKST LVYHQRTSHGEKPFVCRECGGFIQKSTLVKHQITHSEKPFVFC KDCGRGFQKSTFTLHQRTSHSEKPYGCREGRRFRDKSSYNKH LRAHLGEKRFRCDCGRGFTLKNLTIHQRTSHGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFIKSTLLFHQKTH SGEKPFICSECGGFIWKSNLVXHLAHSKGKPFVCKECCGRGFN WKGNNLTHQRTSHGEKPFVNCVCGGFSWKRSLTRHHWRHHSKE KPFVQCQCKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS |
| 6226 | 29 | 266 | TKVSELLGGSQRLFFPLWRRLCRCGLGRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA |
| 6227 | 2581 | 890 | MSASSLLEQRPKGQGNKVQNGSVHQKDGNDLDDDFEPYLSQARP NNAYTAMSDSYLPSYSPSIGFSYSLGEAAWSTGGDTAMPYLT YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFPPSGIDFS AWGNNSQGGSTQSSGYSSNYAYAPSSLGAMIDGQSAFANETL NKAPGMNTIDQMAALKLGSTEASNVKVVGSVAVSGSITSNI VASNSLPPATIAPPKASWADIASKPAKQPKLKTNGIAGSSL PPPIKHNDIGTWDNKGPAKAPSQALVQNIQPTQGSQPQVQ QANNSPVVAQASVGGQTQPLPPPPQPAQLSVQQQAAQPTRWV APRNRSGFGHNGVDGNGVGQSQAGSGSTPSEPHVLEKLSIN NYPKDFDWNLKHGRVFIKSYSEDDIHRSIKYNICWSTBHGK RLDAAYRSMNGKPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRENNENKPVNTSRD TQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQ |

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|------------|--|--|--|
| 6228 | 47 | 1978 | <p> GRRCRRRGAVMELAQEARELGCWAVEEMGVPAARAPESTLRRL CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPOVRRKL ELEAAVTRLRAEIQELDQSLERMDTEAQDTAMEQARQHTQDT QRRALLLRAQAGAMRRQOHTLRDPMQRLQNLRLQDMERKAKV DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLPLPQAKRG SLPTPHDDHFGTSYQQWLSVETLLTNHPPGHVLALEHLAAER EAEIRSLCSGDLGDTISRPAQDQSDSSQTLPMSVHLIQEGW RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERVLGSSERQVL ILGLRRCCLTWELKALHDQSQELQDAAGHRQLLLRELQAKQORI LHWRLVETQEQVRLIKGNSASKTRLCRSPGEVLALVQRKVV PTFEAVAPQSRELLRCLLEEVRHLPHILLGTLLRHRPGELKPLP TVLPSIHQLHPASPRGSSFIASHKLGLPPGKASELLPAAASL RQDLLLLQDQSLWCWDLHMKTSPPGLPTQELLQIQASQBKQ QKENLGQALKRLEKLLKQALERIPELQGIQVGDWWEQPGQAALSE ELCQGLSLPQWRLRWVQAQGLQKLC </p> |
| 6229 | 1571 | 560 | <p> GPSLLGTRGTPNPARTLQIFFLIIGRRITGRMAAVDDLQFEFEG NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG NDDSDKTELLAGQKKSPFWTFEYYQTFDFVDVITYQVFDRIKGS LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFI HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGLMWRNSK VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI ALGISGSLAMTFWPAVREDNRVALATIVITIVLLHMLLSVGCL AYFFDAPENDHLPTTTATPNQTVAANKSS </p> |
| 6230 | 1723 | 600 | <p> SKMSGRSGKKKMSKLSRSARAGVIFPVGRMLRYLKKGTFFKYRIS VGAPVYMAAVIEYLAEILELAGNAARDNKKARIAPRHILLAVA NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP PPEKRGRKATSGKKGGKSKAAKPRTSKSKSPKDSKDEGTSNST SEDGPGDGPFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP TTAIEDLKBIDIGALEKAGGKBFLETVKELRKSGQPLEVAEAAV SQSSGLAAKFVHCHIPQWGSCKCEEQLEETIKNCLSAEDKKL KSVAFPPFPSSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY FLLFDSSEIGIYQEMAKLDAK </p> |
| 6231 | 149 | 870 | <p> LIFSSSTMDRSLRNVLVVSFGFLLFLTAYGGLQSLQSSLYSEEG LGVTALSTLYGGMLSSMFLPPLLIERLGCKGTIILSMCGYVAF SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK AGKRKDMVNQYFGIFFLIFQSSGVWGNLISLVFGQTPSQETL PEEQLTSCGASDCLMATTTTNTSTQPSQQLVYTLGIYTGSGVL AVLMIAAFLQPIRDVQRESE </p> |
| 6232 | 3679 | 1476 | <p> FVAGTTMAGFWGTAPLVAAGRGRWPPQQLMSAALRTLKHVL YYSRQCLMVSRNLGSGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSVDVASSVHVKMADEAVCVGPAPTSSKSYLNMDA IMEAIKKTAAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEAVRIAREIGY PVMIKASAGGGGKMRIAWDDEETRDGFRLLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNRECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHQADIR INGWAVERVYAEADPYKSFGLPSIGRLSQYQEPHLHPGVRVDSG YQPGSDISYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLEVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVSTWNLASPLLSVSDVGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV TEDTSVLSRSPMPGVVAVSVKPGDAVAEGQEICVIEAMKMQNS MTAGTGTGVKSVHCQAGDTVGEGLLVELE </p> |
| 6233 | 1 | 2654 | <p> HSTRENLAGNPNFPSEGHVLRSTGPGGSFAKHMVAQCVPKGP </p> |

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|------------|--|--|--|
| | | | LACSRITYFFGATHVPYVLGGDSKLPKKTQIRLLSQIYAAVIEAV LAGIACYAKTSSLTAKAEVAEQTLGSGLDSEFELIPFKAALRSKM TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC LGSVVFSEFSLTSQILVKEKDGTVTTETSSSVLTAAPRFCSWL VEDNEVKLSEKTHQAVRGDESFLGTLYLTGGEGAYLYSSNLQSWP EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA ALLIDFKSSLLPHLPVHFHGSNNFLMIALFPKSKIYQAFYSEVF SLWKQDQNSGILSKVIQEDGLSVEQKRLHSSAQKLFSAQSOPAG EKRSSLLKLSAKLPEDWFLQHFALSSISQEPVMRTHLPVLLQQ AEINTTHRIESDKVIIISIVTGLPGCHASELCAFLVTLHKECGRW MVYRQIMDSSECFHAAHFQRYLSSALEAQNRSAQSAYIRKKT RLLVVLQGYTDVIDVQALQTHPDSNVKASFTIGAITACVEPMS CYMEHRFLFPKCLDQCSQGLVSNVFTSHTTEQRHPLLVLQQLS IRANPAAAFILAENGIVTRNEDIELILSENSESSPEMLRSRYL MYPGWYBEGKLNAGSVYPIVMVQICVWFGRLPKEKTRFVAKCKAIQS SIKPSPPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL EGPTPPPSKSVSQDSSGQCECYLVFICGSLKEDSIKDWLRQSA KQKPQRKALKTRGMLTQOEIRS IHVKRHLPLEPAGFYFNGTQFV NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQLEQOEYHDLF ELKP |
| 6234 | 1731 | 404 | PRVREDMDHKSPGNKGLSVYAGIKSIVKSSLSGMVESSRHNSGL DKQSDIQNLNEERILALQLCGWIKKGTDDVVGPFLLSLVQEGEW ERAAAVAFNLDIRRAIQILNEGASSEKGDNLNLVAMALSGYT DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG LTKDGVDLMESYVDRDGTQVTSYCMQLQGSPLDVLKDERVQYWI ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQFVSCNFCG KSISSYCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC ALCLINMGTFVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN CRHGGHAGHMLSWFRDHAECFVSACTCKCMQLDTTGNLVPATV QP |
| 6235 | 1 | 571 | EKRDRHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPO DYESDDDSYEVLDLTYARRHQWNRVFGHSSGPMVEKYSVATQ IVMGGVTGWCAGFLQKVGKLAATAVGGGFLLLQIASHSGYVQI DWKRVEKDVNKAQRQIKKRANKAAPEINNLIEATEFIKQNI SSGFVGGFLLGLAS |
| 6236 | 1 | 703 | WDQNKGAAGSGTLPLSLPSARFSAGPPTQSRPTMSNMEKHLF NLKFAAKELSRSAKCDKEEAKAKIKKAIQKGNMEVARIAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMLNEKISALMDKFBHQFETLDVQTQMEDTMSSTTT LTPQONQVDMLLQEMADEAGLDLNMELPQGQTSVGTSVASAEQ DELSQRLARLRDQV |
| 6237 | 312 | 720 | PTAMABEGIAAGGVMDVNTALQEVLTALIHDLARGIREAAKA LDKRQAHLCVLANCDEPMYVKLVEALCAEQINLIKVDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIIEYFK CKK |
| 6238 | 2 | 4666 | EEVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENTMTAAIKDLQVRACPLPVKRGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLLTKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYNNEMFGVWEPLLEPLEIDQTEDFRPWNLGK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNVLKAFTEAATGSSADFVKDLAPFMIINSLGLTISVSPS DSFVSLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI |

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|------------|--|--|---|
| | | | DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDITLLGTASPENEFN IPLGSYRSFIFLKPEDENYQCEGIDFEEIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIESVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPNPKPVLP FSFQPNHFNNNKVQLMVTDSLSNQFSIDTVGSHGAVKCKGLK MDYQVGVITDLSFNITRIVTFTPFYMIKNKSKYHISVAEENGD KWLSDLEQCIPIFWPEYASSKLLIQVERSEDPPKRIYFNKQENC ILLRLDNELGGIIAEVNLAESTVITFLDYHDAATFLLINHTK NELVQYNQSSLSIEDSLPPGKAVFYTWADPVGSRRLKWRCKRS HGEVTKQDDMMMPIDLGEKTIYLVSFEEGLQRIILFTEDPRVFK VTYSEKAELAEQEIIVALQDVGISLVNNYTKQEVAYIGITSSD VWVETKPKKKARWKPMVKHTEKLEREFKBYTESSPSEDKVIQL DTNVPVRLTPTGHNMKILQPHVIALRRNYPALKVEYNTSAHQ SFRIQIYRIQIQNIHGAFFFPVFPVKPKSVTMD SAPKPFDT VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMT AEVTENTVELPHKIDIEAFKEEYKTASLDVQSQVSLYEYFHPIS IKLHLSVLSLSSGREEAKDSKQNGGLIPVHSLNLLKLSIGATLTD VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL GLDLVGNPFGLIREFSEGEAFPEPYQCAIQGPEEFVEGMALG LKALVGGAVGGLAGAASKITGAMAKGVAAMTDEYQQRREAM NKQPAQFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGAAG FFKGVGKGLVGAVARPTGGIIDMASTFGIKRATETSEVESLR PPRFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDESDLNH |
| 6239 | 2108 | 634 | KPGMAGKSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNQA THDLLYHWQDLEQYDHLFPVGVVPTFLGPVVLAVFSSPAVYVL SLEMSKFYSQILVRGVLGLGVI FGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTPNVLALPVVLLALAAWLRHEWARFI WLSAFATVFRVELCLFLGLLLALLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRLTWPEGVWLYNTVLNKSNNWGTSPILL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVALGFMALYSLL PHKELRFIIYAFPMNLNTAARGCSYLLNNYKKS WLKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAQAQTVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVS LNLTLQLPFPNVHLQTKLVLL ERLPRPS |
| 6240 | 2202 | 1176 | HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREARHPRLVPTGPTRHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQAQPGVSETEEVALQPLLPKDEVQLKTTYKSNQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV |
| 6241 | 3 | 1341 | RNAEEKRLSLQREKILARVSDNRTRALVQALRRITDPKLCIT RVEBLTFHLLFPPEGKGVAVKERIIPYLLRLRQIKDETLOAAVR EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSVD FSQNVIVGTVMKSWSHAFYDSQIWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGCCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLNNPSALAMHECKK LWPDVPLECIVSLGTGRYESDVNTVTYTSKTKLSNVINSATD TEEVHIMLDGLLPDITYFRFNPVMCENIPLDES RNEKLDQLQLE GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP |

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|------------|--|--|---|
| 6242 | 198 | 1310 | FFSKL QHFLPGAETWSPGAHVCTARRFPGRSLAAPPRAAPRAVEMGE SSEDIDQMFTLLGEMDLLTQSLGVDTLPPDPNPRAEFNYSV GFKDLNESLNALEDQDLDMADLVADISEAQRTIQAQKESLQ NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPADP VLDLPLPPPPPEPLSQEEEEAAKADKIKLALEKLKAKVKKLV VKVHMNDNSTKSLMVDRLQARDVLDNLFRKTHCDCNVDWCLYE IYPQLQIERFFEDHENVVSVLSDWTRDTENKILFLEKEEKYAVF KNPQNFYLDNRGKESKETNEKMNNAKNKESLLEVRLILQSGRKE KDVCSIFKSFASENNGKI |
| 6243 | 1509 | 614 | RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT TSRASSRRLACGPQTRAGAETRTAMIRANSARDTRRATCRSA AGTPSPPTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA MGQAGAGPAGRGKSEAGGGPGRHAHPSPLPREPRVRTGPPAH SPTPGSIDPSPELSWGSAGVTQESPLLDVDFLLFRTRAVDPLR RVFFFFYQHLTFFSIQPPPPCHAFHPRDPPAGTKRQLILVPLK GPPILAPILSLTPIILSRWSCYFPRSRILAQGWHL |
| 6244 | 2119 | 1745 | FEHAYASQFGTFLGNNESECKLKLQKQTMLSWVWNPSELSK FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP |
| 6245 | 81 | 1148 | LSLRNAKYSFPQELISLFSMTDLNDNICRYIKMITNIVILSLI ICISLAFWIIISMTASTYYGNLRPISPWRWLFVVPVLIVSNGL KKKSLDHSGALGGLVVGFIILTIANFSFTSLMFFLSSSKLTKW KGEVKKRLDSEYKEGGQRNWQVFCNGAVPTBELALLYMIENGGP EIPVDFSQKYSASWMLSLAALACSAGDTWASEVGPVLSKSSP RLITTWKVPVGTNGGVTVVGLVSSLLGGTFVGIAYELTQLIFV NDLDISAPQWPIIAGGLAGLLGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHLAGKPILDNNAVNLFSSVLIALLPTAAWGF PRG |
| 6246 | 1177 | 359 | SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNLFLSLALPKGGNKHLSNLTILWLKLLNLS SGEDGQOMILRLDGLDCLLTEMISKYKHKSPLPLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSIAKKTFFPNSEANPLNAYYKCLE LVQLNLS |
| 6247 | 3 | 1678 | NSRVGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPIKAFYNESWERRHGRPIDPDTLLWSVTV SIFAIGGLVGTILVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIIVGRFIMGIDGGVALSVLPMYLSBISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPLYFGVIVVPAVVQL LSLPLPDSPPRYLLEKHNEARAVKAFQTLGKAHVQSEVEVL AESRVQRSIRLVSVLELLRAPYVRWQVTVIVTMACYQLCGLNA IWFYTNISIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGFGMLMGLFFGTLLTTLTLDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQSQRPAAFIAGTVNWSNFVAVG LLFPPIQKSLDTCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP |
| 6248 | 56 | 1773 | VPPPRMAAVPPGLEPNNRVRIPKAGNRSVTVQNPAAALDLCI AAVIKECHLVILSLKSLTDAETDVLCAVLYSNHNRMRHXPFL ALKQVEQCLKRLKNMNLGSIQDLFELFSSNENQPLTTKVCVVP SQPVVLEVLKVLGACKLLRLLDCCCKTFLTLVKHLGLQEFII LNLVMVGLVSRWLWLYKGVLRKRLILLYEPLFGLLQEVARIQMP YFKDFTFPSDITEFLGQPYFEAFKKMPIAFAAKGINKLLNKL LINEQSPRASEETLLGISKKAKQMKINQNNVLDLQGPVKNKRVF |

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|------------|--|--|--|
| | | | KESSEFDVRAFCNQLKHKATQETSDFDKCSQSRLKTTYSSQK VIGTPHAKSFVQRFREAESFTQLSEIOMAVVWCRSKKLKAQAI FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLRSGGIK TSKHHLRQRRSQNKFLRRQRKPQKQLQSTLLREIQQFSQGRKS ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIQTKMKI HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDI PALMGV |
| 6249 | 56 | 1773 | VPPPRMMAAVPPGLEPWNVRIPKAGNRSVAVTQNPGAALDLCL AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGHKKPHL ALKQVEQCLKRLKNNMLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVLEVLKVLGACKLLRLDCCCKTFLTLVKHLGLQEFII LNLVMVGLVSRWLWLYKGVLRLLIILYEPFLGLLQEVARIQMP YFKDFTFPSDI TEFLGQPYFEAFKKMPIAFAAGINKLLNKL LINEQSPRASEETLLGISKKAKQMKINQNNVDLGQPVKNKRVF KESSEFDVRAFCNQLKHKATQETSDFDKCSQSRLKTTYSSQK VIGTPHAKSFVQRFREAESFTQLSEIOMAVVWCRSKKLKAQAI FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLRSGGIK TSKHHLRQRRSQNKFLRRQRKPQKQLQSTLLREIQQFSQGRKS ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIQTKMKI HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDI PALMGV |
| 6250 | 232 | 1306 | LAALHIMALPFRKDEKYKDLDEDELLGNLSETELKQLETVLDD LDPENALLPAGFRQKNQTSKSTTGPFDRHLLSYLEKEALEHKD REDYVPYTGKKGKIFIPKQKPVQTFTEEKVSLDPELEAL TSA SDTELCDLAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG EKILPVFDEPPNPTNVEESLKRTKENDAHLEVNLLNNIKNIPI TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK SLNVESNFTIGVGILALIDALRDNETLAELKIDNQRQQLGTAVE LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVKRKR VEGDHQ |
| 6251 | 62 | 972 | TPGSGPMSAWAAASLSRAAACLLARGPGVRAAPPRDPRPSHPE PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS KLCLNIRLAVKEGGFNPENHNSNLANILEVCRSKHMPKSTIETAL KMEKSKDTYLLYEGRPGGSSLLIEALSNSSHKQADIRHILNK NGGVMAVGARHSFDKGVIVVEVEDREKKAVNLERALEMAIEAG AEDVKETEDDEERNVFKFICDASSLHQVRKKLDSGLGLCSVSCAL EFIPNSKVQLAEPDLEQAAHLIQAALSNHEDVIHVYDNIE |
| 6252 | 27 | 1897 | EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKKNREL RPQRPKNAYILKKSRI SKKPQV PKKPREWKNPESQRLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLEVAEAEETSIKAARSELLAEPEGFLEGE DGEDTAKICQADIVEAVDIAAAKHFDLNLRFQGPYRLNYSRTG RHLAFGGRGHVAALDWVTKLMCEINVMEAVRDIRFLHSEALL AVAQNRWLHIYDNQGIELHCIRRCRDVTRLEFLPFHLLATASE TOFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVILHGSNG TVSLWSPAMKEPLAKILCHRGVRAVAVDSTGYMATSGLDHQL KIFDLRGTYQPLSTRILPHGAGHLAFSQRGLLVAGMGDVVNIWA GGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQREWEVKALLEKVPABLIC LDPRALAEVDVISLEQKKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHEAKAKPTGARPS ALDRFVR |
| 6253 | 27 | 1897 | EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKKNREL RPQRPKNAYILKKSRI SKKPQV PKKPREWKNPESQRLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLEVAEAEETSIKAARSELLAEPEGFLEGE DGEDTAKICQADIVEAVDIAAAKHFDLNLRFQGPYRLNYSRTG RHLAFGGRGHVAALDWVTKLMCEINVMEAVRDIRFLHSEALL |

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|------------|--|--|---|
| | | | AVAQNRWLHIYDNOGIELHCIRRCDRVTRLEFLPPHFLLATASE TGFLTLYLDVSGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG TVSLWSPAMKEPLAKILCHRGGRVAVAVDSTGYMATSGLDHQL KIFDLRGTYQPLSTRTPHAGHLAFSQRGLLVAGMGDVVNIWA GQKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQRQEWVKALLEKVPALIC LDPRALAEVDVISLEQKGKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR |
| 6254 | 155 | 1139 | HAIGRRGGSQELSAACGCFALRLRAPGSGRPALAPGAAAFAGL GGAPRFPFRGSAAGRMTLLKBYRICMPLTVDEYKIQQLYMISKH SHEQSDRGEVEVVQNEPPEDPHHGNGQFTEKRVYLSKLPSWA RAVVPKIFYVTEKAWNYPPYTITEYTCFPLPKFSIHETKYEDN KGSNDTIFDNEAKDVEREVCFIDIADEIPERYKESDEPKHFK SEKTGRGQLREGWRDSSHQIMCSYKLVTVKFEVWGLQTRVEQFV HKVVRDILLIGHRQAFVWDEWYDMTMDDVREYKMKMHEQTNIK VCNQHSSPVDDIESHAQTST |
| 6255 | 1 | 1444 | PTRPQQELLVSLATVIFVASQKALSVEKAVIKQQLSVSNGWT VYIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS HAEQCLTGLQEENYSSALSCLAESLKFYHKGIALSTAATPLNP LSFQCFVFKLRIDLLQAFSQCITCNSLKTSPPPAIATTIAMTL GNDLQRCGRISNQMQSMEEFRSLASRYGDLQASFDADSATLR NVELOQQSCLLISHAIEALILDPESASFQYEGSTGTAHADSEYE RRMMSVYNHVLVEEVESLNGKYTPVSYMHTACLNALIALLKVP SFQRYFFQKLQSTSILKALSPSPRNPAEPIAVQNNQQLALKVEG VVQHGSKPGLFRKIQSVCLNVSSLTQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLNPAILGTHNITVSSSVKDANGIVWKTG PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF |
| 6256 | 1 | 1542 | CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAECTDEEEK EDRAAQSLNKLIRSNLVDNTNQVEVLQORDPNSPLYSVKSFEEL RLKPQLLQGVYAMGFNRPSKIQENALPMLAEPQNLIAQSQSG TGKTAAPVLAMLSQVEPANKYPQCLCLSPTYELALQTKGVIEQM GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPTVLDWCCKLK FIDPKIKVFLDEADVMATQGHQDQSIQIRQMLPRNCQMLLF SATFEDSVWKFAQKVVPDPNVILKREEETLDTIKQYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVA LLSGEMMVQRAAVIERFREGKEKVLVTNVCARGIDVEQVSVV INFELPVDKGNPDNETYLHRIGRTRGFRGKGLAVNMVDSKHS NILNRIQEHFNKKIERLDTDDLDEIEKIAN |
| 6257 | 210 | 615 | AFIPAMAELIQKKLQGEVEKYQQLQKDLKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAGLQQEFQRAQAAGAPG KA |
| 6258 | 210 | 615 | AFIPAMAELIQKKLQGEVEKYQQLQKDLKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAGLQQEFQRAQAAGAPG KA |
| 6259 | 2 | 1540 | ILEKGFPSQCHPERKWKVDVLESSQENEDHFWELLFHNKTV SVENGDRGSKTFNLGTDVPSLRNPYKICDSCEMNLKNISGLII SKKNCSSRKPKDFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFTNKRSGIGETVCK YNECGRTFIESLKLNIQRPHLEMEPYGCSICGKSFMCNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVS DTWEKSALLKHQIVHMGGSYDYNENGSNFSKSHLTQLRRHT GEKTFECGEGKTFWEKSNLTQHQRHTGKPYECTBCGKAFCQ |

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|------------|--|--|---|
| | | | KPHLTNHRTHHTGKPYECKQCGKTFVCVSNLTHQRTHTGKPYECNACGKSFCHRSALTVHQRTHHTGKPFICNECGKSFVCVSNLTVHQRTHHTGKPYKCNCEGKTFCEKSALTKHQRTHHTGKPYECNACGKTFQSRSVLTKHQRITHRVKALSTS |
| 6260 | 2081 | 1436 | GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVWRFVEDSFDPNINPTIGASFMKTQVQYQNELHKFLIWDTAGQERF RALAPMYRGSAAAIIVYDITKEETFTLKNWVKELRQHGGPPNI VVAIAGNKCDLIDVREVMERDAKDYADSIHAFVETSAKNAINI NELFIEISRRIIPSTDANLPSGGKGFKLRRQPSEPKRSCC |
| 6261 | 3 | 1188 | FWYRLGPGTRSRWRPFRGSWAASLVPRGFSAPALVTSPCPPDPLR SPACEPCRPDFAPRPALLLRSGPRSAVAVTGKPKALGQPGPWPG MAEVSIDQSLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS NVQRNRLVQHDQLQAKQLQEEELKAQAQLQKRYKDLEQQDCEIA QEIQEKLAIEAERRRIQEKDEDIARLLQEKELQEEKKKRKHFP EFPATRAYADSYVYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA ETARKLQEEELLATQVDMRAAQVAQDEEIAARLLMAEEKKAYKKA KEREKSSLDKRRQDFEWKPKTAKAANSKSKESDEPHHSKNERPA RPPPPIMTDGEDADYTHFTNQSSSTRHFSKSESSHKGPHYKH |
| 6262 | 2 | 1759 | FECHSQGLCSVHRPGKVPQARMSGLVLGQDEFPAGHRLSQEELL GSTRLVSQGLEALRSEHQAVLQSLSQTIETCLOQGGHEEGLVHEK ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR LCQENQWLRDELQQLQRLQSEQAQVAQLEBEKKHLEFLGQLRR YDEGHTSEEKEGDKDLSLDDLPNEEEDPSNGLSRGQGFATA AQQGGYEIPARLRLTHNLVIQYAAQGRYEVAVPLCKQALEDLER TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL GPDPHVAATLNNLAVLYGKRGKYKEAEPQCORALEIREKVLGT NHPDVAKQLNNLALLCQNGKYEAVERYQALAIYEGQLGPDN PNVARTKNNLASCYLKQGYAEARTLYKEILTRAHVQEPGSDVD DHKPIWMHAEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV NTLRLNLGALYRRQKLEAAETLEECALRSRRQGTDPISQTKVA ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVESGDSGTLQR SGLGKIRDVLRR |
| 6263 | 1 | 2408 | RELDLSADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSFSPKPEVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT APVNTVMDSPVHLEPSSQGVVIQNKSWEMPVDRLETSTRDFIC PNSNIPDQESSLQSFCSNENKVLKENADFLSLRQTELPNGNSCAQ DPASFMPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ KNAVQIISSALDNDNESTKDTENTFVLGQVQKTDAPVPVYSDST IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK SSSGHEVENSTTDQVISHEKENKLESVLVTHLSRCDSDLCENM AGMPKGNLNEQDPKHCPSEKCLLSIEDEESQQSILSSLENHSQ QSTQPEMHKYQLVKVELEENAEEDDKTENQIPQRMTRNKANTMA NQSKQILASCTLLSEKDSSESSPRGRIRLTEDDDPQIHHPRKRK VSRVPQPVQVSPSLQAKEKTQQSLAAIVDSLKLDEIQPYSSER ANPYFEYLHIRKKIEEKRKLCSVIPAQAPQYDEYVTFNGSYLL DGNPLSKICIPTITPPFSLSDPLKELFRQQEVVRMKRLQHSIE REKLIVSNEQEVLRVHYRAARTLANQTLFSACTVLLDAEVYV PLDSQSDSKTSVRDRFNARQFMSWLQDVDDKFDKLTCLLMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISIIYEQEFYVPLVD VNDDFELTPI |
| 6264 | 143 | 1960 | KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI TQPVVVVAIVGLYRTGKSYLMNKLAKGNKGFSLGSTVKSHTKGI WMWCVPHPKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL SSTLVYNSMGTINQAMDQLYVTELTHIRSKSPDENENEDS ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT |

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|------------|--|--|---|
| | | | SQKDKNFNLPRLCIRKFFPKKKCFVFDLPPIHRRKLAQLEKLQDE ELDPEFVQVADFCSYIFSNSKTKTSLGGIKVNGPRLESVLTY INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV LPAETLQELLDLHRVSEATEVYMKNFSKDVHLPQKKLAAQL DKRDDFCQKQNEASSDRCSALLQVIFSPLEEVKAGIYKPGG YCLFIQKLQDLEKKYEEPRKGIQAEIILQTYLKSRESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI |
| 6265 | 143 | 1960 | KHRQENNALDPAPEIHMTPMCLIENTNGELVANPEALKILSAI TQPVVVAIVGLYRTGKSYLMNKLAKNGKFSLSGTVKSHTKGI WMWCVPHPKPEHTLVLLDTEGLGDVKKGDQNDQSWIFTLAVLI SSTLVYNSMGITINQAMDQLYYVTELTHRIRSKSSPDENENEDS ADPVSPFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT SQKDKNFNLPRLCIRKFFPKKKCFVFDLPPIHRRKLAQLEKLQDE ELDPEFVQVADFCSYIFSNSKTKTSLGGIKVNGPRLESVLTY INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV LPAETLQELLDLHRVSEATEVYMKNFSKDVHLPQKKLAAQL DKRDDFCQKQNEASSDRCSALLQVIFSPLEEVKAGIYKPGG YCLFIQKLQDLEKKYEEPRKGIQAEIILQTYLKSRESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI |
| 6266 | 276 | 1421 | GS HQKQMLVPCFLYSLQNRKPSLYGSLTCQIGLDGIPVETASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSI TCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCRRFF PSGLVVLSSGMDAQLKIWSAEDASCVVTFKGHKGGLDITAVDR GRNVVSASRDGTARLWDCGRSACLGLVADCGSSINGVAVGAADN SINLGSPBQMPSEREVGTEAKMLLLAREDDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIA SQDGS CFIVQQDL DYVTELTGADCD PVYKVATWEKQIYTCCRDLVRRYQLSDL |
| 6267 | 3 | 622 | LGMKKNNNSAKRGPQDGNQPPAPEKVGWVRKFCGKGFIREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYKCEELRKS RSKKNHSKFTLAHSKQPGNTAPNLI FLAVSPEEKESWINALNSA ITRAKNRILDEVTVEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC |
| 6268 | 160 | 1368 | HRELQNLPAGLSSALIDNPLTLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTYRDVMLETFGHLVSVGWETTLLENKELA PNSDIPEEPAPSLKVQESSRDCALSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSALDNTQVSLQKIDNPE SQANSALDNTQVLLHKIPPRKRLRKRDSQVSKMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSTRSTQITFIRIHKGSQVCRCECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKA FRQ SSHLIRHQRHTHTGERPYACNCKGKAF TQSSHLIGHQRTHNRTKR KKKQPTS |
| 6269 | 2886 | 1449 | HASAPTRRNMAAASPLRDC HAWKDARLPLSTTSNEACKLFDATL TQYVKNWTKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQHLVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSDAYFYLYGYEQMRDSVAR IYPFWTPDIPLSSVYKGIYSFGLMETNFYDQAEKLAKAELSINP TDAWSVHTVAHIHEMKAEIKDGLFPMQHSETLWKDSMDLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML YRLQMEGVSVGQRWQDVLVPARKHSRDHILLFNDAHFLMASLGA HDPQTTELTLTLDASESPGENCQHLLARDVGLPLCQALVEAE |

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|------------|--|--|--|
| | | | DGNPDRVLELLLPYRIRIVOLGGSSNAQRDVFNQLLIHAALNCTS SVHKVARSLLMERDALKPNSPLTERLIRKAATVHLMQ |
| 6270 | 23 | 2086 | SVTVTLGSEGDGRPPPTYHLEEMEQEPQNGEPAETIKIIREAYKKA FLFVNKGLNTDELQKKEAKNYYKQGIGHLLRGISISSKESEHT GPWESARQMQQMKMETLQNVTRLEILEKGLATSLQNDLQEVF KLYPEFPFKDMCEKLEPEQSFSSAPQHAENVGNTSTPSAGAVAA PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSEFSSVGE EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS YPGYLRIVRFLDNSLDTVLNRPFGFLQVCDWLYPLVPDRSPVLK CTAGAYMFPDTMLQAGCFVGVVLSSELPEDDRELFEDELLRQMS DLRLQANWNRAEEENEFPQIPGRTRPSSDQLKEASGTDVKQLDQG NKDVRHKGKRGKRAKDTSSSEEVNLSHIVPCEPVPPEKPKELPEW SEKVAHNILSGASWVSWGLVKGAETGKAIQKGASKLRERIQPE EKPVEVSPAVTKGLYIAQATGGAAKVSQFLVDGVCTVANCVGK ELAPHVKKHGSKLVPESLKDKDKGKSLDGMVVAASSVQGFST VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDASV NVGVTAYNINNIGIKAMVKKATATQTGHTLLEDYQIVDNSQRENQ EGAANVNVRGEKDEQTEKVEKAKKDK |
| 6271 | 32 | 1058 | GCGVKTAGMVGREKLSIHFPVPGSCRLVBEVNIPNRRVLVTGA TGLLGRAVHKEFQQNNWHAVGCGFRARPKEQVNLDSNAVHH I IHDFFQPHVIVHCAEERRPDVVENQPDAAASQLNVDASGNLAKEA AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK AVLENNLGAAVLRIPILYGEVEKLEESAVTMFVKVQFSNKSAN MDHWQQRFPPTHVKDVATVCRQLAEKRLMDPSIKGTFHWSGNEQM TKYEMACAIADAFNLPSSHLRPIITDSPVLGAQRPRNAQLDCSKL ETLGIGQRTPPFRIGIKESLWPFLLDKRWQTVFH |
| 6272 | 1136 | 528 | GAVMEDAAAPGRTEGVLERQGAAPAGQGGALVELTPTPGGLAL VSPYHTRAGDPLDLVALAEQVQKADEFIRANATNKLTIVIAEQI QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYLYKRESGQ QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI SMMDTLLSQSVALPPCTEPNFQGLTH |
| 6273 | 256 | 843 | SCPRVSPCCRSLGCVMFSLPLNCSPDHIRRSGCWGRPDQLKIA SAAWNSKCHPGAGAAMARQHARTLWYDRPVVFMFCVBDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKKEVAVPRLTKEDIKPVWLSVDFDNWRDWEDEEME LAHVEHYAEVRDNTYCVLPT |
| 6274 | 56 | 1142 | AAAAAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLPEDPGTPGSETEALYTTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVTVFVKLLNPKCR DVFEPARAQFNGKGSYNGGAMRVAGISLAYSSVDVQKPARLS AQLTHASSLGYNAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSRLKKIGELLDQASVTREEVVS ELGNIAAFESVPTAIYCFRLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGALAGAYYGMQVPESSWQSCGEYEETDILA QSLHRVFKS |
| 6275 | 20 | 565 | SRRGRARCLARGSRPVPFRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQTALGDLKQSAE KCHVM |
| 6276 | 797 | 97 | TLLPLPPLPDTEGMILLNTGLEGTVAENPWPVHTPSGNILTLE SCLQQLATHPGHWGHLQIAEPAALRPSLALLARLSSLGLLHWP VWVGAKISHGFSVPGHVAGRELLTAVAEVFPHTVAPGWFEV LGSGYREQLLTDMLELCQGLWQPVSFQMAMLLGHSTAGAI GRL LASSFRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYRLPQ GYHKDLLAHVGRN |

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|------------|--|--|--|
| 6277 | 4600 | 2744 | MAFRTEMGLYYSYFKTIVEAPSEFLNGVMMIMNDKLTETPLVINT LKRFNLYPBVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSPTESCEGLGDPACFYVAVIFILNGLMMALFFIYGYLSSGSRLLGL VTVLCFFFNHGECTRVMWTPPLRESFSYFPLVLQMLLVTHILRA TKLYRGSIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVG YIDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYASSLVIIWG ILAMKPHFLKINVSELSLWVIQGCFLWFGTVILKYLTSKI FGIANDAHIGNLLTSKFPSYKDFDTLLYTCAAEFDMEKETPLRYTKT LLLPVVLVGFVAIVRKIIISDMWGVLAQQQTHVRKHQFDHGE L VYHALQLLAYTALGILIMRLKFLTPHMCVMASLICSRLFGWLFC KVHPGAIVFAILAAMSIOGSANLQTQWNIVGEFSNL PQEELIEW IKYSTKPDVAFAGAMPTMASVKSALRPIVNHPHYEDAGLRART KIVYSMYSRKAAEEVKRELKIKVNYIILESWCVRRSKPGCSM PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLV EVVKE |
| 6278 | 3 | 823 | ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCGVDNIPSVITDMLTRLSDLLKYFNSRSQCLVLGAG ALQVVGKLTITTKNALSSRCLQLIVHYIPVIRAHFEARLPKQ YSMLRHFHDITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVA PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH LKKQLSHLNVINDGGPQNGLVTAADVFTGNLQALKGLKDLDLN MAEIEWEQKR |
| 6279 | 127 | 1687 | GGAMASDGARKQFWKRSNSKLPQSIQHVYGAQHPPFDPLHGT L LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDDELLAMA AESLNSEVVMETANRVLNRHSQRQGRPTLQEGPGLQKPRPEAE PPSPPSGDLRLVKSVSESHSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKVPVPMTWKLSGYLPANVDRRPTLQKQKQKEYFAP I EHYDYSRNDVHQDTYRQIHIDIIPMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEVDTV DVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDYQSEPDGFSHFHLYVCAAFVVRWKEILEEKDFQELLLFL QNLPTAHWDEDEISLLLAAYRLKFAFADAPNHYKK |
| 6280 | 857 | 2515 | ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRSEEEEEDEE DDLAQVLAYLLRRGQVRLVQGGGANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSDYIHCNIYEGEDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQVPPKAWRKLKLPDSSSLMTYRGH GVLHTLIRCFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVVK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVQSSTPFSSPQ |
| 6281 | 857 | 2515 | ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRSEEEEEDEE DDLAQVLAYLLRRGQVRLVQGGGANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSDYIHCNIYEGEDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR |

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|------------|--|--|---|
| | | | EGMEASRQAATQONWDYRWOQVPPKAWRKLKLPDSSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLSGHIKVK LTNNKACVRDVSWHPFEEKIVSSSWDGNLRWQYRQAEYFQDDM PESEECASAPAPVPQSSSTPFSSPQ |
| 6282 | 125 | 906 | RMAACRALKAVLVDLSGTLHIEDAAVPGAQEQALKRLRGASVIIR FVTNTTKESQKDLLERLRKLEFDISEDEIFTSLTAARSLERKQ VRPMLLVDDRALPDFKGIQTSDFNAVVMGLAPEHFHYQILNQAF RLLLDGAPLIAIHKARYYKRKDGALGPGPFVTALEYATDTKAT VVGKPEKTFLEALRGTCGPEEAVMIGDDCRDDVGAQDVGML GILVKTGKYRASDEEKINPPPYLTCEFPFAVDHILQHL |
| 6283 | 140 | 1043 | LSLFGIHMNPFWSMSTSSVRKRSEGEKTLTGDKVTSPPRTAP KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSL AEFTLVVKQLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVKFK TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR RNHNIWQVLMYARRVYKIDTASPLNPEAAVLYEKDIQLFKSK VDSVKVCTARLFDQPKIEDPYAISFPWNPSVHDEAREKMLTQ KKKPEEQHNKSVHAGLSWVKPGSVQPFSEKKEKTVAT |
| 6284 | 1 | 2879 | RSVIPGSTISSRWPEGLSRPRFMAHEWDWFQREELIGQISDIRV QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI LMALLEVLSGRNLLEYKSSSHRIFRLNNIAKALKFLEDSSNVKL VSDIAAEIADGNPSLVGLIWNIIFFQIKELTGNLSRNSPSS LAPGSGGTSDSSFPPTPTAERSVAISVKDQKAIKALLANVQR KTRKYGVAVQDFAGSWRSGLAFLAVIKADPSLVDKMALENST RENLEKAFSIAQDALHIPRLLEPEDIMVDTPEQSIMTYVAQFL ERFPELEAEDI FDS DKEVPIESTFVRIKETPSEQESKVFVLTE GERTYTVNHETSHPPSKVFCVKPESMKEFRLDGVSSHLSDS STEFMHQIIDQVLQGGFGKTS DISEPSPSSILSSRKENGRSNS LPIKKTVEADTYKDFPFCSKNLSLCFEGSPRVAKESLRQDGHV LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSS CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEGEDDDQLQGVG EELSSSPSSCVSLETLGSHSEGLDFKPSPLSKVSVIPHDLF YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPGYMPDLDSRE EADGSGSSSSSSVPGESLPSASQVLYLSRGGVGTTPASEPAP LAPHEDHQRETENDPMDSHQSQESPENLENIANPLEENVTKES ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSPSR TSHSDSSIYLRHRHTRSSSDHFLCSVEERSRSG |
| 6285 | 2157 | 1331 | SKTENLLEMMWFQQLSFLPSALVIWTSAAFIYSYITAVTLHH IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRYKQVH ALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAAHVS GAVLTFGMGSYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCG VSALSMITCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTA EWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPIN NERTRLRSRDI |
| 6286 | 1619 | 276 | KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV PFSIPAASEIADLSNIINKLLKDKNEPHKHVEFDLIKQQLRM PLDKHMEMENISSREVVEIBYVEKYTAPQPEQCMFHDDWISSIK GAEEWILTGSYDKTSRIWSLEGKSIIMTIVGHTDVVKDVAVWKKD SLSCLLLSASMDQITLLWEWNVERNKVKALHCCRGHAGSVDSIA VDGSGTKFCGSGWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT EQLGLTRTPIVTLSCGHMEAVSSVLWSDAEIICSAWSDHTIRVVD VESGSLKSTLTGNKVFNCSYSPLCRKLASGSTDRHRLWDPRT KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT RSCKAPLYDLAAHEDKVLVDWTDGTLSSGGADNKLYSYRSP |

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|------------|--|--|--|
| | | | TTSHVGA |
| 6287 | 278 | 1482 | MQFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF APAKLQVQKILCDLLLPENLKEGLKESWSLPCTKNRPDFHS VMEESQSLNEPSPKQSEIPEVTSEPVKGSINRAQSAQSINSTE MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIIVNEDGR NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMLRPFPE PVTTPCGHFCKNCLERCLDHAFYCPCKESLKEYLADRRYCVT QLLEELIVKYLPELSEKKIYDEETAELSHLTKNVPIFVCTMA YPTVPCPLHVFEPYRRLMIRRSIQGTGKQFGMVCSDTQNSFADY GCMLQIRNVHFLPDGRSVVDVTVGKRFVLKRGMKDGYCTADIE YLEDV |
| 6288 | 1 | 743 | VTLYPCRGLVGNLLLGASGMASGCKTGPSILNSDLANLGAECRL MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM HMMVSKPEQVWKPMVAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPKRSVINLLRNVCSEAAQKRSLLDR |
| 6289 | 1 | 743 | VTLYPCRGLVGNLLLGASGMASGCKTGPSILNSDLANLGAECRL MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM HMMVSKPEQVWKPMVAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPKRSVINLLRNVCSEAAQKRSLLDR |
| 6290 | 3 | 1856 | TLGRWLLGVYETVAPTILACLPRPRLRRRRRRRRRMRISRYTRKA VPQSLELKGITKHALNHPPPKLEBISPTSDSHEKDTSSQSXS DITRESSPTSADTGNLSAFPSTYTGAGISTEGSSDFSWGYGELD QNATEKVQMTFTAIDELLYEQKLSVHTKSLQEECQQTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSEQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY LAFDHIDIEEGPHGKKSEAAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPVPQSKVLYITSNPMSLCQASRHPNVNDLLVHG MPLQPRNLSLMDKLLDLDKLLMRPGSSTILSTRNWPNAVFEFS TSSLSYTVQSTRRRNPPTLHP ISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSSRAQSAVDEPNYQQPQERLLLPDFFPRPNTTQSFLDIT QYRRSCAVEYPHQARPGRGSGAGPQLHGSTKSQSGGRPVSRTRQG P |
| 6291 | 1732 | 602 | LVAKMASSASARTPAGKRVINQEELRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSASSAPQSVKRAFDADDQDVKRAKATLVPQVQFST SAWTTNFDKIGKEFIRATPSKPSGLSLPDYDEEEEEEEEEEGD GERKRGDASKPLSDAQKEHSVSSSREVTSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKQMDKEWDEFQKAMRQVNTISEAIVAEDEDEGRDLRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKBEEN ADSDDEGELQDLSQDWRVKGALL |
| 6292 | 1835 | 1142 | TCPGAMKMPVAPWTRFYNSNCCCLCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEIYRQLPPNPPYRDDVMSVNPCTCLVLIILFISIIILTFKGY LISCVWNCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA |
| 6293 | 2382 | 1035 | FWCTLGTVDVHPIGWCAINSKILVPPRTIHAFTDWKGYLMKRL VGSRTLVPDFHIKMVESMKYPFRQGMRLVVDKSVQSRTRMAVV DTVIGGRLRLLYEDGSDDDDFWCHMWSPLIHPVGSRRRVGHGKIK |

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|------------|--|--|---|
| | | | MSERRSDMAHHTFRKIYCDVPPYLFKKVRAVYTEGGWFEEGMK LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWNYLEKTKSKA APSRLEFNMDCPNHGFVKGMKLEAVDLMEPRLICVATVKRVVHRL LSIHFDGWDSEYDQWVDCSPDIYPVGWCELTGYQLQPPVAAEP ATPLKAKEATKKKKKQFGKKRKRIPTKTRPLRQGSKKPLEDD PQGARKISSEPVGEIIAVRVKEEHLDVASPDKASSPELPVSVE NIKQETDD |
| 6294 | 354 | 1814 | AQLTTRGRTVAGGVWRWIPSPFPDLELYSCCLGTDRGFPELSHHC KNVIATASDYDMAEITNIRPSFDVSPVAGLIGASVLVVCSVT VFVWSCCHQQAEEKHKNNPPYKFIHMLKGISYIPETLSNKKKIIK VRRDKDGPREGGRNLLVDAEAGLLSRDKDPRGPPSSGSCIDQ LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV DYNFPKKALVVTIQEAHGLPVMDQDQGSDFYIKMTILPDKRHR VKTRVLRKTLDPVDETFYFGIPYSQQLDLVHFLVLSFDRFS RDDVIGEVMPVPLAGVDPSTGKVQLTRDIKRNQKICISRGELQV SLSYQPVQARMTVVVLKARHLQKMDIAGLSGNPVVKNVYGRK RIAKKKTTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD RTTKNEVVGRLLILGAHVSVTASGAHWRREVCEPRKPVAKWHSLS EY |
| 6295 | 2795 | 617 | VSSALLTGATSGSDAAKSEGASAPLSCTNAVAMDRPDEGPPAK TRRLSSSESPQRDP PPPPPPPPLRLPLPPQQRRLQEETAA QVLADMRGVGLG PALPPPPYVILEEGIRAYFTLGAECPGWDS TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVVQSSSFGGE GALETCSAVGWAPQRLVDPKSKEAIIIVEDEDEDERESMRSSR RRRRRRRRKQKVKRESRERNAERMESILQALEDIQLDLAEVNI KAGKAFRLRLKRFIQMRPFLERRDLIIQHIFGFVWKAFLNHPR ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT NMVIVKEFQRNRSRGLVSHSTPIRWHRGQEPQARRHGNQDASHS FFSWFSNHSLEADRIAEIIKNDLWVNPRLYYLRERGSRIKRRK QEMKRRKTRGRCEVVIMEDAPDYAVEDI FSEISDIDETIHDIK ISDFMETTDYFETDNEITDINENICDSENPDHNEVPNNETDN NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY GNNFFKGGFWGSHGNNQDSSDSNEADEASDDEDNDGNEGDNEG SDDDGNEGDNEGSDDDRDI EYKVEDFDKQADYEDVIEII SDESVEEGIEEGIQQDEDIYEENYEEBGSSEVDWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG |
| 6296 | 727 | 1199 | RHCGCDAQGACDSLPTGTSSPVTARNAIPEARCCVWLLDGTTV EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTBRDT LGTSLOFPSPFSGTISFGSFSDSGIFPLGSQCCLGFGQFSGK KVALIHKRVRLSVFGARWGRIYFGK |
| 6297 | 1 | 922 | QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSAALLVGFLS VIFALVWVLHYREGLGWGSALEFNWHPVLMVTGFVFIQGI AII VYRLPWTWKCSKLLMKSIHAGLNAVAAILAII SVVAVFENHNVN NIANMYSLSHWGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL MPIHVYSGIVIFGTVIATAMGLTEKLI FSLRDPAYSTFPPEGV FVNTLGLLILVPGALIFWIVTRPQWKRPKEPNSTILHPNGGTQ GARGSMPAYSGNNMDKSDSELNNEVAARKRNALDEAGQRSTM |
| 6298 | 3 | 985 | SVPLRRLSLSGTLQAGTTTKMAVARLA AVAAWVPCRSGWAAV PFGPHRGLSVLLARI PQRAPRWLPACRQKTSLSFLNRPDLPNLA YKLLKGKSPGIIFIPGYLSYMNKTALAIEEFCKSLGHACIRFD YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSLSGG WLMLHAAIARPEKVVVALIGVATAADTLVTKFNQLPVLLKKEVEM KGVWSMPSKYSEGVYVNVQYSFIKEAEHCHLLHSPIPVNCPIRL LHGMKDDIVPWHTSMQVADRVLS TDVDVILRKHSDHRMREKADI QLLVYTTIDDLIDKLSTIVN |

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|------------|--|--|---|
| 6299 | 512 | 814 | ECDEGIMPVNTISLSLPTNGSPLODILVHPCVTSLSAILTSS SIDAMDDSAFSGPYKFPPTPPLESFNLCFYTSQVPVPPILGFYQ MKEEEVQLRNNH |
| 6300 | 121 | 692 | AAPSCWSQRGVPAAGTPSSPRLVSRRAAPSAGPWGAWRQGARA AQSPFSPINSSSVYPGSDSVHSSPEDGGGGRDRPVGGSPGGPR LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLMCLTKPR ITNEDVLSKDAGECAICLBELQQGDTIARLPCLCIYHKGCIDE WFEVNRSCPEHPD |
| 6301 | 616 | 284 | GKFPVPVNWEPQPLPPFKYLRCYRCLLETKELGCLLGSIDICLTP AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW IFSQYCFDLDFCNDPQNRGLYTP |
| 6302 | 490 | 745 | IFGFLHLFHMESFLVLCALFAHVFFSSSCGSSVALHSDPCLLS PVLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL |
| 6303 | 2 | 1961 | YWNYYGGGLWQSWQEKHPGQALSSPEWNPFDTKEEWQHYSQL YWYYLEQFYWEAQGWTFDASQSCDITDYSKTEADDKNDEKCM KVDLVSLSSPIMGDNDSSTGSDKHSEILDGINSIKLNSEEV QSQDLSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS SGNTNTDPPAEDSQSSGANTSKDRPHASGTDGDESEEDPPEHK PSKLKRSHELDIDENPASDFDSDGSLGFKYSGQKYGGIPNFS HRQVRYLEKNVCLKSKYLDMRRIKMKNNHIFFTKESEKPFKK SKILSKVEKFLTWVKNPMDDEASQSSSHDNGHDASTSCDSEEQ DMSVKKGDDLETNNPEPEKCSQSVSSAGELETENYERDSLATV PDEQDCVTQEVDPDSRQAEAEVKKKKKKKKKKVNGLPPEIAA VPBLAKYWAQRYRLFSRPDDGIKLDREGWFSVTPEKIAEHIAGR VSQSFKCDVVVDAFCGVGGNTIQFALTGMRIAIDIDPVKIALA RNNAEYVGIADKIEFICGDFLLLASFLKADVFLSPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFNNKLKITAYFGDLLIRRPASET |
| 6304 | 1 | 1438 | HRARVDRSRESPGDLRHPGRVRRDITLSGHPRLSTQHVLLRE DEVDPGTGDLGHPQHGSP IQETQSEVVTLVSLPGSDMAALPA WRATSGTLWPHTAEGRDLLGAENRALTGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSRTGQGAAPPWLTDDHDVQMLRL AQGEVVDKARVPAHQVLQVGFSTEALQDLSSPRLSQLCSQGL CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLPYRY TDGGARPVIIWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIIHTEWARLALDFLLQVHDLDRYCCGFEPSPD PCVEERLREKCRNPALRLVHILVRSSDPShLVYIDNAGNLQHP EDKLNFRLLLEGIDGFESAVKVLASGCLQNMLLKSLQMDPVFWE SQGGAQGLKQVLQTLERQGVLLGHIQKHNLTLFRDED |
| 6305 | 99 | 420 | NMIWRGRSTYRFRFRSVPPELIGFMLEPGDEFPQEEPTES RDPAPQGEREDQGAETQVPDLEADLQELSQSKTGDECGDGP VQGKILTKSEQPKMEGR |
| 6306 | 1 | 1874 | PTRPSKVVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDC KFNCHKRCATRVNDCLGEALINGDVPMEETDFSEADKSALMD ESEDGVI PGSHSENALHAS EEEEGEGGKAQSSLGYP LMRVVQ SVRHTTRKSSTTLREGVWVHYSNKDTRKRHYWRLDCKCITLPQ NNTTNRYKKEIPLSEILTVEAQNPSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAARAAGWETAIRQALMPVILQDAPS APGHAFHRQASLSISVNSQIQENVDIATVYQIFPDEVLSGGQF GVVYGGKHKRKTGRDVAVKVIDKLRFPPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVMEKLGHDLMELSSSEKGRLEPRL TKFLITQIILVALRHLHFKNIVHCDLKPENVLLASADPPQVKLC DPGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRLDMWSVG VIMYVLSLGTFFNEDEDINDQIQNAAFMYPASPWSHISAGAI LINNLLQVKMRKYSVDKSLSHPWLEQYQTLWDLRELEGKMER YITHESDARWEQFAAEHPLPGSGLPTDRDLGACFPQDHMQG |

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|------------|--|--|---|
| | | | LAERISVL |
| 6307 | 2136 | 589 | CFLLPGRDPEPPEAGAAAPCAPGAPDMSFRKVVVRQSKFRHVFG QPVKNDQCYEDIRVSRVTWSTFCVAVNPKFLAVIVEASGGGAPL VLP LSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC TVMVWQIPENGLTSPLETPVVVLEBHTKRVGI IAWHPTARNVLL SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHGSLFCS ACKDKSVRIIDPRRGLVAEREKAHEGARPRAIFLADGKVFTT GFSRMSERQLALWDPENLEBPALQELDSSNGALLPFYDPDTSV VYVCGKGDSSIRYFEITEEPYIHFLLNTFTSKEPQRGMGSMPCR GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPD TAG PEAALEAEWVSGRDADPILISLREAYVPSKQRLKISRNVLS DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEV M QELRALRALVKEQGDRI CRLEEQLGRMENGDA |
| 6308 | 2 | 1118 | GRTRPEKMLLSVLHTYSMRYLLPSVVLGTAPTYYVLAWGVWR LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVOILLYGDL PKNKENI IYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK WLPYLGWYFAQHGGIYVVRSAKNEKEMRNKLQSVVDAGTPMYL VIFPEGTRYNPEQTKVLSASQAFAAQRLAVLKHVLTPIKATH VAPDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTTEFLCKECP KIHIIHIDRIDKKDVPEEQEHMRRLHERFEIKDKMLIEFYESP D PERRRKFPFGKSVNSKLSIKTLPSMLILSGLTAGMLMTDAGRKL YVNTWIYGTLLGCLWVTIKA |
| 6309 | 220 | 563 | LVAEVKEPCSLPMLSVDMENKENGSGVGVKNMENGRRPPDPADWA VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL KLGPAKLIYEHVKPLQTKHLKNSS |
| 6310 | 36 | 979 | GPRCWFLLI LSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE AQRGSLAEELNVAAGLWADCDQPLYDCPMGLICTNYHILQEHV DLHLEENSFQQQMDRVQCSGDLQALHQLQQEEDRKRRSEESRQE IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHR KADMESLALGFDDGKTSTSGIIEALHRYQNAATDVRVWLSS VVDHFHSSSLGDKGWGCGYRNFQMLSSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPPQASQLIIRIQGTAKWIGACEVYIL LTSLRV |
| 6311 | 1 | 675 | PVWVNSCEGPRLAAAARTGHGVRRARLACLGEPRVKAAMVMTL ASKLRDGLKGSRTAATASDSTRVSVRDKLLVKEVAELEANL PCTCKVHFDPNKLHCFQLTVPDEGYQQGKQFETEVDPAYN MPPPKVKCLTKIWHFNI TETGEICLSLLREHSIDGTGWAPRTL KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR |
| 6312 | 213 | 1400 | GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVLVCISIPPLT RQISVKALGIGKNVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLSPSYGWIC DELMGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFFVRQNAI IRGIRHVTSDDFCFQMLMGGGVCSTVTLLNFNMPGAFVHEVMV GSAGRLVARGADLYGQKNSATQEEELLRDSLAVGAGLPEQGPQD VPLL YLKGVMYVQALRQSFQGGDRRTWDRTPVSMASFEEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEPDTNQNLCALQRNNL |
| 6313 | 2 | 2071 | QRSGAARLALPSFFSPACVHRSPLSFHGCWFYFVVVFMPLGV L FHRRAHGC TLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHFKAHKAVLAACSKFFYKFFQEF TOEPLVEIBGVSKMAFRHLIEFTYAKLMIQGEENANDVWKAEE FLQMLEAIKALEVRNKENSAPLEENTTGKNAKRRKIARTSNVI TESLPSAESEPVIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSA LALLADITSKYRQGD RKGQIKEDGCPSPDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLPYHFKEHMKSHSTE |

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|------------|--|--|---|
| | | | SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGKPFCEPCNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNWDQPKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTVEVLSVETRVQ TEPVTSMITIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAKAENEDRTALPVLE |
| 6314 | 2 | 2071 | QRSGAARLAFPLSPFSPACVHRSPLSFHGCWFYFVVVPMPLGVL FRRRAHGCITLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHFFKAHKAHLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEENANDVWKAAB FLQMLEAIKALEVRNKNENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPEIEVIEBIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDALALLADITSKYRQGDGRGQIKEDGCPSPDPTSK QVEGIEIIVELQLSHVKDLFHCCKNRSFKLFYHFKHEMKSHSTE SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGKPFCEPCNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNWDQPKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTVEVLSVETRVQ TEPVTSMITIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAKAENEDRTALPVLE |
| 6315 | 1 | 1015 | LGLAVNVVTLTLVLSYCPATATEEAPYWTYLLCALGLFIYQSLDA IDGQARRTNSCPLGELFDHGCDLSLTVFMAVGASIAARLGT PDWFFSCSFIGMFVYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPLHIGLIIILAIMIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDVTFLGP GLLFLDQYFNNFIDEYVVLWMAVSISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQLSSKSHQNNMD |
| 6316 | 1503 | 792 | VSAGAGTGIMGGTSTRRTFEADENENITVVGIRLSENVDR MKESSPSGSKSQRYSGAYGASVDEELKRRVAEBLALQAKKES EDQKRLKQAKELDRERAANEQLTRAILRERICSEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTQYQKAA EEVEAKFKRYESHVPVADLQAKILQCYRENTHTLKCASALATQY MHCNVHAKQSMLEKGG |
| 6317 | 102 | 839 | PEAQTSAVLAREKGLPTMRHEAPMQMASAQDARYGQKDSDDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITATTAYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSADNINVQTFERLVDIICDKMSSELET PAITAAKQNTRLKETPPPPQPNAC |
| 6318 | 1765 | 733 | PWHPLRTLPLHHPHPRPPRAEGREGADSMHPLGLELRREAPPL LGPLLSPPPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAEPLQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGPKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVSGSKDLSTPAQYALM EKDALQVQEMKAENAVSSLTGENVREFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP |
| 6319 | 88 | 717 | AATRLNQNNTLLGKKVVLVPYTSSEHVPSRYHEWMKSEELQRLT ASEPLTLEQYAMQCSWQEDADKCTFIVLDAEKWQAPGATEES CMVGDVNLFLTDLEDLTGEIEVMIAEPSCRGKGLGTEAVLAML SYGVTTLLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV |

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|------------|--|--|---|
| | | | TLRLTVSESEHQWLEQTSHEVEKPYRDGSAEPC |
| 6320 | 90 | 1111 | RPRGTGREKVMAA AVDSFYLLYREIARSCN CYMEALALVGAWYTA RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG IGKAYAEELASRGLNIIILSRNEEKLVVAKDIADTYK VETDII VADFSSGREIYLP IREALKDKDVGILVNNVGVFPYPQYFTQLS EDKLWDIINVNIAAASLMVHVLP GMVERKKGAIVTISGSCCK PTPQLAASFASKAYLDHFSRALQY EYASKGIFVQSLIPFYVATS MTAPSNFLHRC SWLPSPKVYAHHAVSTLGISKRTIGYWSHSIQ FLFAQYMP EWLWVGANILNRSIRKEALSCTA |
| 6321 | 1418 | 341 | HRKAALGALMAGRL LGKALAAVSLSLALASVTIRSSRCRGIQAF RNSFSSSWFHLNTNVMGSGNGSKENSHNKARTSPYPGSKVERSQ VPNEKVGWLV EWDYKPV EYTA VSVLAGPRWADPQISENFSFK FNEKDG HVERKSKNGLYE IENGRPRNPAGRTGLVGRGLLGRWGP NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA IPGGMVDPEKISATLKREFGEALNSLOKTSAEKREIEEKLHK LFSQDHLV IYKGYVDDPRNTDNAMMETEAVNYHDETEIMDNLM LEAGDDAGKVKWVDINDKLKYASHSQFIKLVAEKRD AHWSEDS EADCHAL |
| 6322 | 2047 | 1083 | NQELKNV ESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS WSINCCDDGEGSQQBEVISEDIGASIFNGQKKVLYYADALTEI AFVVPSPVESLTD SLESNISDQSDSDSNMDLMPGILKQPSLTLEL FPNHTDNLNSSQRLSPSSRMRLPQGRPVPLGPETRVSVVWVE RYDDIENFPLSELMTBISTGVETTANSSTSLRSTTLEKEVPVIF IHPLNTGLFR IKIQGATGKFNMV IPLVDGMI VSRRALGFLVRQT VINICRRKRLES DSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT SLFQEVGLKNCSS |
| 6323 | 1 | 656 | PASTTDGAQE ARVPLDGAFWIPRPAGSPKGC FACVSKPPALQA PAAPAPEPSASPPMAPTLFPMESSKSKTDSVRAAGAPPACKHLA EKKMTNPTT VIEVY PDTTEVNDYLLWSIFNFVYLNFCCLGFI A LAYSLKVRDKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW MALSVIATHRGLRSSASILVAEPHDWNTERQVTFRERCAL |
| 6324 | 1 | 2061 | EGAGMRRCP CRGSLNEAEAGALPAAARMGLEAPRGRRRQPGQQ RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGAPAGTES PQAEFWTDGQTEPAAAGLVETERPKQKTEPDRSSLRTHLEWSW SELGTTCLWTETGT DGLWTDPHRSDLQFQPEBASPWTPQGVHGP WBLETHGSGTQPERVKS WADNLWTHQNSSSLQTHPEGACPSKE PSADGSKWEL YTDGSRTOQDI EGPWTEPYTDGSQKKQDTEAARK QPGTGGFQIQQD TDGSWTQPS TDGSGTAPGTDCLLGEPE DGPL E EPEPGE L LTHLYSHLKCSP LCPVPRLIITPETPEPEAQPVGPPS RVEGSGGGSASSFDESEDDV VAGGGGASDPEDRSGSKPWKKL KTVLKYS PFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFQCQ EQRSLEQLMKDPLRPFV PAYYGMVLQDGQTFNQMEDLLADFE GP SIMDCKMGSRTYLEEELVKARERPRPRKDMYEMVAVDPGAPT EEHAQGAVTKPRYMQWRRTMSSTSLGFRIEG I KKADGTCNTNF KKTQALEQVTKVLEDFVDGDHVLQKYVACLEELREALEISPFF KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTL SHRLP WAEGNREDGYLWGLDNMICLLQGLAQS |
| 6325 | 165 | 944 | GLRDPFRKRRLKPOVKMSNYVNDMWPGSPQEKDPSSTSRSGGS SRLSSRSRSRSFSRSSRSRSHRVSSRFSSRSRSRSRSRRRHQ RKYRRYSRSYSRSRSRSRRYRERRYGFTRYYRSPSRYSRS RSRSRSRGRSYCGRAYAIARGQRYYGFRTVYPPEHSRWRDRSR TRSRSTPFR LSEKDRMELLEIAKTNAAKALGTTNIDL PASLRT VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI |
| 6326 | 238 | 680 | GEPSPATQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTTISFT VQTTLQPPGGLPAAPVSGRM AFEPVGRDLARRMVPRAGKRTQTL GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA |

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|------------|--|--|--|
| | | | QAWGGVGQRASSGVP |
| 6327 | 1 | 1337 | SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQKKKKKEEK GAEPTGS AVSAAQCQGPTRREL PESGIQLGTPREKVPAGRSKAE LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR LPEYPQVDDLLRLRLVKPERQVPTRKDYGSKVSLFSLPQYS RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR ALQQVIQDYTTTPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI SRFAYQKISNGDVILVYGCSLSVSRILQEAWTEGRRFRVVVVS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV GGEKV |
| 6328 | 1030 | 276 | HASAEVTTAAARGLGAMEEEMHTDAKTRAENGTSPPRGPGCSL RHFACQNLRLSRPDGSAFLOGDTSVLAVGYGPAEVKVSKEIFN KATLEVILRPKIGLPVGAESRERLIRNTCEAVVLGTLHPRTSI TVVLQVVS DAGSLLACCLNAAACMALVDAGVPMRALFCGVACALD SDGTLVLDPTSKQKKEARAVLTFALDSVERKLLMSSTKGLYSDT ELQQCLAAQAASQHVFRFYRESLQRRYSKS |
| 6329 | 3 | 2016 | SSEVAAGGGTRSAEAGSGEVVTVSATGAANGLNNGAGGTSATT SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENS LRTRNL RGDIERKSLAINEBFVSIFKEVKEELESIEDVQAMSNCCQDMT SRLQAAKEQTQDLIVKTTKQSESKLEIRAQVADAFLSKFQLT SDEMSLLRGTRREGPITEDFFKALGRVKQIHNDVKVLLRTNQQT GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA MEALQDRPVLKYTLDEFGTARRSTVVRGFDALTRGGPGGTPR PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALKHVTQGV ENIQEVVGHITGVCRPLKVRIEQVIVAEPGAVALLYKISNLLKF YHHTISGIVGNSATALLTIEEMHLLSKKIFFNLSLSHASKLMD KVELPPFDLGPSSALNQTMLLREVLASHDSSVVLDPARQADFV QVLSCLVDPLQMCCTVSASNLGTADMATFMVNSLYMMKTTLALF EPTDRRLMLQFQIRAHLDTLINQASYVLTRVGLSYIYNTVQQ HKPEQGS LANMPNLDVSLKAAVMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAMVNPINEYKDPENILHR SPQQVQTLLS |
| 6330 | 1151 | 333 | FFYYTTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQOPL PVHQPHSLVSEGFTVKAMMKNVVRGPPAAGAFKERPTKPTAFR KFYERGDFFIALEHDSKGNKIAWKVEIEKLDYHHYLPFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLQQLIPIKNALNLRN RQVICVTLLKVLQHLVVSABMVGKALVPYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN |
| 6331 | 3 | 495 | QQQQRVTRGRRCASATPLEGCVDLSPYRTHAALLKVAQMVTL LIAFICVRSSLWNTYSAYSIFYEVVTTICDLIMILAFYLVHLFRFY RVLTICISWPLSELHLYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAAV |
| 6332 | 1 | 878 | VTESNKFDELVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTDDLIQLTAMCWMREFIQLAGRVMLEPY SSGILTAVLPCLAYDDRKSKI EVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDALPKQEGTASGEWTPSLHLTSCRGPPEPD VIGVALGPHLSNQDYFMVYVTHITVAATQRSGSSGSPFFCRQDTG KLSTMATHSQLVKGTGTGLEPRQAVSSSH |
| 6333 | 3 | 1467 | TRTPSEAEAGGES PQSCVSAHSDWTAGKPVSLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGHMPMGQRANMPVPHGMMFPQMMFPMGPP MGQMPGMMSSVPMGMMSHMSQASMQPALPPGVNSMDVAAGTAS |

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|------------|--|--|--|
| | | | PALRKVYDQMPEPRYVVSMSGSCANGGGYHYHSYSVVRGCDRIVP VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR |
| 6342 | 2 | 1191 | DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI KPLEBVKILDLTRVLGAPFATMNLGDLGAEVIKVERPGAGDDTR TWGPPFVGTESTYYSVNRNKKSIIVNIKDPKGVKIKELAAVC DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS QRAGYDAVASAVSGLMHTGPEVACLISHIAANYLIGQKEAKRWG TAHGSIVPYQAFKTKDGYIVVGAGNNQFATVCKILDLPELIDN SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG PINNMKNVFAEPQVLHNGLVMEHEHPTVGKISVPGPAVRYSKFK MSEARPPFLLGQHTTHILKEVLRYYDDRAIGELLSAGVVDQHEH T |
| 6343 | 2 | 936 | GTAMVSDDELNLLVIVVDANFIWGWKQALKESQFTLSKCIDAV MVLGNSHLFMNRNKLAVIASHIQESRFLYPGKNGRLGDFGDP GNPPEFNPSSGSKDGYELTSA NEVIVEEIKDLMTKSDIKGQHT ETLLAGSLAKALCYIHRMNEKVDNQEMKSRILVIAAEDSALQ YMFNMNVI PAAQKQNILIDACVLDSDSLQACDITGGLYLKV PQMPSSLQYLLWVFLPDQDQRSQILPPPVHVDYRAACFCHRL IBIGYVCSVCLSI FCFNSP I CTTCTAFKISLPPVLKAKKKKLK VSA |
| 6344 | 2508 | 147 | TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR QSLGPPVPVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDS QTMPEVEDKSDPPEGSEEAEPMDTPEDDQLPPCPEDIAKEKRT PAPEPECEASELPAKRLRSSEEPTEKEPPGQLQVKAQPAQMT VPKQTQTPDLLPEALEAQVLPFRQPRVLQVQAQVQSQTQPRIPS TDTQVQPKLQKQAQTQTSPEHLVLQKQVQVQLQQAEPQKQVQ POVQQAHSQGPQVQLOQAEPKQVQVQVQQAHSQPPRQVQ LQLQKQVQTOTYPQVHTQAQPSVQVQPEHPPAQVSVQPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPDVAEAGGMEKTLPEP VGTQVSMEEIQNESACGLDVGEENRAREMPGVWAGGSLKVTI LQSSDSRAFTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQBEFQDHMSPEQHQQRLGEIQHMSQACLLSLLPVPR DVLTEDEEPPRRWCNTCQLYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCPEGDEEEEDDEDEEEIEVEEELCKQVRSRDIS REEWKGETYSNTAYGVDFLVPVMGYICRICHKIFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRCAINARNALALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT |
| 6345 | 2 | 3483 | PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEEMEIEQLQEKV HELEKQNDTLKNRLISAKQQLQTGGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKQDADVAETPHPMFTKYGNSLLEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSE RIEELQDRINDLEKERELLKENYDKLYDSAFSAHHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERRDQNEKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQDYEKVEQYVHLLDIRA ARIHKLKLAQLKDIAVGTQKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHNKVTFSSEVLQASGDKEPVTFTCTYAFYDFELQTTTPV VRGLHPEYNFTSQYLHVHNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHILEKSGRIFCTASLIGTKGDI PNFGTVEYWFR RVPMQDAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNLHITIRCCNHLQSRASHLOPHPYVYVYKFFDFA DHDTAIIPSSNDPQDDHMYFPVPMNMDLDRYLKSESLSFYVFD DSDTOENIYIGKVNVLISLAHDCISGIFELTDHQKHPAGTIH |

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|------------|--|--|--|
| | | | VILKNKFAYLPPSGSITTEDLGNFIRSEEPVQRLPPASSVST LVLPAPRPKPRQLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN TEKMQQKDDVSLSEGQLAEQSLASSEDETEITLEDLEPEVEED MSASDSDDCIIPGPISKNIKQPSKIRIEIILSLNDSQVTMDD TIQRLFVECRFYSLPABETPVSLPKPKSGQWVYNYNSNVIYVDK ENNAKARDILKAILQKQEMPNSRLRFTTVSDPPEDEQDLECEDI GVAHVLDLDMFQEGRDLEQNIDVDFARADGEGIGKLRVTVEAL HALQSVYKQYRDDLEA |
| 6346 | 2921 | 533 | QDRRLRLRLQKTCQPTSTMSGSHTPACGPFSAITPSIWPQEI AKYTQKEESAEPFYYDFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLFTHNHDVGLTDWDKIAVSLRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSLSYREIVKNSNDETIAAK QIEKDLLRTMPSNACFASMGSGIVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEDAFWMMSAIEDLLPASFYSTTLGLGVQ TDQVLRHLIVQYLPRLDKLLQEHDIELSITLHWFLTAFASVV DIKLLLRIDWDLFFYEGSRVLFQTLGMLHLKEELIQSENSASI FNTLSDIPSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL IADQQLLGAGTLTNLSQVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVDLREAILRVARHFQCTDPKNCSSVSRQLPGLL PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFFPAKFVEVLDERSEKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWSPFLRSPGWVQIKC ELRVLCFAFSLSQDWELPAKREAQQPLKEGVDRMLVKHHLFSW DVDG |
| 6347 | 2921 | 533 | QDRRLRLRLQKTCQPTSTMSGSHTPACGPFSAITPSIWPQEI AKYTQKEESAEPFYYDFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLFTHNHDVGLTDWDKIAVSLRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSLSYREIVKNSNDETIAAK QIEKDLLRTMPSNACFASMGSGIVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEDAFWMMSAIEDLLPASFYSTTLGLGVQ TDQVLRHLIVQYLPRLDKLLQEHDIELSITLHWFLTAFASVV DIKLLLRIDWDLFFYEGSRVLFQTLGMLHLKEELIQSENSASI FNTLSDIPSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL IADQQLLGAGTLTNLSQVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVDLREAILRVARHFQCTDPKNCSSVSRQLPGLL PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFFPAKFVEVLDERSEKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWSPFLRSPGWVQIKC ELRVLCFAFSLSQDWELPAKREAQQPLKEGVDRMLVKHHLFSW DVDG |
| 6348 | 3 | 3679 | AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNLQFKKE KLAEQLQAEELRQYKVLVHSQRELTQLREKLREGRDASRSIN EHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEAEKVQKSSSPBEMQKAEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRLPQLA EKKQQRNLKEKCFLTQLACFLANQKQNKYKYECKDLIKFMLRN ERQFKEEKLAEQLQAEELRQYKVLVHSQRELTQLREKLREGR DASRSINEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEAEKVQKSSAPREMPKAEKEVPEDSLE |

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|------------------|---|--|---|
| | | | ECAITCSNSHGYPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLDSDLCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRICKDQEEEDQGPPCPRLSRELLEVVPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEKXHVGFSLDVGEIE KKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSQCPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPCPRLSGELDEKEPEVLQESLDRCYST TPSGCLELTDSQCPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRICKDQEEEDQGPPCPRLSREL LEVVPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDCYSTPSMYFELPDSFQHYRSVY SFEEHHISFALYVDNRFFTLTSLHLVFGMGVIFPQ |
| 6349 | 3 | 3679 | AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNELQFKKE KLAELQKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDEEDVQVEVAEKVQKSSSPREMKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESSHDECQDALN ILPVPGBTSSATNVSMVVSAGPLSGEKAANILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYECKDLIKFMLRN ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSNLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGYPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLDSDLCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRICKDQEEEDQGPPCPRLSRELLEVVPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKXHVGFSLDVGEIE KKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSQCPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPCPRLSGELDEKEPEVLQESLDRCYST TPSGCLELTDSQCPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRICKDQEEEDQGPPCPRLSREL LEVVPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDCYSTPSMYFELPDSFQHYRSVY SFEEHHISFALYVDNRFFTLTSLHLVFGMGVIFPQ |
| 6350 | 3 | 3679 | AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNELQFKKE KLAELQKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDEEDVQVEVAEKVQKSSSPREMKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESSHDECQDALN ILPVPGBTSSATNVSMVVSAGPLSGEKAANILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYECKDLIKFMLRN ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSNLNEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE |

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|------------|--|--|---|
| | | | ECAITCSNSHGPYDSNQPHRKTITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLBLEPDLGQPYSSAVYSLEE QYLGALDLDVRIKKDQEEEDQGPCCPRLSRELLVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGGKRRGRRSKERRRRGRKEGEEDQNPPCPRLSRELLDEK PEVLQDSLDRCYSTPSGCLELTDSQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCS TPSGCLELTDSQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEYLGALDLDVRIKKDQEEEDQGPCCPRLSRELL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKKGKGGKRRGRRSKERRRRGRKEGEEDQNPPC RLNSMLMEVEEPEVLQDSLDCYSTPSMYFELPDSPQHYRSVFI SFEEHISFALYVDNRFFTLTSLHLVFMQGVIFPQ |
| 6351 | 1291 | 319 | REARRRTERSQGLRMLVVEVANGRSVLVGAFAVQALRERLGVGG RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP DSRHHSALTSFQRQEESEFQESALAAARETRRQELLEKITE GQAACKQKLEQASGASSQAEAGSSQAKEDETSQGQASGEQEEA GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD PLRFHAHYIAQCWAPEDTIPLQDLVAGRLGTSVRKTLTLLCSSPQ PDGKVVYTSQWASLQ |
| 6352 | 235 | 923 | WSEWLSPCAACKGLSMLRITMKTRAISSLAADATEFVQGRSAP AMARSLVHDITVFCYLSVYQVKISPTPQLGAASSAEGHVGQAPG LMGNMNPEGGVNHENGMDGGMIEGGGGNQEPQQPQPPEE PAQAAMEGPPENMQPRTTRTKFTLLQVEELESVFRHTQYPDVP TRRELAENLGVTEKVRVWFKNKRARCRRHQRELMLANELRADP DDCVYIVVD |
| 6353 | 65 | 672 | RFAGAGATPEARARPPDVQAAEEEEKMDLPDSASRVFCGRILSM VNTDDVNAIILAQNMLDRFEKTNEMLLNPNLSSARLQQMSE FLHETRTLVEKMRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS FLEEEDEDPIPPSTTTTIIATSEQSTGSCDTSPTVSPSLSPGFE DLSHVQPGSPAINGRSQTDDEEMTGE |
| 6354 | 965 | 510 | PSLRPMETRDCLPFGGAFSAILPMGAIDVSDLRPVPDNQEVFC HPVTDQSLIVELLEQAHVRGEAAARYHFEDVGGVQGARAVHVE SVQPLSLENLALRGRCQEAWLVSQKQQAIAKENQVAKDVTLHQA LLRLPQYQTDLLLTFFNQPP |
| 6355 | 158 | 1662 | RGSSAARFGSGLRGAMIRRVLPHGMRGLLTRRPGTRRGGFSLD WDGKVEIKKKIKSILPGRSCDLLQDTSHPBHSDDVIVGGGV LGLSVAYWLKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ QFSLPENIQLSLFSASFIRNINEYLAVVDAPPLDLRFNPSSGYLL LASEKDAAMESNVKVRQEGAKVSLMSPDQLRNKFPWINTGVS ALASYGMEDEGWDPWCLLQGLRRKQVSLGVLFQCGEVTRFVSS SQRLMTTDDKAVVLKRIHEVHVKMDRSLEYQPVBCAIVINAAGA WSAQIAALAGVGEPPGTQGTCLPVEPRKRYVYVWHCPQGPGL ETPLVADTSAGYFRREGLSNYLGGRSPTQEEEDPANLEVDHD FFQDKVWPHLALRVPAFETLKVSAGWAGYDYNTFDQNGVVGPH PLVVNMYFATGFSGHGLQAPGIGRAVEMVLKGRFQTDLSPP LFTRFYLGEKIQENNI |
| 6356 | 354 | 633 | TGLTSSCLPLQVMMTKRTKDMGKFSSVTSTIDEBEEEEIEAREV ADSYAQNQAKVIEKQLERKGMKRRRLQELABLEAKKAKMKGTLID NQFK |

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|------------|--|--|---|
| 6357 | 2 | 915 | GLLRNMLLVRLRNQTSISQWVPVCSRLIPVSPQTQGGDRALS RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP QPVEEKVGAFTKIIRAMGFTGPKYSKWKIKIAALRMYTSCVVK TDFEEFFLLRCQMPDTFNSWFLITLLHVWMLVRMKQEGRSQKYM CRIIVHFMWEDVQQRGRVMGVNPPYILKKNMILMTNHFYAILGY DEGILSDDHGLAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL |
| 6358 | 2009 | 1040 | ASDALHSLAPVLRLLSRSAARPATMTEQAISFAKDFLAGGIAA AISKTAAPVIERVKLLQVQHASKQIAADKQYKGIVDCIVRIPK EQGVLSFWRGNLNVIRYFPTQALNFAFKDKYKQIFLGGVDKHT QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADVGSQGT REFRGLGDCLVKITKSDGIRGLYQGFSSVSQGI IYRAAYFGVY DTAKGMLPDPKNTHTIVVSWMIAQTVTAVAGVVSYPFDTVRRMM MQSGRKADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMG GAFVLVLYDELKKVI |
| 6359 | 98 | 1086 | VCRQEEEMKEDCLPSSHVPISDSKSIQKSELGLLKYNCYHE GKSFQLRHREEGTLIIIEGLLNIAWGLRRPRLQMQDDREQVHL PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDS GPLEEAEEAPQLMRTKSDASCMQRPRPKCRAPGEAQRIIRHRFS INGHFYNHKTSTVTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV EDGPSEFALYIVHESGERTKLKDCYPLISRIILHGPCCKIARIF LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEREI I KLT MKFQALRLTLMQLRLEQVEAK |
| 6360 | 1 | 345 | GTRGAVPSTLEEVLPPRSRVRFWIHSGTMSKVSFKITLTSDP RLPYKVLSPVSTPFTAVLKFAAEEFKVPAATSIIITNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVGS |
| 6361 | 615 | 158 | RPGLGQLQHCALAPQAGNRRCRFHGRHLHALTRSTHRGKPMIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHFIQGRCTFTPDGETLHIQAGDALMLPA NSTGIWDIQUETVRKTYLIL |
| 6362 | 350 | 1576 | TTMDGSHSAAKLQQLPPTSSSSAVSEASFYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWLGLFLMLLG ELGVFASAYAFAPLSLIVPLSAVSVIASAIIIGIIFIKEWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLYMLVEIILFCLLLYFYKEKNANNIVVILLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNKKPIPFEPYISMDAMPGMOMMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE |
| 6363 | 21 | 1201 | RRTRLGSSFPRRRDSSAMESYDVIANQPVVINDGSGVIAKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVLVD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRLRLYLKREGY DFHSSSEFEIVKAIKERACYLSINPKQDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLGGSTLFGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVWSKKEYBEDGARS IHRKTF |
| 6364 | 21 | 1201 | RRTRLGSSFPRRRDSSAMESYDVIANQPVVINDGSGVIAKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVLVD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRLRLYLKREGY DFHSSSEFEIVKAIKERACYLSINPKQDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR |

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|------------|--|--|---|
| 6365 | 234 | 1989 | <p>RTLFSNIVLSGGSTLFRGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIRHRTF</p> <p>KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM ASMGTLAFDEYGRPFLLIKDQDRKSRMLGLEALKSHIMAAKAVA NTMRTSLGPNGLDKMMVDKGDVTVTNDGATILSMDVDHQIAK LMVELSKSQDDEIGDGTGVVVLGALLLEAEQLLDRIHPIRI ADGYEQAAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV VNSCHRQMAEIAVNAVLTVADMERRDVPFELIKVEGKVGGRLED TKLIGKVIVDKDFSHQMPKPKVEDAKIALITCFEPKPKTKHK LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDEE ANHLLQNNLPAVRWVGPEIEELIAIATGGRIVPRFSELTAEKL GFAGLVQVEISFGTTKDKMLVIEQCKNSRAVTIFIRGKNKMIIEE AKRSLHDALCVIRNLIRDNRVVYGGGAEEISCALAVSQEADKCP TLEQYAMRAFADALEVIMALSSENSGMNPIQTMTEVRARQVKEM NPALGIDCLHKGNTDMKQHVITLIGKKQISLATQVMVRMLK IDDIRKPGSESE</p> |
| 6366 | 257 | 1898 | <p>GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDILV IGKFNVLIVQKVLHKDKSLENLGLMRNGLLFRMTLLTSGGAG MLYVRWRIMGTGPPAFTEVDNPFASFADSMVRAVNYNYYSINA WLLCPWWLCFDWSMGCIPLIKISISDWRVIALAALWFLIGLIC QALCESDEGHKRRILTLGLGFLVIPFLPASNLFRVGVFVAERVL YLPSVGVCVLLTPFGGALSHTKKKLLIAAVVLGILFINTLRV LRSGEWRSEELFRSALSVCPLNAKVHYNIGKNLADKGNQTAARIYYREAVRLNPKYVHAMNNGNILKERNELQEAEEELSLAVQIQ PDFAAAMWNLGIVQNSLKRFEAAEQSYRTAIKRRKYPDCYYNL GRLYADLNRHVDALNAWRNATVLPKEHSLAWNMIILLDNTGNL AQAEAVGREALELIPNDHSLMFLANVLGKSQKYKESALFLKA IKANPNAASYHGNLAVLYHRWGLDLAKKHYEISLQLDPTASGT KENYGLLRKLEMLMQKAV</p> |
| 6367 | 287 | 1934 | <p>SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSGVKTWKVQNIIEDEYKNPRRNLMLRE KLCESKESHHCGESFNQIADDMNLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFIHSCIQRRHVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCSTDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSGEKPHECKECGVFKYFSSLRHERTHTGEKPH ECKQCGKAFRYFSSLIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHINR</p> |
| 6368 | 1 | 327 | <p>RPVPAKLNPRSWPRTAGALPLRPPPLTMVAFHDEVEIEDFQYDE DSETYFYPCPGDNFSITKEDLENGEDVATCPSCSLIKVIYDK DQFVCGETVPAPSANKELVKC</p> |
| 6369 | 1 | 1745 | <p>AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSGVKTWKVQNIIEDEYKNPRRNLMLREKLCESKESHHC ESFNQIADDMNLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFIHSCIQRRHVMHSGDGPYKCKFCKGAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG EKPKHECKECGVFKYFSSLRHERTHTGEKPKHECKQCGKAFRYF</p> |

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|------------|--|--|---|
| | | | SSLHIHERHTHTGDKPYECKVCGKAFTCSSSIYHERHTHTGEKPY ECKHCGKAFISNYIRYHERHTHTGEKPYQCKQCGKAFIRASSCRE HERHTHTINR |
| 6370 | 1711 | 329 | FVLSBQRLRTERTWPRSPGLGRGAAAGARTAGAGLLRLLLGCG ALVGGRLRPVTMTTPANAQNASKTWELSLYELHRTPEAIMDGTG IAVSPRSLHSELCPICLDMLKNTMTTKCLHRFCSDCIVTALR SGNKECPTCRKKLVSKRSLRPPNFDALISKIYPSREYEYAHQD RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGAPKPRPGGGAGG SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTGPPSPPGAPS PPEPGGEIELVFRPHPLLVKEGEYQTRYVKTGNATVDHLISKY LALRIALERRQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE KFWKVSRLPLELCYAPT KDPK |
| 6371 | 3 | 288 | GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC LHNNNFENALCRKESKEYLECRMERKMLQEPLEKLGFGDLTSG KSEAKK |
| 6372 | 2141 | 625 | RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCMKH LPKVPEKKLKLVMADKELYRACAVEVRRQIQWQDQALFGDEVSP LLKQYILEKESALFSTELSVLHNFSPSPKTRRQGEVVQRLTRM VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRALLMSLHDLVVG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKQGE QVLGLDSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLRLRLALGQGAWMDIDSQVFEKPKMEVELITRFLPMLMSFLVD DYTFNVQDKLPAAEKAPVSYPTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALLRLLPGLVETPGDLAFGDI FLHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL |
| 6373 | 67 | 711 | PSRAARASPARLPAMVSWIISRLVVLIFGLTYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIFLCWPPFYELKIAFVA WLLSPYTKGSSLLYRKVFVHTLSSKEKEIDDCLVQAKORSYDAL VHFQKRGRLNVAATAAVMAASKGQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASASASSGTA |
| 6374 | 535 | 2105 | HKLFCSYISTSEFSPSTRHSCPTHTFCNYTSSTIFLSSTRDHS CPHTFCNYTSSTIFLSSTRDHSCTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVLEDTVLFPEGGGQPDRTGTIN DISVLRVTRRGEQADHFTQTPLDGSGVLRVVDWERRFDHMQQH SQQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMATAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGGKNRTNLI FL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNLNLRLDLAVHIAHSLRNSPDWGGVILHRKEGDESEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQKATKMSRRMEAQALLQDYISTQSAKE |
| 6375 | 1 | 1535 | AIMAAATRPVRLPEAGCEGRERCWNPSSRSRSHSGEGGLAAWSRT CPGRFRPPGQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIATILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAFAWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAPILLALAGALALRNWGENYDRQAFSRTCAGGLRCLLSDR RVLLLTIGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFTSTP QGESPVESPIAFLLIELACGLYFSPMSFLRRKVI PETEQAGVLN |

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|------------|--|--|---|
| | | | WFRVPLHSLACLGLLVLDSDRKTGTRNMFSCSAVMVMALLAV VGLFTVVRHDAELRVPSPTTEPYAPEL |
| 6376 | 380 | 1437 | ISSTDIIDHYRFSPLVNSKMPKESWSGRKTNRAAVHKSQEGRQ QDLLIAALGMKLGSPKSSVTIWIQPLKLFAYSQLTSLVRRATLKE NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCAKDC GLNVHKQCSKMVPNDCKPDLKHVKVYSCDLTTLVKAHTTKRPM VVDMCIREIESRGLNSEGLYRVSGFSDLTIEDVKMAFDRDGEKAD ISVNMVEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD PDEQLETLHEALKLLPPAHCELTLYRLMAHLKRVTLHEKENLMNA ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEIDILF |
| 6377 | 2311 | 1845 | SRIRRRSSRRRPREPPGPPSRRRRRRRRPDPTMPSEKTFKQRTTFE QRVEDVRLIREQHTPKIPIVIERYKGBKQLPVLDKTKFLVPDHFV NMSBELIKIIRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE KDEDGFLVMVYASQETFGMKLSV |
| 6378 | 686 | 191 | GAGPWEAFPDGIGRRRRRLRPQYKRPFGVGGGDSGRRNMAVA DLALIPDVIDSDGVFKYVLIRVHSAPRSGAPAESKEIVRGYK WAEYHADIYDKVSGDMQKQGCDCCELGGRIRISHSQSQDKKHVYG YSMAVGPAQHAISTEKIKAKYPDYEVTWANDGY |
| 6379 | 35 | 378 | BRAGSPSPSRAALRRCAPQRSQAPRPWPDRACRRSPQGSQGRAY LFNSVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA FESSQKYKEGKYIIELAHMIKDNWD |
| 6380 | 1414 | 462 | PAVQQRGAGPPTGRGSGNMARFALTVVRHGETRNFKEKIIQQGQ GVDEPLSBTGFQQAAGIPLNNVKFTHAFSSDLMRKTQTMHGI LERSKFCKDMTKYDSRLRERKYGVVEGKALSELRAMAKAAREE CPVFTPPGGETLDQVKMRGIDPFEFQLCQLILKEADQKEQFSQGS PSNCLETSLAEIIFPLGKNHSSKVNDSGIPGLAASVLVVSHGAY MRSFLDYFLTDLKCSLPATLSRSELMSVTPTNGMSLFIINFEFG REVKPTVQCICMNLQDHLNGLTENSGLNLPSKSNHFEPLKGVPLALFTSLIC |
| 6381 | 1668 | 218 | AVVRAQGSRGFSGAGWRPQAAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTLCDQIQHI EWSADSLFILC AMYKRGVLQVWSLEQPEWHCKIDBGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYSIKYPKACLQGITTFRDGRYMALAE RDKDYVSIIVCSWDQLLRHFDITDQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAVSPSSQFLAVG SYDGKVRILNHVTKMITEFGHPAAINDPKIVVYKBAEKSPQLG LGCLSPFPFPRAGAPLPSSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWVVDIQKLRLFAVLEQL SPVRAFQWDPQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCLWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT |
| 6382 | 2 | 1062 | FEEDEDRNLCIAYPLKGDHGIIVDVSNDCEPKSKLRLWTTNK KHVLETEKTPKDWRVQRHKEEMKSKHLEEFEWLKKSEVLYY TVEKKNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKIFIL LENLTSRYEVPCVLDLKMGTQRHGGDDASEEKAANQIRKQQSTS AVIGVRVCMQVYQAGSGQLMFNMKYHGRKLSVQGFKEALQFF HNGRYLRRELLGPVLKLTTELKAVLERQESYRFYSSSLLVYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E |
| 6383 | 3159 | 1061 | SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTAPAAPCRSPSPGGAPASFPGRAPRSLASQK AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAK PPPAPQPPPPPPAPHPPQHPQHPQHPQNAHQHKGHRGGGGGGKSSSSSSASAAAAAASSSSASCRRRLGRALNFLFYLAIVAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGGQLGVBEQVQVSLQA TGTFTFESILRSSQHKQDLTEKAVKQGESEVSRISIEVLQKLQNEI |

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|------------|--|--|---|
| | | | LKDLSDGIHVVKDARERDFTSLENTVEERLTETLTKSINDNIAIF TEVQKRSQKEINDMKAKVASLERSEGNKQDLKALKEAVKEIQTS AKSREWDMEALRSTLQTMESDIYTEVRELVSLLKQEQQAFKEAAD TERLALQALTEKLLRSEESVSRLEPPEIRLEEELRQLKSDSHGP KEDGGFRHSEAFALQKQSQGLDSRLQHVDEGVLSMQVASARQT ESLESLLSKSQEHEQRLAALQGRLEGLSGSEADQDGLASTVRSI GETQLVLYGDVEELKRSVGEPLPSTVESLQKQVEQVHTLLSQDQA QAARLPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAI SVKIETNENNLESAGLLDLDLRLDFVKEIKHEKV |
| 6384 | 738 | 1904 | IWEVVPVCLTHLLHQQANQPLPPFPSSSINEEDADEANRAIGKEK AAPDSGKKPKTKKQKQDPNEPQKPVSAIALFFRDTQAAIKQG NPNATFGEVSQIVASMWDSLGEQKQVYKRKTEAAKKEYLKALA AYRASLVSKAAESAQAQTIRSVQQTLASTNLTSLLNTPLSQ HGTVSASPQTQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP SNIGAPLISSMGTMTVGSAPSTQVSPSVQTQQHMQQLQQQQQQ QQQMQQMQQQQLQHQHMQQIQQQMQQQHQQHMQHQQHQQHQQH LQQQINQQQLQQQLQQLQQLQHQHMQHQSQSPRQHSVPASQI TSPIPAIGSPQFASQQHQSQIQSQQTQTQVLSQVSI |
| 6385 | 2 | 1584 | PRVRAADVAAGAQAQVVSAGMAKSNGENGPAPAGESLSGTRES LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG ALEEVPLEVLQRRESKWLDMNNWDKWMKXKHKIRLRQCKGIP PSLRGRAWQYLSGGKVKLQONPGKFDELDMSPGDPKWLVDIERD LHRQFPFHEMFVSRGGHQDQLFRVLKAYTLRPEEGYQQAQAP IAAVLLMHMPAEQAFWCLVQICEKYLPGYVSEKLEAIQLDGEIL FSLQKVPVPAHKLRSRQIDPLLYMTWFMCAFRTLPWSSVL RVWDMFFCEGVKIIIFRVGLVLLKHALGSPEKVKACQGGYETIER LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG ELQCRSPFRLHGAAILDAEPGPRPALQPSFIRLPDAPLPGS KAKPKPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAGDACP PQHVPKDSAPKDSAPQDLAPQVSAHHSQESLTSQESSEDITL |
| 6386 | 819 | 195 | TVCGSFYLGIMQASRLKRELHMLATEPPPGITCWQDKDQMDL RAQILGGANTPYEKGVPKLEVIIPERYPFEPQIRFLTPYIYHN IDSAGRICLDVLKLPKGAWRPSLNIAITVLTISQLLMSEPNDD PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKKADEEMLDNL PEAGDSRVHNSQKRAKASQLVGIEKKFHPDV |
| 6387 | 1 | 662 | PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAEVLKR KQELAETLANLERQIYAFEGSYLEDQMYGNIIRGWDRYLTNQK NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSDFHNQENEPSQEDPEDLDGVSQGVKPKKAAS STSSGSHSHSHKKRKNKNRHSPPSGMFDYDFEIDLKLNKKPRADY |
| 6388 | 1 | 662 | PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAEVLKR KQELAETLANLERQIYAFEGSYLEDQMYGNIIRGWDRYLTNQK NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSDFHNQENEPSQEDPEDLDGVSQGVKPKKAAS STSSGSHSHSHKKRKNKNRHSPPSGMFDYDFEIDLKLNKKPRADY |
| 6389 | 1074 | 497 | AEPGDERMAGHRLVLVLGDLHTPHRCNSLPKAFKLLVPGKIQHI LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNPQKVVTVG QFKIGLIHGHQVPIPWGDMAALLQRFVDVILISGHTKFAEF EHENKFYINPGSATGAYNALETNIIPSVFLMDIQASTVVTVVYQ LIGDDVKVERIEYKKP |
| 6390 | 158 | 535 | GEERKEGRAPGKAFAPERNPAKMEKEETTRELLEPNWQSGSHG LTIAGRDDGVFVQEVTONSPAARTGVVKEGDQIVGATIFYDNLQ SGEVTQLLNTMGHHTVGLKLRKGRDRFPFSLGQTWDP |
| 6391 | 5386 | 2897 | VRWNSKTECYLSIQTQENFPANLNLVNCIVISSLVTTORLKA MSLLGSRNQLARAVLNPNPMDFCCKDLLTTTSERIIAYLRDFNE DQKKAIETAYAMVKHSPSAKICLIHGPPGTGSKTIVGLLYRL |

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|------------|--|--|---|
| | | | LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF KEKCKDKKNPLGNCGDINLVRGPEKSINSEVLKFSLDQVNH MKKELPSHVQAMHKRKEFLDYQLDELRSQRALCRGGREIQREL DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS TSGLLLESFAFRGQGGVFPFSCVIVDEAGQSCIEITLPLIHRCN KLILVGDPKQLPPTVISMKAQYGYDQSMARFCRLLEENVEHN MISRLPILQLTVQYRMHPDICLFPSSNYVYNNRNLKTNRQTEAIR SSDWPFQPYLVFDVGDGSERRDNDYINVQEIKLVMETIKLIKID KRKDVSRNIGIITHYKAQKTMQKDLDFDRKGPAEVDTVDVA PQGRQKDCVIVTCVRANSIQSGSIGFLASLQRLNVTITRAKYSLF ILGHLRLTMENQHWNLQIDAQKRGAIKTCCKNYRHDAVKILK LKPVLQSRSLTHPPTIAPEGSRPQGGPSSKLDGSPAKTSVAASL YHTPSDSKEITLTVTSKDPERPFPVHDQLQDPRLLKRMGIEVKG IFLWDPQPSPPQHPGATPPTGEPFPVVDLQSHVQPPAAVVA LSSHKPPVRGEPFAASPEASTCQSKCDDPEEELCHRREARAFSE GEQEKCGSETHHTRNSRWKRTLEQEDSSSKRKL |
| 6392 | 972 | 186 | GRTGVDLASSMAHRLQIRLLTWDVKTLLRLRHLGEAYATKAR AHGLEVEPSALEQGFQRAYRAQSHSPNYGLSHGLTSRQWLDV VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPTQWVLDGAEDTLR ECRTRGLRLAVISNFDRLLEGILGGLGREHDFVLTSEAAGWP KPDPRIFQELRLAHMPEVVAHVGDNYLQDYQGPRAVGMHSFL VVGQALDPVVRDSVPKEHILPSLAHLPLALDCLEGSTPGL |
| 6393 | 2017 | 730 | TGGSMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGT LLIEEDKYNISPLPKYFLAEGIVNGHTLLVASAKEDPANILQ ELPAPLLDDKCKKEFDEVDVNHKTPESNIKMKIAWRYQLLPKME IGPVSSSRFGHYDASKRMPQELIEASNWHGFFLPEKISSSTLKV EPCSLTPGYTKLLQFIQNIIEEGFDGSGNPQKKQRNLRIGIQN LGSPLWDDICCAENGCSHSLTKFLYVLRGLLRTSLSACIITM PTHLIQNKAIARVTTLSDDVVGLSEFIGSERETNPLYKDYHGL IHIRQIPRLNLI CDESVDKDLAFKLKRLFTIERLHLPDDLSD TVSRSSKMDLAESAKRLPGCGMMAGGKKHLDF |
| 6394 | 1418 | 511 | GAAAGGEGARRRPAAMATVMAATAAERAVLEEFRWLLHDEVHA VLKQLQDILKEASLRLPLPGSGTEGPAKQENFILGSCGTDQVK VLTQGDALSQADVNLKMPRNQLLHFAFREDKQWKLQIQDAR NHVSQAIYLLTSRDQSYQKTGAELVKLMDAVMLQLTRARNRLT TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCITYQ LHALQPNSTKNFRPAGGAVLHSPGAMFEGSQRLVSHVHKVEEC VIPWLDALVYFTVSLQQLKDKISVFSSYNSYRPF |
| 6395 | 13 | 658 | PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ DLLEEASSRDMQMGPLFLRMQLVPSIEERETPLTREDRPAEQE PPWSLGCTGLKAAMQIQRVVIVPPTLGHNRNPWVARDSGE |
| 6396 | 1 | 1221 | ANILSSPSKRGQKGTGLIGYSPEGTPLYNFMGDAFQHSQSIPRF IKESLKQILEESDSRQIFYFLCLNLFTFVELFYGVLTNSGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGFLIVIAFFVFMEVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHS SHHMHGSHDHGHGSH GSAGGMNANMRGVFLHVLADTLGSGIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSVDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGSLTGFDHVLAMTKQMES MKYCKDGTIYM |
| 6397 | 391 | 122 | GAGGVGRFEAIRAPARMIEVVCNDRLGKRVKVCNTDDTIGDLK KLIAAQGTGRWNKIVLKKWYTIKDHVSLGDYIEHDGMNLELYY |

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|------------|--|--|--|
| | | | Q |
| 6398 | 353 | 1306 | HKQMGLINRCKKILLPTTVPPATMRIWLGLLPLFLLLSGLQ RPTGSEVAIKIDFDAPGSEDDQYQGCSKQVMEKLTQGDYFTK DIEAQKNYFRMWQKAHLAWLNQGVLPQNMTHAVAILFYTLN SNVHSDFTRAMASVARTPQQYERSPHFKYLHYLTSAIQLLRKD SIMENGTLCYEVHYRTKDVHFNAVYTGATIRFGQFLSTSLLKEEA QEPGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH PRGDWLQLRSTGNLSTYNCLLKASSKKCIFDPIAIASLSFLTS VIIFSRSRV |
| 6399 | 75 | 1245 | PNLETYFGRRCEKDSMNFTPTHTPVCRRKRTVSVKRGVAVSGPTK RRGMADSLSTPLPSPEDRLAKLHPSKELEYQKMAECEAEN EDLLKKLELYKEACEGQHKLECDLQOREEELAEQKALSDMQVC LFQEREHVLRLYSENDRLRIRELEDDKKIQNLALVGTDAEVT YFCKEPPHKVTILQKTIQAVGECEQSESAFADPKISKRRPFR ERKSSEHYQORDIQTLLIQVEALQALGEQTKLSREQIEGLIED RRIHLEEIQVOHQNRQNKIKELTKNLHHTQELLYESTKDFLQLR SENNQKEKSWMLEKDNLMSKI KQYRVQCKKEDKIGKVLPMHE SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM |
| 6400 | 2520 | 1053 | KTMKCEVVYEVQSAILRHNCGYAMKTKGFFHNLMERKDFETWL DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLNLETLLKR DFLKLPLLELSFYLLKWLDPTLLTCLVSKQWNVISACTEVW QTACKNLGWQIDDSVQDALHKKVYLKAILRMKQLEDHEAFETS SLIGH SARVYALYYKDGLLCTGSDDL SAKLWDVSTGQCVYGIQT HTCAAVKFDEQKLVTSFDNTVACWEWSSGARTQHFRGHTGAVF SVDYNDEL DILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL SVSEDRSICLQPRLHPDGKIVCSSLGLYQWDFASYDILRVIK TPEIANLALLGPGDIFALLFDNRVLYIMDLRTESLISRWPPEY RKSKRGSSFLAGEASWNLGLDGHNDTGLVFATSMPDHSIHLVLW KEHG |
| 6401 | 109 | 766 | PGAAWSRPDLRGCTGPQPALRMLVLPSPCPQPLAFSSVETMEG PPRRTCRSPGPGSSSIGSPQASSPPRPNHYLLIDTQGVPTVL VDEESQREPGASGAPGQKKCYSCPVCRRVFEYMSYLQRHSITHS EVKPFECDCGKAPKRAHSHHSIHLAGGGRPHGCPCLPRRF RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP |
| 6402 | 1196 | 279 | TTSCQGGIRQSSAIPVASMFAATCLRNALLLPPEEQDPKQEN GAKNSNQLGGNTESSESSETCSSKSHDGDKFIAPPSSPLRKKQE LENLKCSILACSAYVALALGDNLMALNHADKLLQPKLSGSLKF LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII KRNQLLEPAVKTHSEVRKKPVFPVHP IQPIQMPAFTTVQRK |
| 6403 | 2 | 1690 | RGIHTSVLQGNLQNMYSHNVVIMNLLNLTQVQQRNLTNLQ RSVDDTSQAIQRIKNDQNLQCVFLQAKKDDWLKEKVQSLQTL AANNSALAKANNDTLEDMSQLNSFTGQMENITTISQANEQNLK DLQDLHKDAENRTAIFKNQLEERFQLFETDIVNIISNISTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGRDGSQGPFGPTGNKGQKGEKGEPPGPPAGERGP PAGPPGERGGKSGSGSQGPKSGRSGPGKPGPGQSGDPGPPGPP KKEGLPGPGPPGFGQLQGTVEPGVPGPRGLPGLPGVPGMPG KGPPGPPGPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTRREEQWIKKQMVGREH WIGLTDSEERENKWLDTGTSPTYKNWKAGQPDNNGHGHGPGEDC AGLIYAGQWDFQCEDVNNFICEKDRFTVLSAL |
| 6404 | 1012 | 222 | AAALAMAAAPAGLISVFSSSQELGAALQALVAQRAACCLAGARA |

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|------------|--|--|---|
| | | | RFALGLSGGSLVSMLELPAAPVAPAGPASLARWTLGFCDBRLV PFDHAESTYGLYRTHLLSRLPIESQVITINPELPVEEAABDYA KKLRQAFQGDSPVFDLLILGVGPDGHTCSLFPDHPPLQEREKI VAPISDSPKPPPPQRTLTLPVLNAARTVIFVATGEGKAAVLKRI LEDQEENPLPAALVQPHGTGKLCWFLEAAARLLTVPFEKHSPL |
| 6405 | 1 | 1456 | AALPRPTPRAPLGREGTGSDSEMAASMFGRLVAVATLRNHRER TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYSMELLQE AGSVPKGYVAKSPDEAYAIKKLGSKDVVIAQVLAGGRGKGT FESGLKGGVKIVFSPPEAKAVSSQMGKLFKQTGEGKRICNQ VLVCERKYPREYYFAITMERSFQGPVLIGSSHGGVNIEDVAEE TPEAIKEPIDIEEGIKKEQALQLAKMGFPNIVESAAENMVK LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK KIFLDQDWTQEDERDKDAKANLNYIGLDGNIICLVNAGLAMA TMDIILKHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL VNIGGIMRCDVIAQGIVMVAVKDLKIPVVRLOQTRVDDAKA LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP I |
| 6406 | 1036 | 167 | HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD DDDDHDDHEDNDKMNDSGMDPERLKAFFMVFRLFDENLDRM VPISKQPKKIQAIIESCSRQFPEQERARKRIRTYLKSCKRMK KNGMEMTRTPPHLTSAMAENILAAACESETRKAAKMRLEIYQ SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN YSYRGYALSSNLQPPASLQTNHNSGESGEARALASRPAPSWV CRAALGSGMGRGKQRPVMERGCLTA |
| 6407 | 492 | 150 | VGLCLAVSQTVLAQLDALLVFPQQVAQLSCTLSPOHVTIRDYGV SWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNAC VLTISPQVQPEDDADYCSVGYGFSF |
| 6408 | 1458 | 903 | RGCTSSQAWRLFGGVTGRGNMREIKCYFCSGPIYPGHMMFVR NDCKVFRFCCKSKCHKNFKKRNPRKVRWTKAFRKAAGKELTDN SFEFEKRRNEPIKYQRELWNKTIDAMKRVEEIKQKQAKFIMNR LKKNKELQKVQDIKEVKQNIHLIRAPLAGKQKLEEKMVQQLQE DVDMEDAP |
| 6409 | 150 | 446 | NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDFGP GPACLPKTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS HGRAYLFNSV |
| 6410 | 85 | 607 | RGGTAGCVACLGCGQSSSPKAAPFAGSACLPAADSCPCLLPQAC AISGLFNCITIHPLNIAAGVWMIMNAFILLCEAPFCCQFIEFA NTVAEKVDRLRSWQKAVFYCGMAVVPVIVISLTTLTLLGNAIAPA TGVLVGLSALGKKGDAISYARIQQORQQADEEKLAETLEGEL |
| 6411 | 302 | 772 | RLSIMASSLNEDPEGSRTYVKGDLFACPKTDSLACISEDCRM GAGIAVLFKKKFGGVQELLNQKKSGEVAVLKRDGRYIYYLITK KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ WENVSAMIEEVFEATDIKITVYTL |
| 6412 | 61 | 1709 | RPVTSFSPPLPGSCGGRLGTRTMLGRSLREVSAALKQGITPTL CQKCLSLIKKTKFLNAYITVSEVALKQAESEKRYKNGQSIGD LDGIPIAVKDNFSTSGIBTTCASNMLKGYIPPNATVVQKLLDQ GALLMGKTNLDEFAMGSGSTDGVEGVPVKNPWSYSKYREKRQK PHSENEEDSWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGIILTRCVDDAAIV IGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV PELSSEVQSLWSKAADLFESEGAKEVSLPHTSYISVCVHVLC TSEVASNMARPDGLQYGHRCIDIVSTEAMYAATRREGFNDVVRG RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL TPPTLSEAVPYLEFIKEDNRTRSQQDDIFTQAVNMAGLPAVSIP VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFQVQVFPVQLQE LMDDCSAVLENEKLASVSLKQ |

[illegible]

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|------------|--|--|---|
| | | | FAPMYGGFPVKLRITLGGDEIPYDQPQITAEELAEKTKNAVQALID KHQRI PGNIMSALLERFH |
| 6421 | 1844 | 362 | WALSLRRQPERMSNKLSPHPHSVVLRFSEFKMASSPAVLRSRL YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCW DEPVRIAVRGLAPEQPVTLRASLRDEKGFQAHARYRADTLGE LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA VELEVLDDGHDPPGRLLCQTRHERYFLPPGVRRPVRVGRVGRGT LFLPPEPGPFPGIIVDMFGTGGGLLEYRASLLAGKGFVMAALAY NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPVGLLGISKGG ELCLSMASFLKGITAAVINGSVANVGGLTRYKGETLPPVGVNR NRIKVTGDGYADIVDLNSPLEGPDQKSFIPVERAESTFLFLVG QDDHNWKSSEFYANBACKRLQAHGRRKPQIICYPETGHYIEPPYF PLCRASLHALVGSPIIWGGEPRAHAMAQVDANKQLQTFHKKHLG GREGTIPSKV |
| 6422 | 181 | 2133 | EGENLSWFQEFWGDIAKEFYWKTPCPGPFRLRYNFDVTGKIFIE WMKGATTNICYNVLDRNVHEKLGDKVAFYWGNEPGETTQITY HQLLVQVCQFSNVLKQGIHKGDRVAIYMPMPELVVAMLACAR IGALHSIVFAGFSSESCLERILDSSCSLLITDAFYRGEKLVNL KELADEALQCKQEKGFVRCCIVVKHLGRAELGMDSTSQSPP KRSCPDVQISWNQIDLWHELMQEAGDECEPEWCDADPLFIL YTSGSTGKPKGVVHTVGGYMLYVATTFKYVDFHAEDVFWCTAD IGWITGHSYVTYGFLANGATSVLFEGIPTYPDVNRLWSIVDKYK VTKFYTAPTATIRLLMKFGDEPVTKHSRASLQVLGTGEPINPEA WLWYHRVGAQRCEIVDTFWQTETGGHMLTPLPGATPMKPGSAT PPFFGVAPAILNESGEELEGEAEGYLVFQKPPGIMRTVYGNHE RFETTYFKKPGYYVTGDGCQDQDQGYWITGRIDDLNLSVSHL LSTAEVESALVEHEAEEAAVVGHPHPVKGECLYCFVTLCDGHT FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPFSHRCLTIQ |
| 6423 | 614 | 1237 | ANLKEIPRDLPPETVLLYLDNQTITSIPNETFKDLHQLRVLNLS KNGIEFIDHAFKGVATLQTLDLSDNRIQSVHKQAFNNLKARA RIANNPWCHDCDTLQQLRSMASNHETAHNVICKTSVLDEHAGRP FLNAANDADLCNLPKKTDYAMLVTMPGWFMTVVISYVVVYVRQN QEDARRHLEYLKSLSRQKKADEPDDISTVV |
| 6424 | 1 | 1188 | KKVSWPVAAMVHCSCVLFKRYGNFIDKLRFLTRGGSGMGYPRL GGEGGKGGDVVVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKSGKGDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGG GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFLSSHTQYRTAFETII LLTKELELYKEELQTKFALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEIEELKNCIRKSL DEQANQENDALHKKQLNLNLSIDTMSSTEPSKHAVTTSKMDII |
| 6425 | 1850 | 1144 | LAMEGGGGIPLTLKEESQSRHVLPAFVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPAATMKQIENVVKMLR CRRGSLVDIGSGDRIVIAAAKGFATVGYELNPWLWVYSRYRA WREGVHGSAPFYISDLWKVTFSSQSVNVVIFGVPMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPTSMHFQLPIQA |
| 6426 | 30 | 565 | SRGAAGVGSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIR LHAEFAAERDWEQFHQPRNLLALVGEVGELELQWKTDGEPG PQGSPPRERAAEQEELSVDVLIYVALAARCRVDLPLAVLSKMDI NRRYPALHARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST |
| 6427 | 145 | 959 | AASWGPFPVPRAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK NIREYVRMMYWIWVAFALFMAAEIVTDIFISWFFPYEIKMAFVL |

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|------------|--|--|--|
| | | | WLLSPYTKGASLLYRKFFVHPSLSRHEKEIDAYIVQAKERSYETVLSFGKRGRLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDAPAPAYHDPLYLEDQVSHRRPPIGYRAGGLQSDTEDECWSDTEAVPRAPARPREKPLIRSQSLRVVVKRPPVRBGTSSRLKVRTRKKTVPDSDVS |
| 6428 | 1982 | 444 | SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIREKINAAIQDMPSEEEIAQLLSGSYIHYFHCRLRLDLLKGTEASTKNIFGRYSSQRMKDQWEIIALYEKDNLYLVELSSLVRNVNVEIPSLKKQIAKQQQLQEQYSRKEEECCAGAAEMREQFYHSCQKQYGTGENVRGELLALVKDLPSQLAEIGAAAQQLGEAIDVYQASVGFVCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEELPEQVAEDAIDWGDGVEAVSEGTDGSGISAEAGIDWGIFFPESDSKDPGGDGIDWDDAVALQITVLEAGTQAPGVARGPDALTLEYTETRNQFLDELMELEIFLAQRAVELSEADVLSVSQFQLAPAILQQQTKKEMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVTEFLQQLKQSQLLALKKELMVQKQQAEEQAALPEKLDLLEKTKELQKLIADISKRYSGRPVNLMTSL |
| 6429 | 3413 | 3442 | EPSSWTAAPRGPLAAHPLEAAVQEDDRRLSFDSSRIKVPFANGTLVVKSVTDKADGDLVCARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCAVATGLPNPEISWSLPGSLVNSFMQSDDSGGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVQKDEMVRVVKVVTAPATIRNKTCLAVQVPYGDVVTACEAKGPEMPKVTWLSPTNKVIPTSSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGEDRKTVWIHNVQPPKINGNPNPITTVREIAAGGSRKLDCKAEGIPTPRVLWAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGHTISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLHISGLSSVDAGAYRCVARNAAGHTERLVSLKVGKPEANKQYHNLLVSIINGETLKLPTPPGAGQGRFSWTLPNGMHLEGPQTIGRVSLDNGTLTVREASVFDRTGYVCRMETEYGPSVTSIPVIVIAYPPIITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPKSHLKAGVQARLYGNRFLHPQGSLLTIQHATQRDAGFYKCMKNILGSDSKTYIHFV |
| 6430 | 1946 | 602 | RTRVSTGLRRTLLWSEAVGASSTRGDTGIPSGEGGAGPGGGEGAMLEAMAEPSPEDPPPTLKPETQPPKRRRTIBDFNFKCSFVLAYAGYIPPSKEESDWPASGSSSPLRGESAADSDGWSAPSDDLRTIQTFVKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKMKLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTVPVPLSQGDLSHPPRKDKRKNRKLGPAGAGFVLRPRPTPGDGEKRSRIKKSCKRKLKKAERGDRLLPPGPPQAPPSTDSEEEEEEEEEEEBEMATVVGGEAPVPVLPPTPEAPRPPATVHPEGVPPADSESKEVGSTETSQDGDASSSEGENRVMDEDIMVESGDDSDDLITCYCRKPFAGRPMIECSLCGTWIHLSCAKIKKTNVPDFFYCQCKELRPEARLGGPCKSGEP |
| 6431 | 3 | 605 | WNNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGRLEEEALRRKERLKALEKTRKDKEDGEPKTKHLREEEEEGEKHRELRLRNYVPEDEDLKRRRVPQAKPVAVEEKVKEQLEAAKPEPVIIEVDLANLAPRKPDWDLKRDVAKKLEKLKRTQRAIAELIRERLKGQEDSLASAVDAATEQKTCDS |
| 6432 | 56 | 1692 | GGLGTMGSRIKQNPETTFEVYEVAYPRTGGTLDPEVQRQFPEDYSDQEVQLTLTKFCFFPYVDSLTVSQVGNFTFVLTDIDSKQRFGRCLSSGAKSCPCILSYLPWFVYFVYKLLNILADYTTKRQENQWNELLETLHLKLPIDPGVSVHLSVHSYFTVPDTRLPSPENRNLTIFYVAVDVNNMLHLYASMLYERRILIIICSKLSTLTACIHGSAAMLYPMYQHVYIPVLPPhLLDYCCAPMPYILIGIHLSLMEKVRNMALEDVVILNVDNTLTETPFDDLQSLPNDVISSLNRLKKVSTT |

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|------------|--|--|---|
| | | | TG DGVARAF LKAQA A FFGSYRNAL KIEPEEPITFCB EAFVSHYR SGAMRQFLQNATQLQ LFKQFIDGR LDDLNSGEGFSDVFEE EENM GEYAGSDKLYHQWLSTVRK GSGAILNTVKT KANPAMKTVYKF DI AENGCAPTPEEQ LPKTAPSP LVEAKDPKLRDRRPITVHFGQVR PPRPHVVKRPKSNI AVEGRRTSVPSPEQNTIATPATLHILQKSI THFAAKFPTRGWTSSSH |
| 6433 | 1524 | 484 | APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA PTTPPQPGWCLCGDKFSSCQTPGREKERRLATMHGSCSFLMLL LP LLLL VATTGPVGALTDEEKRLMVELHNLRYRAQVSP TASDML HMRWDEELAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDV PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVNAKTERIGG SHFCEKLQGVETNIELLV CNYEPPGNVKGKRPYQEGTPCSQCP SGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRA TEASDRKMG AEGDPKPSVSVGLNSGPGHVWGPLLGLLLLPLVLGIF |
| 6434 | 40 | 2002 | MPQLNFGMADPTQMGLSMLLLAGEHALGTPEVFSGTCRPDVSE SPELRQKSP LQFAEISSSTSHSDASTKQCQTSA LFQFAEISSN TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKL IKAKES DGGRIKELEKGKEEKEIKMEKTDETR LQKEAEFEKSAKENLRDS KELRNFEALQIDDI MAIKMEDPK EIRKEELEEDHKCSHFPDFSY SASSKIIISDVPSRKDHMCHPHGIMI IEDPAALNKPELKKKKK KSKMDRHGNDKSTPKKTKCKRQSSSEDI ESVIYTI EAVAKGDWG IEKLGDTPRKKVRTSSSGKGSILDAKPPKKVK SREKKMSKEKS SDTTKESRPDPFISISASKNISGETPEG IKAEP LTPMEDALPPS LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS LRANVDRGKRSSSGKGNSSDHEGCWNEESWTFSSQSGTSGSKFPK TKPKEDCLLGS AKLDEEFKFNLSLPQYSPTV FDRKCVPVPRKK KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPT EAI FSED RNT MEPVHKVNKIPSI FNTPEPTTARTFGGQPKESKENPDYS PCQ DTQRAGYHHEEVLWMTNLMN NCGVYLKQLRHTAMTNA |
| 6435 | 2227 | 657 | ALQRDAAAAYAHPEYEEERFLQEETVSQQINSIELLQTRPLALPE VVKSRQLRQVHLRGRPASQPTVIRGITYYKAKVSEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQSPQVPATTVAHTATQQPAAPAPPAVS PREALMEAM HTVPVPPTTVRTSLGKDAPAGRGTTPASPTLSFEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFQGRWSNSYKLPYSWIGTGHVYNGAFYNNR AFTRNIIKYDLKQRYVAAWAMLDVAYEEATPWRWQHSDVDFA VDENGLWLIYPALDDEGFSQBEVIVLSKLNADLSTQKETTWR TG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHNTQTIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY |
| 6436 | 1295 | 341 | GACRPPVRQDPDSGPDYEALPAGATVTHMVAGAVAGILEHCV YPIDCVKTRMQSLQPDPAARYRNVL EALWRIIRTEGLWRP MRGL NVTATGAGPAHALYFACYEKLKKTLSDVHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTD CVRAVWQNEGAG AFYRSYTTQLTMNVFPQAIHFMTYEFLQEBFN PQRYPNPSSHVL SGACAGAVAAAAATPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIANSVYEFFKYLIT KRQEEWRAGK |
| 6437 | 1828 | 360 | FPAPAPPASPARHVTRTARGHLEGGSRAPLLQAVFLQIKNMVK LIHTLADHGDDVNCCAFSFL LATCSLDKTI RLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKHA DLGITCCDFSSQPVSDGEQGLQFPRLASCGQDCQVKIWI VSFTH ILGFELKYKSTLSGHCAVLACAFSHDQMLVSGSVDKSVIVYD |

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|------------|--|--|---|
| | | | TNTENILHTLTQHTRYVTTCAFAFNTLLLATGSMKDTVNIWQFD LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM NNIDGKELLNLTKESSLADDLKIESLGLRSKVLRIEELRTKVKS LSSGIPDEFICPITRELMKDPVIASDGYSYEKAMENWDPAKRN RTSP |
| 6438 | 109 | 901 | EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV NPALPLSPTGLAGSLTNALSNGLSGGLGILENPLLDILKPG GGTSGGLLGGLLGKVTSPVPLNNIIDIKVTDPLLELGLVQSP DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD KQERIHVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN KVLPELVQGNVCPVNEVLRGLDITLVHDIWNMLIHGLQFVIK |
| 6439 | 23 | 412 | SIQTASAITTEMASQSQGIQQLQAEKRAEKVADARKRKARRL KQAKESAEQMEVEQYRREREHEFQSKQQAAMSGQNLSAEVEQAT RRQVQGMQSSQQRNRERVLAAQLGMVCDVRPQVHPNYRISA |
| 6440 | 3 | 517 | RARWNSDMGDLPLVRLSLALRIQPNDDGPFYKVDGQRFQGNRT IKLLTGSSYKVEVKIKPSTLQVENISIGGLVLPLELKSKEPDGD RVVYTGTYDTGEGVTPTKSGERQPIQITMPFTDIGTFETVMQVKF YNYHKRDHCQWGSPPFSVIEYECKPNETRSLMWVNKESFL |
| 6441 | 234 | 1373 | KSGGLRRRRQRPGRSAAGVEEELPPGMEKFKAAMLLGSVGDALGY RNVCKENSTVGMKIQEELQSRSGGLDHLVLPSPGEWPFVSDNTIMHI ATABALTDDYWCDDLYREMVRCEIVEKLPERRPDPATIEGC AQLKPNYLLAWHTPFNEKSGSGFAATKAMCIGLRWYKPERLET LIEVSVECGRMTHNHTGFLGSLCTALFVSFAAQGKPLVQWGRD MLRAVPLAEFYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK DSENKAI FPDNYDAEERBKYRKWSSEGRGRRGHADPMIAYDA LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK GLYQDLEDKEKLEDLGAALYRLSTEEK |
| 6442 | 34 | 796 | AEDFAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS LQORQLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ DGTWRTVAPQAAERAPLDRLVSTELCRAAWGQEGAHPASGLGD GHTQGPVSDLCPVTSQAAPRHLQSSAWEMDGPRENRSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLGTGMMGGARPGPC EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET |
| 6443 | 2 | 555 | MASPAASSVRPPRPKKEPQTLVIPKNAEEQKLERLMKNPDK AVPIPEKMSWAPRPPPEFVRDVMGSSAGAGSGEFHYRHLRRR EYQRQDYMMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ KLKEKKLLAKMKLEQKKQEGPGQPKQEGSSSSAEASGTEEBEE VPSFTMGR |
| 6444 | 390 | 899 | GSTPRGKMRAPIEPKPGDLIEIFRPFYRHWAIYVGDGYVWHIA PPSEVAGAGAASVMSALTDKAIKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVI I AASVAGMGLAAMSLIGVMFSRNKRQKQ |
| 6445 | 2 | 753 | AGAAGAAGAARSPPQAHTKGVRLPSRRRSPDCGRMELAGSF SEEQFWEACAEALQPPALAGADWQLLVETSGISYRLLDKKTGLY EYKVFVLEDCSPTLLADIYMSDYRKQWDQVVKELYEQECNGE TVVYWEVKYPPFMSNRDYYLRQRRDLMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGOIP SWLINWAAKNGVFNFLKDMARACQNYLKK |
| 6446 | 1 | 1651 | RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDDEDADLPHGKQQTPLCFNRLFTSAERTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNISYNPV PWEKEEYLPVLEDDLLQFDVEDLYEPVSVFSPYNGLSENTS VVEKLKHEARALSAAALARAREDLQMKQFAQDFVMHTDVRT CSSSTSVIADLQEDBDGVYSSYGHYGIHEEMLKDKIRTESYRD FIYQNPFIHKDKVVLDVGCCTGILSMFAAKAGAKVLGVDQSEI |

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|------------|--|--|---|
| | | | LYQAMDIIRLNKLEDTITLIKGTIEEVHLPVEKVDVIISEWMGY FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA DRIAFWDDVYGFKMSCMKAVIPEAVVEVLDPKTLISEPCGIKH IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN RVVFTSGPQSTKTHWKQTVFLLEKPPSVKAGEALKGKVTVHNK KDPRSLTVTLTNNSTQTYGLQ |
| 6447 | 1554 | 1068 | RLGPAEWHLSGPGCHATLGAANRGRALGVRAAWRGAPLQCRVMMP SRINLATGIPSSKVYSRLSSTDDGYIDLQFKKTPPKIPYKAIA LATVFLIGAFLLIIIGSLLSGYISKGGADRAVPVLIIGILVFL PGFYHLRIAYVASKGYRGYSYDDIPDFDD |
| 6448 | 74 | 559 | GQVLSHCYHYRSSRRRGGLSRGRGAGVMALVPYEBTTEFGLQK FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAIVLSTYLEMG AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER QFIVRVKHYDPEKDVHIYEAKRKNQKEDL |
| 6449 | 597 | 1876 | EYGVCCENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG GLLNVDVDFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA ATVECMYGHKGPHGHGHIQVKKDEFSTKCNQTDHHRMSGGRQEE FRTNLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCCLTYRRI YLPSPSRPDDLKPGLFKGTGSHGLEIVMLSFHGRRARGTKITG DPNIPAGQQTVEIDLHRHIQLPDLENQRNFNELSRIVLEVREVR RQEQQEGGHEAGEGRGQGPRESQPSPAQPAEAPSKGPDGTPG EDGGEQGDVAAAEQPAQCGGQPFVLPVGVSSRNEDYPRTCRM CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY SRVQATFRNADAPSPQAFDEMLKNIQSLTS |
| 6450 | 848 | 269 | FVPAPRTVSGKRSPLGEWEERGEQRTGREFSNGGRAVEAAR MRLLCGLWLWLSLLKVLQQTPTPLPLPPMQSFGNQFQGEWF VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAQQLVAAS RDAGPVHLPGQSSGPLG |
| 6451 | 232 | 939 | HSPTPTSPRATMEDVKLEFFSLPQCKEDABEWYTPMRREMGE ILPGLFLGPYSSAMKSLPVLOKHGITHIICIRQNIENFIKEN FQQLFRYLVDIADNPVENIIRFPMTKEFIDGSLQMGKVLVH GNAGISRSAAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF VHQLQYEYAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE EEDDFGTMQVATAQNG |
| 6452 | 1 | 652 | RTRGESSNMEPLAAYPLKCSGPRAKVFVLLSIVLCTVTLFLLQ LKFLPKINSFYAFEVKDAKGRVTSLEKYKGKSVLVNVASDCQ LTDNRNVLGLKELHKEFGPSHFSVLAPPCNQFGESEPRPSKEVES FARKNYGVTFPIPHKIKILGSEGEPAFRPLVDSSKKKEPRWNFWK YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL |
| 6453 | 827 | 223 | HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKNCKVVFSSQQLRKRLTPLQYHVTOEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD FSYGMHVRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL |
| 6454 | 827 | 223 | HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKNCKVVFSSQQLRKRLTPLQYHVTOEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD FSYGMHVRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL |
| 6455 | 1042 | 173 | RVHLATVSASAAWDALGLFVRSHMQGSTRMGVMTDVHRRFLQL LMTHGVLEEDVKRLQTHCYKVHNRNATVDKLEDFINNINSVLE SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF RKALELIIDSETGFASSTNINLVDQLKGKMRKKEAQVLQKF VQNKWLEKEGEFTLHGRAILEMEQYIRETPYDAVKICINCHSL |

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|------------|--|--|---|
| | | | LIQGQSCETCGIRMHLPCVAKYFQSNAPRCPCNDYWPHEIPK VPDPEKERESGVLSKNKSLRSRQH |
| 6456 | 2 | 555 | RPQSRISIMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCCKGA TVEAEALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR RPAPFEVVFVSADGSSQEMLDPMRELHGAWLALPFHDPYRHELK KRYNVTAIPKLVIKQNGEVITNKGRKQIRERGLACFDQWVEAA DIFQNFVS |
| 6457 | 23 | 892 | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFDPDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS |
| 6458 | 23 | 892 | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFDPDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS |
| 6459 | 23 | 892 | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFDPDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS |
| 6460 | 23 | 892 | PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFDPDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS |
| 6461 | 1653 | 360 | LQQRTRLRITAVGQTHPIAWMAWEPISLGAFYGPASFITFVNCMYF LSIFIQLKRHPERKYELKEPTEEQORLAANENGEINHQDSMSLS LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYPL DLVFSFVFGATSLSFSAFFVHVHCNREDVRLAWIMTCCPGRSS YSVQVNVQPPNSNGTNGEAPKCPNSSAESSTCNKSASSFKNSSQ GCKLTNLQAAAAQCHANSPLNSTPQLDNLSTEHSMDNDIKMHV APLEVQFRITNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE GSVQNGLPKSRILGNNEGHSRSRRAYLAYRERQYVPPQDSSDAC STLKSSRNFEKPVSTTSKKDALRKPAVVELENQKSYGLNLAI QNGPIKSNQEGPLLGTSTGNVRTGLWKHETTV |
| 6462 | 3 | 773 | SEELDREKCLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH PDSQSMESKLNDDRKTTPVNWKDSRGTRVAVSSPMSQHQSYIQ YLHAYPYQMYDPSHPAYRAVSPVLMHSPGAYLSPGFHYVPYG KMSGRETEKVNTPSPVNTKTTTESKALDLLQHANQYRSKSPA PVEKATAEREREAEERDRHSFPQGRHLTHHHTHVGMGYPLIP GQYDFPQGLTSAALVASQVAAQASAGMFPQQRRE |
| 6463 | 2 | 350 | VILCILGGWIFKNADRSMBKKKGEPRTAEARFPWVDEDLKDSSD LHQAEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL NKRRSVRFISNEQVPMVEIDNVIRTAGL |
| 6464 | 12 | 1154 | GILRQKEREERNRIHKKEILFLEHLLVVPSEMSSSLGKVQTVLG |

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|------------|--|--|--|
| | | | LVPEPSKLGRTLTTHEHLAMTFDCCYCPFPFPCQEAISKEPTVMKNL YWIQKNAYSHKENLQNLQETEAKEELLYFKANGGGALVENTTT GISRDTQTLKRLABETGVHIISGAGFYVDATHSSSETRAMSVEQL TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH AQAQLGCPVIIHPGRSSRAFPQIRILQEAGADISKTVMSHLDR TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR IRRVRLVVEEGCEDRILVAHDHTKTRLMKYGGHGYSHILTNVV PKMLLRGITENVLDKILINPKQWLTFK |
| 6465 | 126 | 1396 | KMTVFFKTLRNHWKKTAGLCLLTWGGHWLYGKHCNLLRRAAC QBAQVFGNQLIPPAQVVKATVFLNPAACKGKARTLFEKNAAPI LHLSGMDVTIVKTDYEGQAKLLELMENDTVIIVAGGDGTLQEV VTGVLRRTDDEATFSKIPGFIPLGETSSLSHTLFAESGNKVQHI TDATLAIKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV KVSKEYWLEPLKIKAAHFFSTLKEWPQTHQASISYTGTPERPEN EPEETPVQRPSPLYRRLRLASYWAQPODALSOEVSPEVWKDVQ LSTIELSITTRNNQDPTSKEDFLNICIEPDTISKGDPFITIGSR KVRNPKLHVGEQTECLQASQCITLLIPEGAGGSFSDSERYEAMPV EVKLLPRKLQFFCDPRKREQMLTSPQ |
| 6466 | 1134 | 828 | VARGTELSQLEKAHPADMGRRKSKRKPFPFKKMTGTLETQFTC PFCNHEKSCDVKMDRARNRGVISCTVCLEEFQTPITYLSEPV DV YSDWIDACEAANQ |
| 6467 | 301 | 2571 | GRLRVLALAHGELACHAVLTASLLSLRSLRMSDMDYERPNVET IKCVVVDNAVKGKTRLCARACNATLTQYQLLATHVPTVWAIQ YRVCQEVLEERSRDVDDVSLSRLWDTFGDHKKDRRFAYGRSDV VVLCSFIANPNLSLHVKTWMPYKIKHFCPRAPVILVGCQLDLRY ADLEAVNRARRPLARPIKPNELPPEKGREVAKELGIPYETS VAQFGIKDVFDAIRAAALISRRHLQFWKSHLRNVQRPLQAPFL PPKPPPIIVVPDPSSSEECPAHLLDPLCADVILVLQERVRI FAHKIYLSSTSSKFYDLFLMDLSEGLGPGSEPGGTHPEDHQGH SDQHSHHHHHHGRDFLRAASFVDCESVDEAGSGPAGLRAST SDGILRGNGTGYLPGRGRVLSWSRAFVSIQEEMAEDPLTYKSR LMVVVKMDSSIQPGPFRAVLKYLTYTGELDENERDLMHIAHIAEL LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT FSDVTFILDDGTISAHKPELLISSCDWMAAMFGGPFVESSTREVV FPYTSKSCMRVLELYLTGMFTSSPDLDMMKLIILANRLCLPHL VALTEQYTVTGLMEATQMMVDIDGDVLVFLLELAQFHCAYQLADW CLHHICTNYYNNVCRKFFPRDMKAMSPENQYEFKRWPPVWYLKE EDHYQRARKEREKEDYLHLKRPKRRLFWNSPSSPSSSAASS SPSSSSAVV |
| 6468 | 3 | 1374 | DAWAGTNMAALAPVGSFASRGPRLAAGLRLPLMLGLLQLLAEPG LGRVHHLALKDDVRHKVHLNTFGFFKDGMYVNVVSSLSLNEPED KDVITIGFSLDRTKNDGFSSYLEDVNYCILKKQSVSVTLILLDI SRSEVRVKSPEAGTQLPKIIFSRDEKVLGQSQEPNVNPNASAGN QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFFNIS TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA GEIPLPKLYISMAFFFFLSGTIWIHLKRRNDVFKIHWLMAAL PFTKLSLVFHAIDYHYISSQGFPIEGWAVVYITHLLKGALLF ITIALIGTWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES TEEGTTEYGLWKDSLFLVDLLCCGAILFPVWVSIIRHLQEASATD GKGKFSRAHFVLLSL |
| 6469 | 3 | 1374 | DAWAGTNMAALAPVGSFASRGPRLAAGLRLPLMLGLLQLLAEPG LGRVHHLALKDDVRHKVHLNTFGFFKDGMYVNVVSSLSLNEPED KDVITIGFSLDRTKNDGFSSYLEDVNYCILKKQSVSVTLILLDI SRSEVRVKSPEAGTQLPKIIFSRDEKVLGQSQEPNVNPNASAGN QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFFNIS TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA |

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|------------|--|--|--|
| | | | GEIPLPKLYISMAFFFFLSGTIWIHILRKRNDVFKIHWLMAAL PPTKSLSLVFHAIDYHYISSQGFPIEGWAVVYIYTHLLKGALLF ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLNVAYIIIES TEEGTTEYGLWKDSLFLVDLLCCGAILFPVWVSIRHLQEASATD GKGKFSRAHFVLLSLL |
| 6470 | 2726 | 1437 | AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS GPLPREDGCRTPGPQLPLPGALLRPRTLLSSAAETGRSRHPDT QHPSSGGRRCRGGTESPSAAGRPAASMAEAEEDCHSDTVRADDE ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG SLQKTSADTKGKQEQAKEKARELFLKAVEEENQNGALYEAIFY RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDSKMADLLS YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS SDLRLSLEQLSLVCRGFYICARDPEIWRACLKVGWGRSCIKLV PYTSWREMFLEPRPRVFDGVYISKTTYIRQGEQSLDGFYRAWHQ VEYYRYIRFFPDGHVMMMLTTPPEPQSIVPRLRTR |
| 6471 | 1750 | 299 | FFFDKMAAGSGVGKRSKSDADSGFLGLRPTSVDPALRRRRR GPRNKKRGWRRLAQEPGLGLEVDQFLEDVRLQERTSGGLLEAPN EKLFFVDTSKEKGLTKKRTKVQKSSLLKKPLRVDLILENTSK VPAPKDVLAHQVPNAKLLRKEQLWEKLAKQGELEPREVRAQAR LLNPSATRAKPGPQDVERPFYDLWASDNPLDRPLVGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLIS AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE ESDGEPEGQEGEGPEAGDAEVCPTPARLATTEKKTEQQRREKA VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRLTKPEG NILRDRFKSFQRRNMIEPRERAKFKRKYKVLVEKRAFREIQL |
| 6472 | 3 | 897 | SCGSDRAQWAMEFFFDVDALEPFRITVLDQHLRPFARRPGTTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSARPAGKGAIGFIKVGYKKLFVLDREAHNEVEPLCLL DFYIHESVQRHGHGRELFQYMLQKERVPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATHRSRAA AVDPTPAAPARKLPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP |
| 6473 | 22 | 912 | SSAVEFVWEGEKMAAEFNKTEIQTLFKRLRAVPTNKACFDGAK NPWSASITYGVFLCIDCSGVHRSGLVHLSFIRSTELDSNNWFQ LRMCQVGGNANATAFFRQHGTANDANTKYNSRAAQMYREKIRQ LGSAAALRHGTDLWIDNMSSAVPNHSPKKDSDFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNLDLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSIERQAQVAE KLREQQAADAKKQAEESVMASMLAYQELQIDR |
| 6474 | 3 | 462 | LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPENTGKDG KVTKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRGA KGKKEEKQEGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP PSTLSVKQIETVRVKGTEN |
| 6475 | 3 | 462 | LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPENTGKDG KVTKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRGA KGKKEEKQEGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP PSTLSVKQIETVRVKGTEN |
| 6476 | 106 | 1090 | ARAMAQYKGTMRAGRAMHLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRE RQLAKRQHLEEQRLQQRERQREQRRERKRKISCLSFALDDLLD QADAAEARRAGNLGNPDVDTSLPDRDREEEENRLREELRQW EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNVTQQFLKKAL QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYKXKHIF PASRWEAYDPEKKWDKYTIR |

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|------------|--|--|---|
| 6477 | 227 | 915 | LQGHLMGIMAASRFLSRFWENGKNIVCVGRNYADHVREMRSAVL SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELVVMGKRRCR AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTAKSFTA SCPVSFAFVPKEKIPDPHKLKLWLKVNGLRQEGETSSMIFSIPIY IISVYSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM TFKVEKPEY |
| 6478 | 2 | 1495 | FVSSRILPESLASSEASTLEAMGRKEEDDCSSNKKQTTNIRKTF IFMEVLGSGAFSEVFLVKORLTGKLFALKCKIKKSPAFRDSSLEN BIAVLKKIKHENIVTLEDIYESTTHYYLVMLVSGGELFDRILE RGVYTEKDASLVIOQVLSAVKYLHENGIVHRDLKPENLLYLTP ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA VDCWSIGVITYILLCGYPPFYEETESKLFKEIKEGYEFESFPW DDISESAKDFICHLEKDPNERYTCEKALSHPWIDGNTALHRDI YPSVSLQIQKNFAKSKWRQAFNAAAVVHMRKLHMLHSPGVRP EVENRPPETQASETSRSPSPETITTEAPVLDHVSVALPALTQLPC QHGRRTAPGGRSNLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC SSCLNIGSKGSSYCSBPTLLKKANKKQNFKSEVMVPVKASGSS HCRAGQTVCLIM |
| 6479 | 3 | 949 | SCRGPWGHFAGGQAGAMELLSALSGLGELALSFSRVPLFPVFDLS YFIVSILYLKYPEGAVELSRRHPIASWLCAMLHCFGSYILADLL LGEPLIDYFSNNSSILLASAVYLIFFCPLDLFYKCVCFPLPKL IFVAMKEVVRVKIAGVIHHAHHHHYHGWFMVMTAGWVKGSGLVA LMSNFEQLLRGVNKPETNEILHMSFPPTKASLYGAILFTLQQTRW LPVSKASLIFITFLFMVSCKVFLTATHSHSSPFDALGYICPVL FGSACGGDHHHDNHGGSHSGGPGAQHSAMPAKSKEELSEGRSK KKAKKAD |
| 6480 | 192 | 514 | DFMSIYFPIHCPDYLRSAKMTVEVMNTQPMEEIGLSPRKDGLSY QIFPDPSDFDRCKLKDRLPSIVVEPTGEVESGELRWPEEFL VQEDQDNCEETAKENKEQ |
| 6481 | 110 | 1131 | KSRMDLDVVMFVIAGGTALPILAFVASFLWLPSALIRIYYWY WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCDMPGHEGTTRSSLDLSDIQQVKRIH QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYPSDVSSLWLVC AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRI PHNNFYRKLFLEIVSEKSRYSLHQ NMDKIKVPTQIINGKQDQVLDVSGADMLAKSIANCQVELLENC HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD |
| 6482 | 2517 | 568 | EPVSKVSQSRKAGVPTANIEESQAVEAAMANVPWAEVCEKFOA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDDE RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVLAVIBFHLGV NHIDTEELSAGEEHLVKCLRLRLRYRLSHDCISLCIQAQNNLGI LWSEREEIETAQAYLESSEALYNQYMKVGSPPLDPTERFLPEE EKLTEQERSKRFEKVYTHNLYLAQVYQHLEMFKAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKEDEESIRKKAQVQGT GELCDAISAVEEKVSYLRPLDFEARELFLGQHYVFEAKEFFQ IDGYVDHIEVVQDHSALFKGLAFFETDMERRCKMKHRRIAMLE PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD SHIVKINNLNKSAKYQLFLDSLRLDPNKVFPHEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP EAAQIEVELELSKEMVSLLPKMERFRTKMALT |
| 6483 | 3 | 623 | NSHLLCGLRARAPLSANGREARAMEQRLAEFRAARKRAGLAAQP PAASQGAQTPGEKAEAAATLKAAAGWLKRFLVWKPRPASARAQP GLVQEAQPGSTSETPWNTAIPSPCWDQSFNTITFLKVLW LVLLGLFVELEFGLAYFVLSLFYWMYVGTGROPEEKKEGEKSAYS |

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|------------|--|--|---|
| 6484 | 201 | 965 | VFNPGCRAIQGTLTAEQLERELQLRPLAGR QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF MILWLKGVKFNVTVDVMTKPEELKDLPAGTNPFFLVYNKELKT DFIKIEEFLEQLTAPPRYPHLSPKYKESFDVGCNLFAPKFSAYIK NTQKEANKNFEKSLLEKPKRLDDYLTPLDDEIDPDSEAEPPVS RRLFLDGDQLTLADCSLLPKLNIIKVAACKYRDFDIPAEFSGVW RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS |
| 6485 | 6 | 1091 | FVDLVRAVEFLPCPDQSKLEKECQSSSESMGNSMRISILEEDEE DEEPPRVLLYHEPRSEFVGMVLVWHKHKYPPFWPAVVKSVRQDK KASVLYIEGHMNPMMKGFVTVSLKSLKHFDCKEKQTLNQAQEDF NQDIGWCVSLITDYRVLGCGSFAGSFLEYAADISYPVRKSIQ QDVLGTLKLPQLSKGSPPEEPVVGCPGQRPCKRMLPDRSRAARD RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTLFSSSQYVT CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD VLLPEAIIICASAGDEVYKTABEKYIKGPSLSYREKEIFDNQL LEERNRRRR |
| 6486 | 10 | 581 | LVLQAGGAHLSPSRVTOGIYMLAFSEMPKPPDYSELSDSLTLA GGTGRFSGLPHRAWMMNFRQRMGWIGVGLYLASAAAFYVFE ISETYNRLALEHIQQHPEEPLEGTWTHSLKAQLLSLFFWVWTV IFLVPYLMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV KASNQISRLQLIDT |
| 6487 | 352 | 863 | SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNLIKGFVMTQDPTGTGRGGNSIWGKKFEDEYSEYL KHNVRGVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPPAQ |
| 6488 | 878 | 241 | TALQFEGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFFGSGGSISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPPGQALRPLDLSIQIPPGSSVGRPNGQS |
| 6489 | 1457 | 375 | KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYYRRLCML YHPDKHRDPELKSQAERLFLNVHQAYEVLSDPTQTRAIYDIYGKR GLEMEGWVVERRRTPAEIREEFERLQREERBRRLQRTNPKGT ISVGVDATDLFDYDEEYEDVSGSSFPQIEINKMHISQSIAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAGKGGELEFGAG DLQGPLFGLKLFRLNLTFRCFVTTNALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSLQVORPHRNTACAPESFRPFLHVP TWDACSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLTTPR SKRRTGGG |
| 6490 | 3 | 1183 | HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSTIADH KDLIHDVSPDFHGRMATCSSDQSVKVDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLPVKRKELTSSGGPTKFEIHIWAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQTSNPSLGSNIPSLQNSLNGSSAGRKHS |
| 6491 | 3 | 1183 | HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSTIADH KDLIHDVSPDFHGRMATCSSDQSVKVDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLPVKRKELTSSGGPTKFEIHIWAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL |

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|------------|--|--|--|
| 6492 | 34 | 2573 | <p>KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS</p> <p>IPFLKSCCCCLFDFPPPPPLDQVQEECEVERVTEHGTTPKPFRRK PDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI KRQEVINELFYTERAHVRTLKVLQDVFFYQVRSREGILSPSELRK IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG PGEEKLKHAATFCSNQPFALMIKSRQKKDSRFQTFVQDAESN PLCRRLLQKDIIPQMQRLTKYPLLDNIATYTEWPTEREKVKK AADHCRQILNYVNOAVKEAENKQRLQEDYQRRLDTSCLKSEYPN VEELRNLDLTKRKMIHEGPLVWVKNRDKTIDLYTLLEDILVLL QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSLTVLRQVATDN KALFVISMDSNGAQIYELVAQTVSEKTVQDLICRMAASVKEQS TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG LESTLISGKQSHSLSTSGKSEVRDLFVAERQFAEQHTDGTLLK EVGEDYQIAIPDShLPVSEERWALDALRNLGLLQLLVQQLGLT EKSVDQEDWQHFPYRTASQGPQTDVSIQNSENIKAYHSGEGHMP FRITGTGDIATCYSPTSTESFAPRDSVGLAPQDSQASNILVMDH MIMTPPEMPTMEPEGGLDSDGEHFFDAREAHSDENPSEGDGAVNK EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLPMTGIP AVESTHQQHSQPNTHSDGAI SPFTPEFLVQQRWGAMEYSCFEI QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTLICQLRAGS ALTDKHSKDS</p> |
| 6493 | 557 | 1147 | <p>TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAVPVSRSEVA KEONTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT VGHITTHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN VHINTRTSAPSPTALKLATVAASMDRVPKVTTPSSAISSIARENH EPERLGLNGIABTTVAMEVT</p> |
| 6494 | 2425 | 1052 | <p>AVAGGARPCSTPSSPHRRRHRPRPLRPPPAAIMSASAVVYLD LKGVLCICRNYRGDVMSEVEHFMPILMKEEEMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK PLIWIESVIEKSHSRIEYMIKAKSQFKRRSTANNVEIHIPVFN DADSPKFKTTVGSKVWPENSEIVWSIKSPFGGKEYLMRAHFGL PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ</p> |
| 6495 | 2425 | 1052 | <p>AVAGGARPCSTPSSPHRRRHRPRPLRPPPAAIMSASAVVYLD LKGVLCICRNYRGDVMSEVEHFMPILMKEEEMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK PLIWIESVIEKSHSRIEYMIKAKSQFKRRSTANNVEIHIPVFN DADSPKFKTTVGSKVWPENSEIVWSIKSPFGGKEYLMRAHFGL PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ</p> |
| 6496 | 247 | 559 | <p>LRAVSLPLQLVLPEYSIHSFLFCIMFLCAQEWLTGLNVPLLFY HFWRIFYHCPADSSSELAYDPPVVMNADTLSCYQKEAWCKLAFYLL SFFYYLYCMIYTLVSS</p> |
| 6497 | 1053 | 352 | <p>ANTQICRLCPRRHLPCCGAKMNGTEEDYNFVFKVVLIGESGV GKTNLLSRFRNEFSDHSRTTIGVEFSTRVMTGLTAAVKAQIWD TAGLERYRAITSAYYRGAVGALLVFDLTKHOTYAVVERWLKELY DHAEATIVVMLVGNKSDLSQAREVPTTEARMFAENNGLLFLETS ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGAQAQO</p> |

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|------------|--|--|--|
| 6498 | 2636 | 272 | <p>EPGPGEKRACCISL</p> <p>SLRLCPWGTHTLAGPTTMRLLSSLLALLRPALPLILGLSLGCSLSL LRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDDEDFKPRI VPYYRDPNPKYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTL AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSNGDERPAWIM SETLRHLHHTHFGADYDWFIMQDDTYVQAPRLAALAGHLSINQD LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG DILSARPDWLGRLCLIDSLGVGCVSQHQGGQYRSFELAKNRDP KEGSSAFLSAFVHPVSEGTLMYRLHKRFSALELERAYSEIEQL QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWDYFTE QHTFSCADGAPKCPQGASRADVGDALETALEQLNRRYQPRLRF QKQRLNLNGYRRFDPARGMEYTLDLLLECVTQRGHRRLARRVSL LRPLSRVEILPMPYVTEATRVQLVPLLVAAEAAAAPAFLEAFAA NVLEPREHALLTLLLVYGPREGGRGAPDFLGVKAAAELEERRY PGTRLAWLAVRAEAPSQVRLMDVVSXKHPVDLFFLTTVWTRPG PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP DPPSPGADPSRGAPIGGRFDRQASAEAGCFYNADYLAARARLAG ELAGQEEEEALEGLEVMDFLRFSGHLHFRVPEGLVQKFSRLRD CSRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST</p> |
| 6499 | 3 | 2040 | <p>SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACL GHPVVRPQVSGGPGAMPDPAHLFFFYGSISRAEAEHKLKLAGM ADGLFLLRQCLRSLLGGYVLSLVHDVRFHHFPIERQLNGTYAIA GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRESGLEPQPGVDFC LRDAMVRDYVRQTKLEGEALEQAIISQAPQVEKLIATTAHERM PWYHSSLTREEAERKLYSGAQTGKFLLRPRKEGQTYALSLIYG KTVYHYLISQDKAGKYCIPGTFKFDTLWQLVEYLLKADGLIYC LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNL LIADIELGCGNFGSVRQGVYMRKKQIDVAIKVLKQGTETKADTE EMMREAQIMHQLDNPIYVRLIGVQAEALMLVMEMAGGGPLHKF LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYRTASAGKPLKMYAPBCINF RKFSRSDVWSYGVMTWEALSYGQKPYKMKGPVEMAFIBQGR MECPPECPPELYALMSDCWIYKWEKDRPDFTVEQRMRCYYSLA SKVEGPPGSTQKAEACA</p> |
| 6500 | 1773 | 726 | <p>TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPAVLDAK MLESSESLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHL QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLLAAVKE TWTKHCDKAEFFSSENVKVFESINMDTNDMLMMRKAYKYAFDK YRDQYNWFFLARPTTFIIEENLYFLLKKDPSQPFYLGHTIKSG DLEYVMEGGIVLSVESMKRLNSLLNIPEKCPQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNKSVGLSKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGPYFQ</p> |
| 6501 | 1 | 570 | <p>LVGMSGGGTETFPVGEAAPGGGSKKRDLSLGTAGSAHLIIKDLGE IHSRLDHRPVIQGETRYFVKEFEKRLREMRVLENLKNMIEHE TNEHTLPKCRDTRMDSLSQVLQRLQAANDSVCLQQREQERKKI HSDHLVASEKQHMQLQWDFNMKEQPNKRAEVDDEHRKAMERLKEQ YAEKEDLAKFTF</p> |
| 6502 | 213 | 1650 | <p>AGNKEDPWAGNRRTAVLPDVSFVHREDVGWNRSLQSSVQAVKE KSSEALEFMKRDLEFTQVQVQHDCTACTIAATASVVEKELATEGS SGATEKMKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTAKARLSLQSDPATYCNEPDGPPPELFDWLSQFCLBEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHOLEQ EQARRDALQRAEQSISEEPGWEEEEEELMGIISPISPEAKVPV AKISTFPPEGEPQSPCEENLVTSVEPPAEVTPSESSSESISLVT QIANPATAPEARVLPKDLQKLLLEASLEEQLAVDVGETGSPSP</p> |

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|------------|--|--|---|
| | | | IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFEINSDSG KSTPSNNGKKGSSDISEDWEKDFDLDMTEEEVQMALSKVDASG EVSGPGGSEGSEPNPGPCESSPQPAQLSPQEGPCSCLR |
| 6503 | 213 | 1650 | AGNKPDPWAGRNRTAVLPDVSVFHRREDVGVWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVOHDTACTIAATASVVKEKLATBGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTAKARLYSLQSDPATYCNEPDGPPPELFDWLQFCLLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLQEQ EQARRDALQRAEQSISEEPGWEEEEELMGI SPISPEAKVPV AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESESISLVT QIANPATAPEARVLPKDLSQLLEASLEEGLAVDVGETGSPFP IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFEINSDSG KSTPSNNGKKGSSDISEDWEKDFDLDMTEEEVQMALSKVDASG EVSGPGGSEGSEPNPGPCESSPQPAQLSPQEGPCSCLR |
| 6504 | 2131 | 1294 | GKVCILVAHWVCLSLSPPPAGMKT PNAQEAEGQQTAAAGRATG SANMTKKKVSQKKQGRGPSSQPCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPTTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVVDLVKKS |
| 6505 | 2131 | 1294 | GKVCILVAHWVCLSLSPPPAGMKT PNAQEAEGQQTAAAGRATG SANMTKKKVSQKKQGRGPSSQPCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPTTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVVDLVKKS |
| 6506 | 1 | 1350 | EVSPPTSCCLTVAVADPGVSEGFGRFGAGCEMPGRGRCPDCGST ELVEDSHYSQSQLVCSDCGCVVTEGVLTTFSDENLREVITYSR STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQAY RHSGIRARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD LDVFSSTYMQIVKLLGLDVPSLCLAEVLKTYCSSFKLFQASPSV PAKYVEDKEKMLSRMTQMLVELANETWLVTRHPLPVITAATFLA WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA EQLAWLRVLRDLKRSVVKHIGDLLQHRQSLVRSFAFRDGTAEVET REKEPPGWGGQGEVGNNSLGLPQGRKPASFALLPPCMLKS PKRICPVPVSTVTGDNISDSEIEQYLRTQBEVRDFQRAQAAR QAATSVPNPP |
| 6507 | 1878 | 929 | RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD IAWIAADEEETVARVRS DTRPLRHTWKPSPLIVMQRNASVFNLR GSEERLLALKKPPALPALSRTTELQDELSHLSQIAKIVAADAAS ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE VPPELPSVPLLCASPECCCKPEHKAACSSSEEDDCVSLSKASSFA DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRKPFALKE EDISRKGN |
| 6508 | 862 | 342 | WEARKRPQRWPSERREVRVPPPHLQGRSGLEPGTFRKMAAARP SLGRVLPGSSSVLFLCDMQEKFRHNIAFFQIVSVAARMKNTTL DLLDRGLQVHVVDACSSRSQVDRVLVALARMRQSGAFLSTSEGL ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGNSSLH |
| 6509 | 2 | 1053 | FVWNPRGGKRKRRAAVTQAATRASGTPSPRDGMTQGLSVAN KAPTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHDLFTTFSWDDQKV RRVFVRKYVTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWY ASYAVVFATYTLTACCSGPRRHFPWNLLLTFTLSMAYLTGML |

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|------------|--|--|--|
| | | | SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL LMTLFFSGILAILLPQYVPWLHAYVYALGAGVFTLFLALDTQ LLMGNRRHSLSPPEYIFGALNIYLDIIYIPTFFLQFLGTNRE |
| 6510 | 37 | 1156 | PCALDGCPCQGAHVHPLSSAMGLLAFKTKQFVLHLLVGFVFWVS GLVINPVQLCTALWPVSKQLYRRRLNCRLAYSLWSQLVLMLEWW SCTECTLFDTQATVERFGKSHAVIILNHNFEIDFLCGWTMCERF GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCRKRWEEDRDTVV EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEEVAAKGLFVL KYHLLPRTKGFTTAVKCLRGTVAAVYDVTNFRGNKNPSSLGIL YGKKYEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY NQKGMFPGEQFKPARRPWTLNFLSWATILLSPLFSFVLGVFAS GSPLLILTLFGFVGAGNGHCR |
| 6511 | 2541 | 1425 | GEEQLAAAPTECLEQVIGGAGDPGTWASFPSPFGPAPLKGKK TMAFNFSDIVKQGYVKMKSRKLGIRRCNLVFRKSSSKGPQRLE KYPDEKSVCLRGCPKVTETISNVKCVTRLPKETKRQAVAIIFDD SARTFTCDSELEAEWEYKTLSEVCLGSRLNDISLGEPLDLAGV QCEQTDTRFNVFLPCPNLDVYGECKLQITHENIYLDIHNPRVK LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTOGEQEI YQRVHSATLAIABQHKRVLLEMEKNVRLNKGTEHYSTPPTT MLPRSAWWHITGSQNIABASSYAGEGYGAAQASSETDLLNRFI LLKPKPSQGDSSSEAKTPSQ |
| 6512 | 159 | 807 | FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSFGFGEPRDSGA EVPSSGSRATGCGERGVRGARQGRAPGSSIWRKEPRMVCTRKT TLVSTCVILSGMTNIIICLLYVGWVTNYIASVYVRGQEPAPDKKL BEDKGDTLKIERLDHLENIKQHIQEPAPKEAEAEPTDSS LFAHWGQELSPGRRVALKQFYGYGNAYLSDRPLDRP |
| 6513 | 2 | 756 | FVSPFPGFSLAQLNLIWQLTDTKQLVHSFAEGDQGSAYANRTA LFPDLLAQGNASLRLQVRVVADEGSFTCFVSIIRDFGSAAVSLQV AAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDQV GVPLTGNVTTSMANEQGLFDVHSILRVVLGANGTYSCLVRNPV LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGDQGSAYANRTALF PDLLAQGNASLRLQVRVVADEGSFTCFVSIIRDFGSAAVSLQVAA PYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDQGV PLTGNVTTSMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP EPGFSLAQLNLIWQLTDTKQLVHSFTEGR |
| 6514 | 985 | 302 | VGIPGFTISSAAEMEDLLDLDEELRYSLATSRKMGRRQQESA QAENHLNGKNSSLTLTGETSSAKLPRCROGGWAGDSVKASKFRR KASEIEDFRLRPQSLNGSDYGGDIPIDPLEVQEEDFVLQVA APPSIQIKRVMTYRDLNDLMKYSATQTLDEIDLKLLTKVLAP EHEVRERNPSWQDDVGDWDHFLTEVSSSVLTWDPLQTEKEDP AGQARHT |
| 6515 | 1345 | 305 | GRVGSRRRGAAPVGGCGAGSTQLEVSASASCGALGSADMNPIV VHGGGAGPISKDRKERVHGMVRAATVGYILREGGSADVAVEG AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLGAGVSA VQCIANPIKLARLVMEKTPHCFLLTDQGAQFAAAMGVPEIPGEK LVTERNKKRLEKEKHEKGAQKTDCCQKNLGTGVAVALDCKGNVAY ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL KVNLARLTLFHIEBQKTVEEAADLSLGYMKSRVKGLGGLIVVSK TGDWVAKWTSTSMWAAAKDGKLFHFGIDPDDTTITDLP |
| 6516 | 1 | 1402 | FRRLRYLGQDATAAARLDLRLTRGLQGYCPSATARQQVLVSALQQL KGRRSEHRNENQEMPYSTNKEILIGIMVGTAGISLLLLWYHKVR KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTFVPOERQLQI LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK ISPQHRARKRLPTIQSSATSNSSSEAESEGGYITANTDTTEEQS |

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|------------|--|--|--|
| | | | FPVPKAFNTRVEELNLDVLLQKVDHLRMSSESGKSESFELLRDHK EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA INRAPMNGHCHLWYAVLCGYVSEFEGQLQNKINYGHLFKEHLDIA IKLLPEEPFLYYLKGRCYTVSKLSWIEKKMAATLFGKIPSSTV QEALHNFLKAEELCPGYSNPNYMLAKCYTDLEENQNALKFCNTL ALLLPTVTKEDKEAQKEMQKIMTSLKR |
| 6517 | 3 | 1414 | GRVWGSSSSLNAMVYVRGHAEDYERWQRQARGWDYAHCLPYFR KAQGHHELGAARYRGADGRLRVSRGKTNHPLHCAFLEATQOAGYP LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA EAETLVSRVLFEGTRAVGVEYVKNQSHRAYASKEVILSGGAIN SPOLLMLSGIGNADDLKKLGI PVVCHLPGVGNLQDHLIYIQQ ACTRPTLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR SQPGVPHFDIQFHLFSPQVIDHGRVPTQGEAYQVHVGPMTGTSV GWLKLRANPDQHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRKADSAYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA EKAADIKQGPALWDDKDVVYKPRTLATQR |
| 6518 | 242 | 1098 | PAWNPGESEPTTRVPRARSFPLPPRPRRRRRHLLRAVPGPSR RHRERRRAPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN LCSKCFADFKQKQDDDSAPSTNSQSDLFSEETSDNNNTSIT TPTLSPSQQLPTELNVTSPSKEEGCPCTDTAHVSLITPTKRSC GTDQSSENEASPVKRPRLLENTSEETSRSKQSRRCFCQCQT KLELVQQLGSCRCGYVFCMLHRLPEQHDCTFDHMGGRGEEAIM KMKLDRKVGSRQCRIGEGCS |
| 6519 | 3 | 1113 | ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSL AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAAASANAKSRPKKREKERRRHGL GGAREAGGASREENGVEVKPLPRDKIKDKIKERDKEKEREKKKH VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKVKKKKKKKHK ENKRRKPKMYSKSIQITCSGLLTDVEDQAAGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLRLDTLEFKQLI HIEHQPNGGASVIHCLQ |
| 6520 | 3 | 1113 | ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSL AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLLPAAAAAASANAKSRPKKREKERRRHGL GGAREAGGASREENGVEVKPLPRDKIKDKIKERDKEKEREKKKH VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKVKKKKKKKHK ENKRRKPKMYSKSIQITCSGLLTDVEDQAAGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLRLDTLEFKQLI HIEHQPNGGASVIHCLQ |
| 6521 | 184 | 1798 | KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETTPPKSLAEGEEKEPEPDISSESVSTVEEQNE TPPATSSAEQPKGEPENBEKEENKSEETKKDEKQSKKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFLKKSGEKPLLGGSLMEYAIL AIAAMNBPKTCSTTALKKYVLENHPTNSNYQMHLKKTLOKCE KNGWMEQISGKGFSGTFLCFYPPSPGVLFPPKEPDDSRDEDE DEDESSEEDSEDEEPPKRRRLQKTPAKSPGKAASVKQSGSKPA PKVSAAQRGKARPLPKKAPPAKTPAKKTRPSSTVIKPSGGSS KKPAT SARKE |
| 6522 | 1042 | 391 | NKWLRPSPRSHRTPESGRVLSLFRLLPFPFGMALSGSTPAPCWEEED |

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|------------|--|--|---|
| | | | ECLDYVGMLSLHRMFVVGGLTECELELLAFLLEAPGAAGGLSRARSGLKLLLELERRGQCDESNRLRLGQLRLVLAHDLPLHLARKRRRPFVSPERYSGTSSSSSKRTEGSCRRRRQSSSSANSQQGSPPTKRQRRSRGRPSGGARRRRRGPPHPSSSQSPDPLPLKAK |
| 6523 | 2 | 1097 | ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNNDIVKQGYVKIRSRKLGIFRRCWLVFKKASSKGPRLLEKFPDEKAAYFRNFHKVTELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC KHLCECLGTRLNDISLGEPLDLAGVQREQNERFNVYLMPTFNLDIYGECTMQITHENIYLWDIHNKVKLVMPPLSSLRRYGRDSTWTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAEQHERLMLEMEQKARLQTSLTEPMTLSKISLPRSAWWHITRQNSVGEIYSLQGNHNRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLFMDTSTCKVVHDL |
| 6524 | 2 | 1097 | ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNNDIVKQGYVKIRSRKLGIFRRCWLVFKKASSKGPRLLEKFPDEKAAYFRNFHKVTELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC KHLCECLGTRLNDISLGEPLDLAGVQREQNERFNVYLMPTFNLDIYGECTMQITHENIYLWDIHNKVKLVMPPLSSLRRYGRDSTWTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAEQHERLMLEMEQKARLQTSLTEPMTLSKISLPRSAWWHITRQNSVGEIYSLQGNHNRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLFMDTSTCKVVHDL |
| 6525 | 1 | 1859 | GESPFSEBESIEFNPSSSGRSARTVSSNFCSDDTGWPSQSQSVSPVKTPSDAGNSPIGFCPSGDEGFTRKCKTIGMVGEISIQSSRYK KESKSGLVKPGSEADFSSSSSTGSIAPVHMSTAGSKRSSSRNRGPHGRSNGASSHKPGSSPSPREKDLLSMLCRNQLSPVNIHPSYAPSSPSSSNSGYSKGSDCSPIMRRSGRYMSCGENHGVPPNP EQYLTPLQQKEVTVRHLKTKLKESERLHERESEIIVELKSQLARMREDWIEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKKGIIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDSPEKSLTLNPPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTDLEFDEIVTATTESGDLELVHSTPGANVLELLPIVMQEEGSSVVVERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDSESDSMESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANRLMRELDFAACVEERLDGVIPLARGGVVRQYWSSFLVDLLAVAAPVVPVTLWAFSTQRGGTDVYNIGALLRGCCVVALHSLRRTAFRIKT |
| 6526 | 2 | 2034 | SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQOLEEAYSSGKGCN GRVVPDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKNKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIILHNP KLMVHYQPVAGSDDWGSTMEOGRPRTVKRGVENISVDIHCGEPLQIDHLVFFVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFKKAQENQQIGRVEFLPVNWHSPHISTGVVDLQRLTLP SINRLRHFTNDTILDVFFYNSPTYCQITVDTVASEMNRIYTLFLQRNPDFKGGVSIAGHSLGSLILFDILTQKDSLGDIDSEKGS LNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEI GIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQSVKYPRLIYKPEIFFAFGSPIGMFLTVRGLKRIDPNYRFPTCKGFFNIYHPDPVAYRIEPMVVPGVFEFPMPLIPHKKGRKRMHLELREGLTRMSMDLKNLLGSLRMAWKSFTRAPYALQASETPETEAEPESTSEKPSDVNTEETSVAVKEEVLPINVGMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLVLKEIYQQTQGIFFLDQPLQ |
| 6527 | 1 | 922 | GWVFLLSRIPLPSDACKIYKQGINIRLDTTLIDFTDMKQCRGDLSFIFNGDAAPSESFVLDNEQKVYQRIHHEESEMTEEEVDILMS SDIYSATLSTKSI SFTRAQTGWLFRDKTERVGNFLADFYLVNG |

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|------------|--|--|---|
| | | | LVLSESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRQSLTPPPQNTITWEEYISAENGKAPHLGRELVCESKKTFFKATIAMSQEFPLGIELLLNVLEVVPFKHFNKLREFVQMKLPPGFPVKLDIPVFPPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL |
| 6528 | 1 | 1073 | LTGPAAAEPRCAADAGMKRALGRRKGWLRRLRKLFLFCVLGLYIAIPPLIKLCPGIQAKLIPLNFVRVPYFIDLKKPQDQGLNHTCNYYLQPEEDVTIGVWHTVPAVWKNAGQKQDMWYEDALASSHPILLYLHGNAGTRGGDHRVELYKVLSSLYGHVVTFDYRGWGDVSGTPSERGMTYDALHVFWDWIKARSGDNVPYIWHGSLGTGVATNLVRLCERETTPDALILESPTNIREEAKSHPFVVIYRYPFGFDWFFLDPI TSSGIKFANDENVKHISCPILLHAEDDPVVPFQLGRKLYSIAAPARSFRDFKVQFVPFHSDLGYRHXYIKSPPELPRILREFLGKSEPEHQH |
| 6529 | 363 | 2215 | THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLFEGVEDESEFLKWFPCGNVNBQNVLSERELEAFSILQXSGKPILEGAALDEALKTKTSDLKTPRLDDKELEKLEDEVQTLKLKLNKIQRRNKCQLMASVTSHKSLRLNAKEEATKKLQSQGILNAMI TKISNELQALTDEVQTLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSEEQSTAALTLYTKKQFFQGIHEVVESSESQFFNFKIQTPSICDNQEILEERRLEMARQLAYICAOHQLIHLKASNSMKSSIKWAEESLSLSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPAVRENAQLLNMPVVKGDFDLQIAKQDYTTARQELVLNQLIKQKASFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEMLTDPVSQSQINPRNTIDTKDYSTRHLYQVLEGENKKELFLTHGNLEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRKNKDVMCLCDTL YQGGNQLLLSDQELTEQPHKVESQLNKLNLHLLTDILADVKTTRKTLANNKLHQMEREFVYVFLKDEDYLDKDIVENLETQSKIKAVSLED |
| 6530 | 128 | 2986 | GAHHGAIVQVHPLLPSSSTIMHDLCLVFPAPAKAVVYVSDIQELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA SPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQRINSAPQQIEVFPPRLMPRKVTLIGATMQVTSEGGPQPSNILLSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVIISQDLVQVEVLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPFSFGNAVPLTFHWSVTKRDVLDLGRGRHHEASIRLPSQYNFAMNV LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV VHVDEKGFSLAGSMIGTSTIEVIAQEPFGANQTIIVAVKVPVS YLRVMSGSPVLHTQNKALVAVPLGMTVTFTVHFHDNSGDVFAHSSVLNFATNRDDFVQIGKGTNTNTCVVRTVSVGLTLRLVWDAKH PGLSDFMPLPVLQAI SPELSGAMVVGDVLCATVLTSLLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYEVAGHLRTYKEVVV SVPQRIMARHLHPITQTSFQBATASKVIVAGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVDFPSPQDVFTVEPQFDTALG QYFCSITMHRITDKQRKHLMSKKTALVVSASLSSSHFSTEQVGA EVFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSGFWPSFITVTGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFFVDRRGPYPGASLFQHFLLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH |
| 6531 | 845 | 1425 | PSASIPPSASDPVPDIRTCHFLVEDPSVGCISGSEKCTISSSLCMVITIIYDVKVRFIIVRGCGQYISYRCQEKNTYFAEYWQA QCCQYDNCNSWSSPQLQSSLPBPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLNLSNLGLSFAELRRMYLFLNSGLLVLPQAGLLTPHPS |
| 6532 | 2 | 954 | AAGPPSEVVNQDSLFEPEPGPAPQVLLGPQGGPLIKGVAPPTL |

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|------------|--|--|---|
| | | | ITDSTGTHLVLTVTNKNHSPGLSRGSPQQPSSQPGSPAPAPSA QMDLEHPLQLPFGTPTSLKKKEPPGYEAMSQQPKQQENGSSSQ QMDLFDILIQSGEISADFKKEPSPSLPGKEKPSKPTVCWSPLAAQ PPSAELPQAAPPPPGSPSLPGRLED FLESSTGLPLLTSGHDGP EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSMTGL DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD LQLHWDSC |
| 6533 | 1798 | 373 | STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGIEG GAKLCSKLKAEKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES AENLEEVSVLHVFGYDTLGEKQTLVVDVANGGHTWVKAIGR KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQPPVQYSNPHII FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSSES ESDDEGPPELLQVTRVDRENILASVAFPTKIVDVCKRVNLDITT LITVVSALS YGGCHFI FKEKVLTEQAEQERKEQVLPQLEAFMKD KELFACESAVKDFQSILDTLGGPGERERATVLIKRVNVPDQPS ERALRLVASSKINSRSLTIFGTGDTLKAITMTANS GFVRAANNQ GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH |
| 6534 | 47 | 596 | KATRFISAAPVVLNKGQVSPAKLPHTSWWSLQTLSPFLSGDLA EKS LQCFCPSAMLELIPLLGIHFVLR TARASVTQPDIIHITVS EGASLELR CNYSYGATPYLFWMERTVEEAFILVCLKPWRVASS LEKKEKEDES FQLLLGSRYNVLKAHCLLP LIRWLTS GDSLLSAQ PHCPQGL |
| 6535 | 250 | 964 | LIKTFFRDVAIQRDLLPKEKNLETLTLTAPLEIDKAFSSHARLS ADATLLTSGTTATVALLRDLGVASVGDRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHADDSPVLVLTDDGINFMVNSQEIW DFNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINF SFRS FASSGRWA |
| 6536 | 242 | 1174 | SLVKEMTNQYGI LFKQEQAHDDAIWSVAVGTNKKENSETVVTGS LDDLVKVKWRDERLDLQWSLEGHQLGVVSDIISHTLP IAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYS PDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMP IRS LTFSPDSQLLV TASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCDDTHFVSSSSDKSVKVV DVGTRTCVHTFFDHQDQVWGVKYNNGSKIVSVGDDQEIHIYDC PI |
| 6537 | 1638 | 921 | NRFNPPPTQGPDP SLVYRPD VDPEVAKDKASFRNYTSGPLLD RV FTTYKLMHTHTQTVDFVRSKHAQFGGFSYKMTVMEAVDLLDGLV DESDDVDVFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALPGEPQWAVVGDTFPVGC RPQASVVFCDSTFQDNPDLDQPRY STELGMYQPHCGLDRLVMSWGHGDEARGGQWGGGGRWGTVG GGG AEAVPAGDTLSPQSTCTR |
| 6538 | 3345 | 2412 | PYLYDFLDALITCOTAPEEAFIKLDGLAGMLTEQLRRLTKQVQB ARHNRDDEAIKAVNEYDETMEXYIPVLMQAQKIYWNLENYPMV EKI FRKSV EFCNDHDVWKLNVAVLFM QENKYKEAIGFYEP IVK KHYDNI LNVSAILANLCVSYIMTSQNEKAEELMRKIEKEEBQL SYDDPNRKMVHLCIVNLVIGTLYCAKGNVEFGISRVIKSLPEYN KKLGTDTWYAKRCFLSLENMSKHMIVIHDSVIEQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGNKNTVTDESRLKALIYEIIGW NK |
| 6539 | 218 | 339 | FLGAASPHPHFSS LAPHPDQPEFTPVQDELEAMELWGPV |
| 6540 | 3 | 391 | LERLWLLLRRRPEDAMAECP TLGEAVTDHEDRLWAWK FVYLDE KQHAWLPLTIEIKDRLQLRVLLRRREDVVLGRMPTPTQIGPSLLP IMWQLYPDGRYSSDSSFWRVLYHIKIDGVEDMLLELPDD |

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|------------|--|--|---|
| 6541 | 1165 | 536 | RTLVRRLMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFF RFEGGRKPDSDGNREPFGPGHEHFRDTPRDPHPPHGHSPASRE RSSSLQGMASLPPRKRPHWDGPGTSEHREMEAPGGPSEDGGRG KGRGGPGPAQRVPKSGRSSLDGEHHDGYHREDFGPGPPGSGTP SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR |
| 6542 | 3 | 3775 | SWPRGRGETGGHFGALRTRTMQKSVRYNEGHALYLAFLARKEGT KRGFLSKKTAESRWHEKWFALYQNVLFYFEGEQSCRPAAGMYLL EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGEHGGKPLE LRCEEEQDQKEWMAIHQASYADILIEREVLQKQYIHLVQIVET EKIAANQLRHQLEDQDTEIERLKSEI IALNKT KERM RP YQSNQE DEDPDIKKIKKQSFMRGWLCCRKWKTIQDYICSPHAESMRKR NQIVFTMVEASEYVHQLYLIVNGFLRPLRMAASSKKPPISHDD VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM LNIYQEFVRNHQYSLQVLNCKQNRDFDKLLKQYEANPACEGRM LETFTLYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSTQTFIRQG SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLETKHFLICTRS SGGKLHLLKTGGVLSLIDCTLIEEPDASDDSKSGSQVFGHLDF KIVVEPPDRAAFTVLLAPSRQEKAAWMSDISQVDNIRCNGLM TIVFEENSKVTVPHEIKSDARLHKDDTDICFSLTNSCKVPQIR YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSLSD TYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP PPLAVSRTSSPVRARKLSLTSPNSKIGALDLTTSSSPTTTTQS PAASPPPHGTQIPLDLSRGLSSPEQSPGTVEENVNDNPRVDLCKN LKRSIQKAVLESAPADRAGVESSPAADTTLSPCRSPSTPRHLR YRQPGGQTADNAHCSVSPASAFIAATAAGHGSPPGFNNTERTC DKEFIIRRTATNRVLNVLNRHWSKHAQDFELNNELKMNVLNLE EVLRLDPLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC MKAECFESLSAMELAEQITLLDHVIFRSIYBEFLGQGWMLDK NERTPYIMKTSQHFNDSNLVASQIMNYADVSSRANAIEKWWAV ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKQTKALMD KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMVLTDLAFIEBGT PNFTEEGLVNFPSKMRMISHIIREIRQFQQTSYRIDHQPQVAYL LDKDLI IDEDTLYELSLKIEPLPA |
| 6543 | 1857 | 950 | FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLGSGVSLAGGFVG TPADLVNVRMNDVKLPQGGRRNYAHALDGLYRVAREGLRLRF SGATMASSRGALVTGQLSCYDQAKQLVLTGYLSDNIFTHFVA SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCVETAKLGP LAFYKGLVPAGIRLIPHTVLTFFVLEQLRKNFGIKVPS |
| 6544 | 630 | 79 | PSPCFIRSLDGGQPMWAGLEAWLSQNFSLHQPSRVVRRASIS EPSTDPEPRTLNPSPAGWFVQQHPELELMSSFRERFGRNWLQY RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPPPPQBEAR GPQES PQKMSEEVRAEPQEEEE3KEGKEEKEEGEMAPLPEAHIG EGKQKECP |
| 6545 | 176 | 560 | PPHSHAALLPAAMTPLLTLILVLMGLPLAQAALDCHVCAYNGDN CFNPMRCPAMVAYCMTTRTYTPTRMKVS KSCVPRCFETVYDGY SKHASTTSCCQYDLNCTGLATPATLALAPIILLATLWGLL |
| 6546 | 1657 | 364 | HLLNGLDEVAFFVADLGAIVRKHFCLKCLPRVRFYAVKCNCS SPGVLKVLQQLGLGFS CANKAEMELVQHIGIPASKIICANPCQ IAQKYAAKHGIIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS HSLSCLSLKFGVSLKSCRHLENAKKHHEVVGVSFPHIGSGCPD PQAYAQSIADARLVFEMGTGLGHKMHVLDLGGGFPGTGAKVRF EEIASVINSALDLYFPEGCGVDIFAELEGYYVTSAPTVAVSIIA KKEVLDDQPGREEENGSTSKTIVYHLDEGVYGFNSVLFNDNICP |

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|------------|--|--|---|
| | | | TPILQKKPSTEQPLYSSSLWGPVAVDGCDCVAEGLWLPQLHVGDW LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM |
| 6547 | 1 | 541 | LHASKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLPLVLL PPLAAAAAGPNRCDTIYQGFACELIRLGDSMRGGELETICRSW NDFHACASQVLSGCPEEAAVWESLQQEAPAPRPNLHTLCGA PVHVRERGTGSETNQETLRATAPALPMAPPLLAALALAYLL RPLA |
| 6548 | 2 | 219 | FVSRLSVRDVRFPFTFLGGHGDAMHTDDPYSAAYVPIETDAEDG IKGCGITFTLGKGTVEVGELKILSRFQNA |
| 6549 | 73 | 1490 | ETGRVCEADARPACGSRSRRRRKEAAGIPTPSPSSSSPTSSRPA ARAFASKAPARLSRPRAREPPDPGRRIYQEEIIQARKHKLIKMC SSVAAKLWFLTDRIREDYPQKEILRALKAKCCEELDFRAVVM DEVVLTIEQGNLGLRINGELITAYPQVVVVVPTPWVQSDSDIT VLRHLEKMGCRMLNRPQAILNCVNKFWTQFELAGHGVPDPDTS YGGHENFAKMIDEAEVLEFPMVVKNTGRHGRKAVFLARDKHHLA DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST DGRMQSNCSLGGVCMMSLSEQKQLAIQVSNILGMDVCGIDLL MKDDGSFCVCEANANVGFIADFACNLVDVAGIADYAASLLPSG RLTRRMSLLSVVSTASETSEPELGPASTAVDNMSASSSSVSDS PESTERELLTKLPGGLFMNQLLANEIKLLVD |
| 6550 | 2293 | 922 | FRVSRDGPADCGIEQMGLAMEHGGSYARAGSSRGWCWYLRVFF LRVSLIQFLIILGLVLFMVGNVHVSTESNLQATERRAEGLYSQ LLGLTASQSNLTKEINFTTRAKDAIMQMWLNARDLDRINASFRC QCGDRVIYTNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEQVECVKTR E LQHQRQLAKEQLQKVQALCLPLDKDKFEMDLRLNLRDSSIIPRS LDNLGYNLYHPLGSELASIRACDHMPMSLSSKVEELARSLRAD IERVARENSDLQOKLEAQOGLRASQEAQKQVEKEAQAREAKLQ AECSRQTQLALEEKAVLRKERDNLAKELEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG |
| 6551 | 157 | 748 | IQPPDPNRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIENNFIKMAKEKLAQKMSNKENREAHLAAMLERLQ EKDKHAEVVRKNKELKEEASR |
| 6552 | 157 | 748 | IQPPDPNRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIENNFIKMAKEKLAQKMSNKENREAHLAAMLERLQ EKDKHAEVVRKNKELKEEASR |
| 6553 | 2 | 1807 | FVWSKMAAHLISYGRVNLNVLREAVRRELREFLDKAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFLLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTTRDFHILFVPRRSLCEQRLKD LGVLGSFIHREYSLDLIPFDGDLMSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVLLTPLATQLTYEGLIDEIYGIONS YVKLPPEKFAPKKQGGDKLPTEAKKLQNSAERLYAEIRDKN FNAVGSVLSKKAKIIISAAFEERHNAKTVEIKQFVSQPLPHMQAA RGSANHTSIAELIKDVTTSDDFFDKLTVEQEFMSGIDTDKVN YIEDCIAQKHSIKVLRVLVCLQSVCSGLKQKVLDYKREILQT YGYEHILT LHNLEKAGLLKPTGGNNNYPTIRKTLRLWMDVNE QNPTDISVYSGYAPLSVRLAQLLSRPGWRSIEEVLRIPLGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL EDGTEYVIATTKLNGTWSWIEALMEKPF |

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|------------|--|--|---|
| 6554 | 119 | 1244 | FEMGSQVSVESGALHVIVVGGGFGGIAAASQLQALNVPFMLVDM KDSFHHNVAALRASVETGFAKKTFFISYSVTFKDNFRQGLVVGID LKNQMVLQGGGEALPFSHLILATGSTGPPPGKFNEVSSQQAIIQ AYEDMVRQVQSRFIVVVGGSAGVEMAABIKTEYPEKEVTLIH SQVALADKELLPSVRQEVKEILLRKGVLQLLSERVSNLEELPLN EYREYIKVQTDKGTEVATNLVILCTGIIKINSSAYRKAFESRLAS SGALRVNEHLQVEGHSNVYAIGDCADVTPKMAAYLAGLHANIAV ANIVSVKQRPLOAYKPGALTFLLSMGRNDGVGQISGFYVGRIM VRLTKSRDLFVSTSWKTMROSPP |
| 6555 | 1552 | 498 | IHMALLRKINQVLLFLIVTLCVILYKKVHKGTVPKNDADDESE TPEELEEEIPVVICAAAGRMGATMAAINSISNTDANILFYVVG LRNTLTRIRKWIHESKLRINFKIVEFNPMGLKGIKIRPDSSRPE LLQPLNFVRFYLPPLIHQHEKVIYLDLDDVIVQGDIIQELYDTTLA LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIDKLG ISPTCSFNPGVIVANMTWKHQRITKQLEKWMQKNVEENLYSS SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL QEAKLLHWNGRHKPWPDPSPVHNDLWESWFPDPAGIFKLNHHS |
| 6556 | 241 | 1449 | ASLCKGCFVTHVLVILPISLQSPPTFGFLDDIGVLVRGHRVI PAALKAFAFRRLVNSQGGQLRVVVFVTNAGNILQHSKAQELSALLG CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR NVVTVDLRLMAFPLDMVDLERRLKTTPLRNDFPRIEGVLLLG EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPLPVLASNMDLL WMAEAKMPRFGHGTFLCLETIYQKVTGKELRYEGLMGKPSILT YQYAEGLIRROAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY LQKATHDGAPELGAGGTROQQPSASQSCISILVCTGVYNPRNPQ STEPVLGGGEPPFHGHRDLCPSPGLMEASHVVDVNEAVQLVFR KEGWALE |
| 6557 | 2598 | 1534 | RMCGRTSCHLPRDVLTRACAYQDRRGQRLPEWRDPDKYCFPSYN KSPQSNPVLRLSLHFEKDADSSERIAPMRWGLVPSWFKESDP SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT MAGIFDCWEPPPEGGDVLYSYTIITVDSCKGLSDIHRMPAILDG BEAVSKWLDGFEVSTQEALKLIHPTENITFHAVSSVNNRNT PECLAPVDLVVKELRASGSSQRMQLQWLATKSPKKEDSKTPQKE ESDVPQWSSQFLQKSPLPTRKGTAGLLEQWLKREKEEPEVAKRP YSQ |
| 6558 | 21 | 1138 | FHGRRRGGGRKMELGSCLEGGREAAEEGEPEVKKRRLLCVEFAS VASCDAAVAQCFLAENDWEMERALSIFYEPPEESALERPETI SEPPTYVDLTNEETDSTTSKISPSSEDTOQENGSMFSLITWNID GLDLNNLSERARGVCSYLALYSPDVIIFLQEVIPPYYSYLKKRSS NYEIIITGHEEGYFTAIMLKSRVKKLSQEIIPFPSTKMMRNLLC VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMLKMQEAPES ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTW DQMNNSNLGITAAKLRFDRIFFRAAAEERGHIPRSLDLLGLEKL DCGRFPDSDHWGLLCNLDIIL |
| 6559 | 3 | 364 | GPESGLPTRPKKLANQTPIAMDCASRSCSVPTGPATTICSS DKSCRCGVCPLSTCPHTVWLEPTCCDNCPPCHIPQPCVPTCF LLNSCQPTPGLETNLNLTFTQPCCEPCLPRGC |
| 6560 | 3 | 1435 | TATSGGIWLRKWKCHWRPLPQSCVGTGGGLQVRDTSRIAGK GVDHTKMSLHGASGGHERSDRRSSDRSDSSHERTESQLTPC IRNVTSPTRQHHVEREKDHSSSRPSSPRPKASPNGISISSAGNS SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSEVTLIVD NTRFVVDPSIFTAQPNMLGRMFGSGREHNFTRPNEKGEYEVAB GIGSTVFRAILDYKGTGIRCPDGISIPELREACDYLCISFEYS TIKCRDLSALMHLSNDGARRQFEFYLEEMILPLMVASAQSGER ECHIVVLTDDDDVDWDEEYPPQMGEYSQIIYSTKLRYFFKXIE |

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|------------|--|--|--|
| | | | NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKRPGGRBEVTYN YVQRPFIRMSWEKEEGKSRHVDFOCVKSKSITNAAAAADIPOD QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPM |
| 6561 | 3 | 1086 | PGRRFRKKESSSRWFADCLLGLRGPASSLLSPFSPSPWFSHS PCPMAALTDLSFMYRWFKNLGNLVGNLSEKVFITGCDSGFGNLL AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNELTKDDFVKV INVNLVGLIEVTLHMLPMVKRARGRVNMSSSGGRVAVIGGGYC VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES RMRKLERLQETRDSYGEDYFRIYTDKLNIMQVAEPVRVDVI NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY LPRPADSV |
| 6562 | 1 | 1562 | MSTLYDIRAHKAQLRRFFASSDSNKALEQRRTLHTPKLEHLDRV LYEWFGLGRSEGVPSGPMLEKAKDFYEQMQLTEPCVFSGGWL WRFKARHGIKKLDASSEKQADHQAEEQFCAPFRSLAAEHGLSA EQVYNADETGLFWRCPLNPTPEGGAFFGPKQGDRLTVLMCANA TGSRLKPLAIGKCSGPRAFKGIOHLEPVAYKAQGNAWVDKEIFS DWFHHIFVPSVREHFRITGLPEDSKAVLLLDSSRAHPQEAELVS SNVFTIFLPASVASLVQPMEQGIRRDFFMRNFINPPVPLQGPBAR YNNMDAIFSVACAWNAVPSHVFRARWRKLWPSVAFAGSSSEEE LEAECEFFVKPHNKSFAHILELVKEGSSCPQLRQQAASWGVAG REAEGGRPPAATSPAENVVSSBKTPKADQDGRGDPGEGEVVAWE QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQVRRRR GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN |
| 6563 | 1319 | 2694 | LARPAQVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA HEHPLPCDQMFWRQMGHLMVBANSRGVVMGIGYDHTAWVYTG GYGGGCFQGLASSTSNITYQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMWDASGLQECTKAGTKPPSLQWAVVSDWVDFSVFPG TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARCKLVTSGPWL EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS ELNPAGSSWLHVGTQDPFASISIGACYQVWAVARDGSAFYRGSV YPSQPADDCWYHIPSPRQRLKQVSAGQTSVYALDENGNLWYRQ GTFPSYPQSSWEHVSNNVCRVSVGLDQVWVIANKVQSSHLS RGTVCHRTGVQPEPKGHGWDYIGGGWDHISVRANATRAPRSS SQEQEPSAPPEAHGPVCC |
| 6564 | 1 | 975 | APGSCALWSYCGRGWSRAMRGCOLLGLRSSWPGDLLSARLLSQE KRAETHFGFETVSEEEKGKVYQVFESVAKKYDVMNDMMSLGI HRVWKDILLWKMHPLPGTQLLDVAGGTGDIARFLNYVQSQHQR KQKRLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCINKEMLK VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTLAFGIRNV THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKMDIEDAGFHKVT YESLTSGIVAIHSGFKL |
| 6565 | 1464 | 999 | RSAVANGLTKRRMGLKNGRYISLILAVQIAYLVQAVRAAGKCD AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTCTYWFEDFHSCT VTALTDQEGAKDMWDKLRKESKNLNIQGSFLFCGSGNGAAGS LLPAFPVLLVLSLAALATWLSF |
| 6566 | 3 | 1385 | KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLPFGAWAQG HVPFGCSQGLNPLYNNLCDSGAWGIVLEAVAGAGIVTTFVLT ILVASLPFVQDTKKRSLGTQVFFLLGTGLFLCLVFACVEKPDF STCASRRFLFGLVFAICFSLAAHVFAFNFLARKNHGPRGWVIF TVALLTLVEVINTENLIIITLVRSGEQGGPQGNSSAGWAVASP CAIANMDFVMALIYVMLLLGAFGLAWPALCGRYKRWKRGVVFV LLTTATSVAIWVWVIMYTYGNKQHNSTWDDPTLALALANAW AFVLFYVIVEVSQVTKSSPEQSYQGDMPYTRGVGYETILKEQKG QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTMAL |

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|------------|--|--|--|
| | | | MHKVPSEGAIDYIILPRATANSQVMGSANSTLRAEDMYSAQSHQA ATPPKDGKNSQVFRNPYVWD |
| 6567 | 125 | 863 | TKRSNLKAYACSIHHIRTSYVFNVDSSQTNVPLLQACIDGDFN YSKRLLSESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD LLATDYQGNLTALHLGCHVDTIQPLVSNGLKIDICNHQGATPLVL AKRRGVNKDVIRLLESLEEVEKGFNRGTHSKLETMQTAESESA MESHSLLNPNLQQGEGVLSFRFTWQEFVEDLGFWRVLLIFVI ALLSLGIAYVSVGVLPFVENQPELVH |
| 6568 | 3 | 1183 | HASDRLLVLPDNYSHFSQASANLQGPSRTTELPHPTLASISSPM LEGAELFYNVHDGYLEGLVRGCKASLLTQQDYINLVQCETLEDL KIHLLQTTDYGNFANHTNPLTVSKIDTEMKRRLCGEFYFRNHS LEPLSTFLTYMTCSYIMIDNVILLMNGALQKKSVKELGKCHPLG RFTMEAVNIAETPSDLFNAILIETPLAPFPQDCMSENALDELN IELLRNKLYKSYLEAFYKFCNKGDVTAEVMCPILEFEADRRAF IITLNSFGTELSKEDRETYPTFGKLYPEGLRLLAQAEFDQMK NVADHYGVYKPLFEAVGSGGKTLEDVFYEREVQMNVLAFNRQF HYGVFYAYVKLEKEIRNIVWIAECISQRHRTKINSYIPIL |
| 6569 | 205 | 1532 | RRRGFQRLGHRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDP RMSWLFPLTKSASSAAGSPGGLTSLQOQKQRLIESLRNHS AEIQKDVEYRLPFTINNLINILLPPQFPQEKPVISVYPPIR HHLMDKQGVYVTSPLVNNFTMHSGLGKIIQSLLEDFWKNPPVLA PTSTAPPYLYSNPSGMSPYASQGFPLPPYPPQEAANSITSLV ADTVSSSTTSHTAKPAAPSGVLSNLPLIPTVDASIPTSQNG FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLLEQFLTLPQLK QIITDKDDLKVSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTFEKKMQRQHELESSESASALQARLKVAHEAEESDNIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAAMHSQFHA PL |
| 6570 | 330 | 1304 | ARLFRLTFLREGFLYVLLSHWVFGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPILPHPSLQLTINYSFLQAVNTFPATVDHLQ LYGLSAVQTMHMHNTLGYPNVHEITRSTITEMAAQGLVDARF PPPALPFTTHLFHPKQGAIAHVLPALHKDRPRDFANLAVAATQ EDPFKMGDLKSLSPGLGSPISGLSKLTPDRKPSRGRPLPSKTKKE FICKFCGRHFTKSYNLLIHERHTDERPYTCDICHKAFFRRQDHL RDHRYIHSKEKPFKCQECGKFCQSRTLAVHKTLLHMQTSSTPTAA SSAAKCSGETVICGGT |
| 6571 | 169 | 656 | APDMNRKKLQKLTDTLTKNCKHLFRGFDKNDGCVNVLEWIGHL SLFLRGSLEEKMKYCFEVDLNGDGFISKEEMFHLKNLLKQP SEBDPDEGIDKLVETLKKMDHDHDKLSFADYRLAVREETLLL EAFGPCLPDPKSKMEFEAQVFKDPNEFNDM |
| 6572 | 49 | 1646 | TPERAQPGALLGAAGCCVCGGRWWRPSHERGYFSSAKMGSKRRN LSCSERHQKLVDNBYCKKLHVQALKNVNSQIRNQMVQENENDNV QRKQFLRLQNEQFELDMEEAIQAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQVRENSIELRELEKLLKAAVMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQBAEQLLKEKLMIDEIVRKIYBED QLEKQKLEKMNAMRRYIEEFQKEQALWRKKREEMEEENRKII EFANMQQREEDRMKVQENEEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAELKLRKQKEMKQDFEEQMA LKLVLQAAKEEENFRKTMKFAEDDRIELMNAQKQRMKQLE HRAVEKLIERRQOFLADKQRELEEWQLQORRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK |
| 6573 | 767 | 275 | GGGGESQSFRAGDQTRTPATDCLMYLQGPRLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELQORNILKPRNEQEEQEEKREIKRRL TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR |

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|------------|--|--|--|
| 6574 | 204 | 1159 | <p>LTAAADKVSRGECWRVGGRTVCWVSLGSPLGSV</p> <p>LESSVPVSVGVFWACGVSWTGAAGLQDGLSDTMARNAEKAMTA LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRIIGEISK KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY KVGPKMLDHEGKEVPGNRYKYFGAAKDLPGVRELFEKEPLPP PRKTRAEMLKAIDFEYGYLDEDDGVIVPLEQYEEKLRAELVE KWKAEERARLARGEKEEEEEEEINIYAVTEESDEEGSQEKG GDDSQQKFIAHVPVPSQOEIEEALVRRKMKMELLQKYASETLQAQ SEEARLLGY</p> |
| 6575 | 117 | 820 | <p>SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFFPPFPFP ASPERQDGEGETEPDEESGNGAPVPPPKRTVTKRNIPKLDARLI SERGLPALRHVFDKAKFKGKGHEADLKMLIRHMEHWAHRLFPK LQFEDFIDRVEYLGSKKEVQTCCLKRIRLDLPILHEDFVSNNDDEV AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQRIER NKQLALERRQAKLP</p> |
| 6576 | 1 | 1060 | <p>PEPQALVGQKRGALRLRLVARLVLTVSAPAEVRRRVLRLPVLWMD RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR GFLLPNLPVCFSSAFTQGWGSRRRWVTPAGRPFDFHLLRTYGDV VVPVANCQVQYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGL YLKDNHLCRDFPVEDVFTLPVYFSSDWLNEFDALDLDVDDYRFVY AGPAGSWSPPHADIFRSFSWSVNVCGRKKWLLFPFGQEEALRDR HGNLPYDVTSPALCDTHLHPRNQLAGPPLBITQEAGEMVFPVPSG WHQVHNLVMCCFSCPLSGAFIQEDGSTTSPLSQPELGWNGVAH G</p> |
| 6577 | 2271 | 987 | <p>SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKDYPSNTTSS TSNSGNETSGSSTIGETSNRSRDRDRYRRNRNSRSRSPGRQCHRR RSRWDRRHGESRSRDRHREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV KGVDRVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKNGGPMRLYVGSLLHFNITD MLRGI FEPFGKIDNIVLMKDSDTGRSKGYGFI TFSDEECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLABGAGIQLPSTAAAAAQAALQALNGAVPLGA LNPAALTALSPALNLASQCLQLSSSLTPQTM</p> |
| 6578 | 377 | 1489 | <p>PSSSATMNRAPLKRATILHMAITGASDPSAAEANGKEPFLRLRA LQIALVVSLEYWVTSISMVFLNKYLLDPSLRDLTPIFVTIFYQCL VTLLCKGLSALAACCPGAVDFPSLRDLRLVARSVLPLSVVFIG MITFNNLCLKYGVAFYVNGRSLTTVFNVLLSYLLKQTTSFYA LLTCGIIIGGFVLGVDQEGAETLSWLGTVPGLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYEETKSFLWNTSNMMVLGGSSAYTNVRGWEMK KTPEEPSPKDSEKSAMGV</p> |
| 6579 | 2 | 711 | <p>RPRRVWYPELRELSAAAPRWSHRTAPGIMVIFYTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRHLKGENI EDI PKEVLMDCALVKANS IQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIIVTBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEMKKREMDLRYSYSSLMKV ENMSSNQDGNDSDEFM</p> |
| 6580 | 62 | 1571 | <p>LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEGKYLPSLEMFRRQFRQFGYHDTGP PREALSQRLVLCCEWLRLPEIHTKEQILELLVLEQFLTILPQELQ AWVQEHCPESAERAATLLEDLERELDEPGHQVSTPPNEQKPVWE KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA QDPRKVRDCRLSTQHEESADEQKGSAAEGLKGDIIISVIANKPE ASLERQCVNLNEKGTKPPLQEQAGSKKGRESVPTKPTPGERRYI</p> |

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|------------|--|--|---|
| | | | CAECGKAFSNSSNLTKRRRTHTGKPYVCTKCGKAFSHSSNLTTHYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEAPYQCKDCGKAFSGKGSIRHYRIHTGKPYQCNECGKSFSQHAGLSSHQRLHTGKPYKCKCEGKAFNHSSNFNKHRIHTGKPYWCHHCCKTFC SKSLSKKHQRVHTGEGEAP |
| 6581 | 228 | 476 | RVFLKDLSTPMASNNASTIAQARKLVEQLKMEANIDRIKVSKAADLMAYCEAHAKEDPLLTVPASENPFREKKFFCAIL |
| 6582 | 1428 | 718 | CFTTKTHCSFVSPYLSPLVLRKELESLENEGQVHTSSFIN QHP IIFWTLVWYFRRLDLPNLPGILITSEHCNEGQLPLSSLS QDSKLVYIQLLDNINLHQEPREPLYVSWRNFNSEKSSLLSEE QQETSTLVETIRQSIQHNNVLKPINLLSQMKPGMKRQRSYLYRE ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP PSASVEWCRKCGAPLI |
| 6583 | 487 | 41 | RIFMSTSGRLRWCTWRPATALWSASLRGLTSSMHPSPRSISLP LSMMLSPSPNTRGLSPALFRSPDSEHATSCPRHLHWRCRAPL RSPSPGLRLQVLRPSPLHVHTHNSGKEVLGLQVQSRSGTGPAC SQAGSGAVQGGNWCIF |
| 6584 | 189 | 1750 | PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN FAT WNQARLERDLSNKKIYQEEEMPESGAGSEFNRLREBARCKYGV LKKEFRPEDQPWLLRVNGKSGRKFKGIKKGVTEINTSYIIF TQ CPDGAFAFPVHNWYNFTPLARHRTLTAEEAEWERRNKVLNH FSI MQRRRLKDQDQDEDEEEKEKRRRKASELRIDHLEDDLEMS SDASDASGEEGGRVPAKAKKAPLAKGGRKKKKKGSDDAEFDS DDGDFEGQEVDMYSDGSSSSQEEPESEKAKAPQEEGPKGVDEQS DSSESEEEKPPEEDKEEEEEKAPTQEKRRKDSSESSESSE ESDIDSEASSAFFMAKKKTPPKRERKPSGSSSRGNSRPGTSAE GGSTSSSTLRAAASKLEQGRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE |
| 6585 | 3 | 1678 | GPINRSRIDDFVGGDPRAEASCSVLHSPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKNLNVITVGRGPILLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVDRPRGFVAVFYTEDGNWDL VGNNTPIFFIRDPILFSPFIHSQKRNPQTHLKDPPDMVWDFWSLR PESLHQVSFLFSDRGI PDGHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYP SW TFYIQVMTFNQAEFFPNPFDLTKVWPHKDYPLIPVGKLVNRRN PVNYFAVEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLH IPVNCOPYRVRVANYQRDGPMDQDQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLINE EQRRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL |
| 6586 | 32 | 804 | PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNRGRGSSQAGG SGAGQYGSDDQHHLGSAGGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHTVFKTYISPWERAMGVDPQQKXELGIDLLA YGAKAELPKYKSFNRTAMPYGGYKASKRMTFQMPKV |
| 6587 | 75 | 1117 | RRVPSLGKMEPCWDGENDIETPYGLLHVIRGSPKGNRPAILTY HDVGLNHLKCFNTFFNFEDMQEITKHFFVCHVDAPGQVQV GASQF PQGYQFPSMEQLAAMLPSVVOHFGFKYVIGVIGVAGAYVLAKFA LIFFPDLVEGLVLVNIIDPNGKWIDWAATKLSGLTSTLPDVTLSH LFSQEEHLVNNTLVQSYRQQIGNVVNQNANLQLFWNMYNSRRDL D INRPGTVPNAKTLRCPVMLVVGDNAPAEEDGVVECNKLDPTTTT FLKMADSGGLPQVTQPGKLTFAFKYFLQGMGYMPSASMTRLARS RTASLTSASSVDGSRPQACTHSESSEGLQGVNHTMEVSC |

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|------------|--|--|--|
| 6588 | 137 | 501 | LGLOAQLLELRNNYQLSDELKNGVELTSRQKVAYLDKEFSK AQKALS KSKKAQEVEVLLSENEMLQAKLHSEEDFRLQNSTLMA EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP |
| 6589 | 2 | 1405 | RPWGSAMATFSRQEFFQQLLQGCCLLPTAQOGLDQIWLILAICLA CRLWLRLGLPSYLYKHASTVAGGFPSLYHFFQLHMVWVLLSLLC YLVLFLCRHSSHRGVFLSVTILYLLMGEMHMDVTVTWHKMRGA QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGITVFGPW ISFHSYLAQVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL PPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV TSWNLPMYSYWLNNYVFNALRLGTFSAVLVTYAASALLHGFSFH LAALLSLAFITYVEHVLRLRLARILSACVLSKRCPPDCSHQHR LGLGVRALNLLFGALAI FHLAYLGLSLFDVDDTTBEQGYGMAY TVHKWSELWSASHWVTFGCWIFRYRLIG |
| 6590 | 2177 | 656 | VRAYEHVLSLLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN GSLSLDDFRNTQKRGESEFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFEDPSSERKEKKERIPVFCIDVERNDRAVGHEPEHWSVYR RYLEFFVLESKLTEFHGAFFDAQLPSKRIIGPKNYEFLKSKREE FQBYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPFIMNFINSCEPKPKPSRPELTIL SPTSENNKKLFNDLFKNANRAENTERKQONQYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYYVLLDI VIQELFPELNKVQKEVTSVTSWM |
| 6591 | 2177 | 656 | VRAYEHVLSLLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN GSLSLDDFRNTQKRGESEFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFEDPSSERKEKKERIPVFCIDVERNDRAVGHEPEHWSVYR RYLEFFVLESKLTEFHGAFFDAQLPSKRIIGPKNYEFLKSKREE FQBYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPFIMNFINSCEPKPKPSRPELTIL SPTSENNKKLFNDLFKNANRAENTERKQONQYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYYVLLDI VIQELFPELNKVQKEVTSVTSWM |
| 6592 | 3 | 1861 | APFPLGSTISSGSMIDANLKLQBAEQRLKAIVAEKFAIATKEG DLQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAENLLMV LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNLMRNS TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISDFEVGDS MASEEVKQEHQKCLDKLLNCLLSCTMQELIGLYVTMEEFMRE TVNKAVALDTYEGQQLTSSMVDVFIIVKCCIGRALSSSIDCL CAMINLATTELESDFRDVLCNKLRMGFATTQDIQGVTSVAVN IMHSSLQQKPDTKGIESTDCAKMSFLVTLNNVEVCSENISTLK KTLES DCTKLFSGIGGEQAQAFDSCLSDLAAVSNKFRDLLQE GLTELNSTAIKPVQWPWINSFFSVSHNIEEEFNDEYANDPWVQ QFILNLEQQMAEFKASLSPVIYDSLTLGLMTSLVAVELEKVVLS TFNRLGGLQFDKELRSLIAYLTVTWTWTRDKFARLSQMATILN LERVTEILDYWPNSGPLTWRLTPAEVRQVLAALRIDFRSEDIKR LRL |
| 6593 | 3 | 1837 | EAFSAGSRRRRLALQRGVLLGGYCPCCRRRGRLLVLLLLVR RGGBGGGRGRGDKRRRRQARRRRRPEAEARGGKMADVLSVL RQYNIQKKEIVVKGEVIFGEFSWPKNVKTNVYVWGTGKEGQPR |

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|------------|--|--|---|
| | | | EYTLDSILFLLNNVHLSHPVYVRRRAATENIPVVRPDRKDLLG YLNGEASTSASIDRSAPLEIGLQRSTQVKRAAEVLAEAKKPRI EDEBCVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA IKAKIMAKKRSTIKTDLDDITALKQRSFVDAEVDVTRDIVSRE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRFAPN AAPVDPTLRTKQIPAAAYNRYDQERFKGKEETEGFKIDTMTGYH GMTLKSVTGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIPAAATSLITMLNAKDLQDLKFVPSDEKKKQGCORENETL IQRRKQMQPGGTASVTVPYRVVDQPLKMPQDWDVAVFVQ GPAWQFKGWFWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW DVTVLELSYHKRHLDRPVFLRVWETLDRYVMVKHSHLRF |
| 6594 | 1 | 1096 | EFFGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA DILSTIGYDNIHQHLNNGRNCKEFEDPLKRAAIBERYGKDLL NLSRKPCPGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE ARKMEEFREKQKLQRKKTELIMDAIHKKQSLQFKKTMADAKNYE QKCRDKDEAEQAVSRANLVNPKQKEKLFVKLATSKTAVEDSDK AYMLHIGTLDKVBREBQSEHIKACEFAEAQECERINFFRNALWL HVNQLSQQCVTSDEMYEQVRKSELMCSIQRDIYFVNQRKTGQI PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLLYQ |
| 6595 | 57 | 781 | PLGTMSDSDLGDEGLLSLAGKRRRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLPDMLRKD GKDPNQFTISRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA GSPTGGLFNTPTPTPEQDKEDFSFQLLVEVALQRAAEMELQK QDPSLPLLHTPIPLVSENPO |
| 6596 | 2 | 1026 | PLPVRRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLPVVCVKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFQDCEDDGETA AGGRLHLMEILNVKNVMVVSRYGGILLGPDPRFKHINNCA ILVEKNYTNPSPESSKALGKKNKVRKDKKRNEH |
| 6597 | 2 | 1026 | PLPVRRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLPVVCVKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFQDCEDDGETA AGGRLHLMEILNVKNVMVVSRYGGILLGPDPRFKHINNCA ILVEKNYTNPSPESSKALGKKNKVRKDKKRNEH |
| 6598 | 1099 | 419 | PRVRWATTMAMSFEPWPQYRFPFFFTLQPNVDTRQQLAAWCSL VLSPCRHLKQSSMTVMEAQESPLFNNVKLQRLPVESIQIVLEE LRKKGNLEWLDKSKSFLIMWRRPEEWGKLIYQWVSRSGQNNV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQEQHKAEITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRRTQCPPKTGTVTPPD SKGLQS |
| 6599 | 164 | 1593 | KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVQKLGGSVELVDIGKQLPDGSEIPLPPIILGRLGS DPQKKTVCITYGHLVDQPAALDGDWSEPFVTLVERDGKLHGRGST DDKGFVAGWINALEAYQKTGOEIPVNVRFCEGMEESSGSEGLDE LIFARKDTFFKDVVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKLHSGVYGGSVHEAMTDLILLMGSVDKRGNIIIPGIN EAVAAVTEEHKLYDDIDFDIEFAKDVGAQILLHSHKIDILMH RWRYPSSLHGIEGAFSGGAKTVIPRKVVGKFSIRLVNMTPE |

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|------------|--|--|--|
| | | | VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKWPVSDFSHPHYL AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS ADDGAHSQNEKLNRYNYIEGTKMLAAYLYEVSQDKD |
| 6600 | 2 | 934 | PGRLFRVAAMESAGLEQLRELLLPDTERIRRATEQLQIVLRAP AALSALCDLLASAADPQIRQFAAVLTRRLNTRWRLAAEQRES LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLQLL QHSTHSPHSPEREMGLLLSVVVTSRPEAFQPHHRELLRLNET LGEVGSPLGLFYSLRTLTTMAPYLSTEDVPLARMLVPKILIMAMQ TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR NVALGNAIRIRILCCLTFLVKVSKALLKNRLLATLAHPFPHC GC |
| 6601 | 529 | 1420 | PRAAARAPPPAVLRDRRAATAPGAGEMTLHGPLAQRYFLNHIE KITTWQDPRKAMNQFLNHNMLHPAVSSTFPVQSRMAVSQPNLVM NHQHQQQMAPSTLSQQNHPTQNPAGLMSMPNALTTQQQQQKQL RLQRIQMERERIMRQEELMRQEAALCRQLPMEAEATLAPVQAAV NPPTMTDPMRSITNNSSDPFLNGGPHYHSREQSTDGSLGLGCYSV PTTPEDFLSNVDEMTGENAGQTPMNINPQTRFPDFDCLDCLPGT NVDLGTLESEDLIPLFNDVESALNKSEPFLLTWL |
| 6602 | 127 | 617 | LLDFPALPKFVLAQSPKAGKPSMTSMTQSLREVIKAMTKARNF ERVLGKITLVSAAPGKVICEMKVEEHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSDMNITYMSPAKLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIQAQRHXTKHLGN |
| 6603 | 79 | 660 | PVGFSSLAARTGLGHLFPFLHRLASSRGLDMDLLQFLAFLFVLLL SGMGATGTLRTSLDPSLEIYKKMFVKKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGFPPQDEKLD AFSHVVENTAFFGDVVLRFPRIVHYFDHNSNWNLLIRWGISFC NQTGVFNQGGPHSPILSLM |
| 6604 | 3 | 688 | TSTAQRQGGGRMSFRGGGRGGFNRGGGGGFFNRGSSSNHFRGGG GGGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPEPVLLGEFL HPCEDDIVCKCTTDENKVYPFNAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSNEMKASSFKKLQKFYIDPYKLLPLQRFPLRPPGEG GPPRGGGRGGGRGGGRGGGRGGGRGGGRGGGGGGFRGGGRG GGFRGRGH |
| 6605 | 7 | 848 | SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV ALVAVAEHSGEFEKIMQLSERYNGFVLPCLVHVPVQGLPPEQR SVTLKDLDAVLPFIENYKDRLLAIGEVGLDFSPRFAGTGBQKEE QRQVLIRQIQLAQRNLNLPVNVHSRSAGRPTINLLQEQAQKVL HAFDGRPSVAMEGVVAGYFFSIPPSIIRSGQQLVKQLPLTSLIC LETDSPALGPEKQVRNEPWNISISARYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK |
| 6606 | 2 | 1682 | FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGLPATLSPAEEBKAGPHEKYGVNSYLSE KISLDRSIPDYRPTCKCEKYSKDLQISIIIFIVNEALSILR SVHSVAVNHTPTHLLKEIILVDDNSDEBELKVPLEEYVHKRYFGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAE VLSRIQENRKRVLPSIDNIIQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTAMIGCSFVVRNKKFGEIGLLDPG MDVYGGENIELGIKVNLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVMDDYKSHVYIAWNPLENPGIDIDGVSER RALRKSLSKCKNFQWYLDHVPYEMRRYNNVAYGELRNNAKDV LDQGFLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLPL DTRCLVDNSKSRLPQLDQDKVKSLSLYKRWFIQNGAIMNKG TGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK |
| 6607 | 137 | 986 | VPACAGLKKEARSLASPPRLNLTKLQASCALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSSLQTKQRRPSK KIEDELEMTMVCHRPEGLEAQTNFTKRELQVLYRGFKNECP |

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|------------|--|--|--|
| | | | SGVYVEDTFKQTYAQFFPHGDASTYAHYLFNAFDTTQTGSKVFE DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA IYMMGKYTYPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEFLE SCQEDDNIMRSLQLFQNV |
| 6608 | 224 | 1140 | RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQSPSPPMVSATRS TGTLQLPPQKPPGQEAASPLAGEEELSKGGEQDCALEELCKPLY CKLCNVTLNSAQQAQAHYQGNHKKLRNYAANSCPPPARMSN VVEPAATFVVPVPPQMGSKPGGRVILATENDYCKLCDASFSSP AVAQAQHYQGNHAKRLRLAEASNSFSESSELGQRRARKEGNEF KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTFSGQPYC SMCNVGAAGEEMEFRQHLESKQHKSKVSEQRYNEMENLGIV |
| 6609 | 1 | 443 | FRLCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT PAAEPGNFQLSPAEPGRGLASPVRAAPRACPAAMSELNKTTS PATNQAAQGEKKGAGNVKKAEEEEIDIDLTAPETEKAALAIQ GKPRRFQKRKKDPSS |
| 6610 | 319 | 881 | GRKSLCNLHIFIRFLTPYDMMGMCTAKKCGIRFQPPAILI YESEIKGKIRQIMPVRNFSKFSQDCTRAAEQLKNNPRHKSYLEQ VSLRQLEKLPFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL DDKELAKRKSIMDELFEKNQKKDDPNFVYDIEVEFPQDDQLQS CGWDTESADEF |
| 6611 | 978 | 212 | PGCSGAGSRVWVLPALRHLAMGSTESSEGRVSVFGVDEERVV LQGVRLSENVNRMKEPSSPPAPTSTFGLQDGNLRAPHKEST LPRSGSSGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREA TKHSKASLPTGEGSISHBQKSVRLARELESREABLRRTDFYK EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL QAQILHCYDRDPHEVLLCSDLVKAYQRCVSAAHKG |
| 6612 | 1724 | 992 | VSTHASALSRTQGPQRPRAASGAGAGTAGGGGSGGAGBSKM STEAQRVDDSPSTSGSSSDGQRESVQGEPEREQVQPKKKEGKI SSKTAALKLSTSAKRIQKELAEITLDPNCSAGPKGDNIYEWRS TILGPPGSVYEGGVFFLDITFSPDYPPKPPKVTFRTRIYHCNIN SQGVICLDILKDNWSPALTISKVLLSICSLTDCNPADPLVGS IATQYMTNRAEHRMARQWTKRYAT |
| 6613 | 130 | 748 | ELELSNNMEQSNDRYVAVFGAGGVGKSSLVLFVKGTFRSEYI PTVEDTYRQVISCDKSICTLQITDTTGSHPFAMQRLSISKGHA FILVYSITSRSLEELKPIYEIQICEIKGDVESIPIMLVGNKCD SPSREVQSSEABALARTWKCAFMETSAKLNHNKELFQELLNLE KRTVSLQIDGKSKQKKRKEKLKGCIVM |
| 6614 | 3 | 1191 | SSAAEAMRVLVRRCWGPPLAHGARRGRFSPQWRALARLGWEDCR DSRVREKPPWRVLFPGTDQFAREALRALHAARENKEELIDKLE VVTMPSPSPKGLPVKQYAVQSOLFVYEWPDVGSGEYDVGVASF GRLLNEALILKPPYGIINVHPSCLPRWRGPAPVIHTVLHGDTVT GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN MLISVLKNLPESLSNGRQPMEGATYAPKISAGTSCIWEEQTS EQIFRLYRAIGNIIPLOTLMANTIKLLDLVEVNSSVLADPKLT GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKSLTATDFY NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTAMQQCIE |
| 6615 | 832 | 35 | GRVGAGASAMSELPDVRAPLREHPSLRQLTDARKVRCILTGHE LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH QLFCKLTLRHINKCPEHVLHRTQGRYQALCKYBECQKQGVY VPACLVHRRRRREDQMDGGRPREAFWEPTSSDEGGAASDDSM TDLYPPELFTRKDLGSTEDGDTDDFLTDEDEKAKPPREKATD EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS G |
| 6616 | 347 | 1886 | LLPPCQGARPLSSPHASEDNLFWNCILCAFPHPSPQPLQYP VWPLLLVITQIPAPRHNRNPFPSRGGLDSSGSLSTPSICRS |

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|------------|--|--|--|
| | | | PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPWLQSPPPQSSP PPQHPCHTCRGLVDSFNKGLERTIRDNPGGGNTAWEENLSKY KDSETRLVELEGVCSKSDFECHRLLELSELVESWWFHKQEA PDLFQWLCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYQCEG EGTRGGSGHCDQCAGYGGACGQCGLGYFEARNASHLVCSACF GPCARCSGPESNCLQCKKGWALHHLKCVDIDECGETEGANCGAD QFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC LDVDECETEVCPEGNKQCENTEGGYRCICAEGYKQMEGICVKEQ IPESAGFFSEMTEDELVLVQQMFPGIIICALATLAAKGLVFTA IFIGAVAAMTGYWLSERSDRVLEGFIKGR |
| 6617 | 118 | 673 | VWMAWQVSLLELEDRLQCPICLEVFKBSLMLQCGHSYCKGCLVS LSYHLDTKVRCPMCWQAVDGSSSLNPNVSLAWVIEALRLPGDPEP KVCVHHRNPLSLFCEKDQELICGLGGLGSHQHHPVTPISTVCS RMKEELAAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC LGPATFTFL |
| 6618 | 548 | 136 | DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR NVPKMTSERSRIPCLSAEAGTGKKQEGRAMATLDRKVPSP AFLGKFWSSWIDAALHCSNDVLEEAGKEGKSRVEMRLNKEA WKYGT |
| 6619 | 246 | 842 | PASSEVLTAAMVFLLLNCIVAVSONMGIGKNGDLRPPPLRNEFR YFQRMTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGSSV YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG ILSDVQEGKHIKYKFEVCEKDD |
| 6620 | 3 | 1879 | NSRVDDFVARARMAAENEASQESALGAYSVPDYSITSFPRLP DEPAPAAPLRGRKDEDAFLGDDPTDPSFLKSARLQRLPSSSE MGSQDGSPLRETRKDPFSAAAECSCRDGLTVIVTACLTATG VTVALVMQIYFGDPQIFQQGAVVTDAACTSLGIEVLSSKQSSV DAAVAAALCLGIVAPHSGLGGGVMLVHDIRNESHLDIFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHLQYGRPLWS QVLFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG RPPLPGSLLHRPDLAELVDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPHTPGALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFSGSLITPSGILLNSQMLDFS WPNRTANHSAPSLNSVQPGKRPLSFLPTVVRPABGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCLDCRCLSYLWL SIPHAANMG |
| 6621 | 1 | 662 | VQGITSYQORLQALRKEKSRDAARSRRGKNEFFYELAKLLPLP AAITSQLDKASIIRLTISYLMKMRDFANQGDPPWNLRMEGPPNT SVKVIGAQRSSPSALAEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYGLGSQVELTGSSVFDYVHPGDHVEAEQLGMK LPPGRGLLSQGTAEAGASSASSSSQSETPEPVVCFPPASDQFLL |
| 6622 | 2 | 319 | GRASQAEBETEAGGPERARAMEANMPKRKEPGRSLRIKVISMG AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVDRREIKVN IFDMAGHPFFFEVRKPF |
| 6623 | 1886 | 189 | KALFEKVKFRHLHVEEGDILYAMYVRQTVLKVIFLIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTYLWLFYRSLREYSFEYVRQETGFDDIPDVKNDF APMLHMDQYDPLYSKRFVFLSEVSENKQLQNLNNEWTPDKL RQKIQTNANHRLELPLIMLSGLPDTVFETTELQSLKLEIIKVM IPATIAQLDNLQELS HQCSVKIHSAAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVLTLESRLDLKSLKI LSIKSNVSKIQAQVVDVSSHQKMCIHNDGTLVMLNLLKMTN LTELVLHCDLERIPHAVFSLLSLQELDLKENNLKSIIEIVSFQ |

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|------------|--|--|---|
| | | | HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP DELYFCKKLKTLKIGKNSLSVSPKIGNLLFLSYLDGKGNHFEI LPPELGDCRALKRAGLVVEDALFETLPSPDVRQMKTE |
| 6624 | 218 | 1786 | GSRRGGGSRIPAVSTHVAPGRSVLRPPFASGALRLRLSVLKALGGC RGRPSGLAHLSEQETSHWRAKRSGRACLGDFFGEILRSFIMKCTA REWLRTVTVLFMARAIAMVVPNATLLEKLEKYMDEDEGEWWIA KQGRKRAITDNDMQSILDLHNKLSQVYPTASNMEYMTWDVLE RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPTTFHVQSW YDEVKDFSPYPEHECNPYCPFRCSGPVCTHYTQVWVATSNRIGC AINLCHNNNIWQIWPKAVYLVNYSFKGNWNGHAPYKHGRPCS ACPPSFGGGCRENLCKEGRSDRYPPREBEETNEIERQQSQVHDT HVRTRSDSSRNEVISAAQMSQIVSCEVRLRDQCKGTTCNRYEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR QGRKHFIKSNRNGIQTIGKYQSANSFTVSKVTQAVTCETTVE QLCPFHKPAHCPRVYCPKLYASKSTLCSCNWNSSLF |
| 6625 | 1124 | 543 | PGPRGGGSLSTKALGRSRLGMPGSPSGGTEGGVPTALRPP GPLVPSTSDNLLKNIELFDKLALRFHGRLLFLKDLVLDGDEICCW SFYGGQRKIAEVCCTSIYATEKKQTKVEFPPEARIFEETLNILI YETPRGPDPALEATGGAAGAGGAGRGEDENREHRVRRIHVRR HITHDERPHGQQIVFKD |
| 6626 | 3 | 1498 | SAVEFVYTRDFHLILGISVEFLCSLRSDATMESITACLHALQAL LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEV RQIIICAAQEHVKEKRRAEVDGAAEKETLPEFGEGKDTGGVLV GKSLVFATLELCVCILVRQLPELNPKLGTGSPGVKATKPQILLED GSRVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRATAV KLPGGQLSSTVAASLQALKGILSSPMARARKSRTATWDLRLSAL TTILDCWDVDPVDETHQELDEVSLTITVFIILSTSEVTTIPCLQ KRCIDKFATLEIKDPVVQIKTYQLLHSIFQYPNPVSPYPIYS LASCIMEKLQEIHKRPENTAELEIFQEGIKVLETLVTVAAEHH RAQLVACLLPILISFLDENSLSGATSIMRNLDHDFALQNLQMIG POYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS PGKNSSIQLKTSFL |
| 6627 | 1 | 697 | GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSFSDLTGKVMLL GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV KLQIWDTAGQERFRSVTHAYYRDAQALLLYDITNKSSFNIRA WLTEIHEYAQRDVVIMLLGNKADMSSSERVIRSEDGETLAREYGV PFLETSAGTKMNVLAFLAIAKELKYRAGHQADEPSFQIRDYVE SQKRSSCCSFM |
| 6628 | 1 | 1861 | QCAEFGGGSGGGGGSGGGSGGGGAGGEEENKENERPSAGSKAN KEFGDSLSEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR KTLNFKMGNRHKFTGKKVTEELLTDNRVLLLVLMDAERAWSYAM QLKQEAANTEPRKRPHLLSRLRKAVKHAEELERLCESNRVDAKTK LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE EQAVLYNQRVEEISPNIYCAYNIGDQSAINELMQMLRSLSGGTE GLLAEKLEALITQTRAKQAATMSEVWGRGRTVPVKIDKVRIFLL GLADNEAAIVQAESEETKERLFESMLSECRDAIQVREELKPDQ KORDYILEGEPGKVSNLQYLHSYLYTYIKLSTAIKRNNMAKGLQ RALLQQQPEDDSKRSRPPQDLIRLYDIIILQNLVELLQLPLGLEED KAFQKEIGLKTIVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK YANBVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA NDAHQTETSSSQVKONKPLVERFETFCLDPSLVTKQANLVHFPF GFQPIPKPLPFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF GFRS |
| 6629 | 5653 | 4549 | GATFLGSGGRTGKMDAATLTIDTLRFAEFEDFPETSEPVWILG RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC |

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|------------|--|--|---|
| | | | MLRCGQMI FAQALVCRHLGRDWRWTQKRPDSYFSVLNAFIDR KDSYYSIHQIAQMGVGEKSGIQWYGPNTVAQVLKKLAVFDTWS SLAVHIAMDNTVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF PAGAEVTRNRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCPI PDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM TRKTFGFLRFFFSMLG |
| 6630 | 2 | 423 | LVQCGGIRRRSAWGA MPGRHVSVRVLYKRVLQLHRVLPDDLKS LGDQYVKDEFRRHKT VGSDEAQRFLQEWVYATALLQOANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQRATKPNRQFSI SESMPKPF |
| 6631 | 2 | 423 | LVQCGGIRRRSAWGA MPGRHVSVRVLYKRVLQLHRVLPDDLKS LGDQYVKDEFRRHKT VGSDEAQRFLQEWVYATALLQOANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMPKPF |
| 6632 | 1273 | 588 | WNSRGRTQRGAAPLAPAAAMKAVVQVRVTRASVTVGGEQISAIGR GICVLLGISLEDTQKELEHVMVRKILNLRVFEDESGKHWKSVMD KQYEILCVSQFTLQCVLKGKPKDFHLAMPTEQAEGFYNSFLEQL RKYRPELIKDGKFGAYMQVHIQNDGPVTIELESAPGTATSDP KQLSKLEKQQRKEKTRAKGPSSESSKERNTPRKEDRSASSGAEG DVSSEREP |
| 6633 | 1145 | 617 | ATGRHEGVFTLEGIIQQLVNGIITPATIPSLGPWGLVHSNPM DY AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV GSGLECPVCKDDYALGERVRLPCNHLFHDGCI V PWLEQHDSCP VCRKSLTGQNTATNPGLTGVSFSSSSSSSSSSSPSNENATSNS |
| 6634 | 1 | 1134 | CGGIPRKSGSPRRRLPMARLDRCLPRLMLTLRSLLFWSLVYCYC GLCASIHLLKLLWSLKGKPAQTFRPAREHPPACLSDP SLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRVQLREF KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLI V INFPHPNVFTEYI LRHPAQLLKSSYYYFQI PWFPEMF SINDFKVLKHLFTSHSTG IGRKG CQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCPLPKH HMTTPTLLLGENDAFMEVEMA EVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTF LKEETRKKD |
| 6635 | 1420 | 470 | EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAFSSSSG GRGGAEPRLPLSYRLLDGEAALPAVFLHGLFGSKTNFNSIAK ILAQTGRRLTV DARNHGDSPHSPDMSYEIMSDQLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRP ELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDA LTQHLDKILAFPPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLF PRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV |
| 6636 | 1514 | 1801 | SFCMF SHKQDSHFQAVPVQEKKKRLRRAPWRAFAQ PQLKHPAE QPIVRQCLQRPFPLCGVLGVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF |
| 6637 | 2 | 1501 | CSSSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEAGSKSI KASEDSL SVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQNGEWSGKQPICIKACREPKISD LVRRRVLP MVQVSRETPLHQLYSAAFSKQLQSAPT KKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPAQAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSFQBSHITVAGWNVLADVRSPGFKNDTL RSGVVSVDSSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC TAETGGIAAVSFGRASPEPRWMLMGLVSWSYDKTCSHRLSTAF |

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|------------|--|--|---|
| | | | TKVLFPKDWIERNMK |
| 6638 | 1391 | 224 | GGIPQAGGKMAAPWWRAALCECRRWRGFSSTAVALGRRTPLPGPM PNSDIDLNSLERLEKYRSFDRYRRRAEQEAQAPHWRTYREYFG EKTDPKKIDIGLPPPKVSRTOQLLERKQAIQELRANVEEERAA RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF VPRVPLHVAYAVGEDDLMPVYCGNEVTPTAAQAPEVTYEAEEG SLWTLTLLSLDGHLLLEPDAEYLHWLLTNIPGNRVAEQVTCPYL PPFPARGSGIHLAFLFLFKQDOPIDFSEDARPSPCYQLAQRTPR TFDFYKKHQETMTFAGLSFFQCRWDDSVTYIFHQLLDMREPVEF FVRPPPYHFKQKRFPHRQPLRYLDYRDSHEPTYGIY |
| 6639 | 2046 | 1268 | IGCFIMDGGDDGNLTIKKRFVSEAELEDRKRKRQEWKVRKPE DPBECPEEYVDPRSLYERLQEQKDRKQEQYEEQFKFKNMVRGLD EDETNFLDEVSRRQELIEKQRREBELKELKEYRNKVKVIGISQE NKKVEVEKLTVPKPIETKNKFSQAKLLAGAVKHKSSSEGSNSVKRL KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPAAVCIGILPGL GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP |
| 6640 | 117 | 1043 | VLEPPDVSMASEDRSLRVLVVGKTSKGSKSATANTILGEEIFDS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE ISRCIISCPGPHAIVLVLLGRYTEEQKTVALIKAVFGKSAM KHMVILFTRKEELEGGQSFHDFIADADVGLKSIKCEGNCRCFAFS NSKKTSAEKESQVQELVELIEKMQVCNEGAYFSDDIYKDTTEER LKQREEVLKRIYTDQLNEEIKLVEEDKHKSEKKEIKLLKLK YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS |
| 6641 | 1 | 894 | SAAVGRRSEVRGCAPRPLRRSARRMDVPVGTDSAPLAGLAWSS ASAPPPRGFSAISCTVEGAPASFGKSAQKSGYFLCLSSLSGLE NPQENVVADIQIVVDKSLPLGFSVPCDPMDSKASVSKKRMVCV KLLPLGATDTAVFVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVVKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEYNYGVFVEKTAARLPSSVS |
| 6642 | 22 | 1296 | PLEERMMTKMDPNDQAQRDIIFELRRIFAFAESDPSNAPGSGTE KHKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSREDKHECPFGSAIETKMLCEILQVGELP NEGRNDYHPMFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQLNRLCEGSSFRKIG NRRRQERFWYCRALNKHVLYHYGDLDDNPQGEVTFESLQEKIPV ADIKAVTGKDCPHMKEKSAKQNKVELELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSSELTKSDDLTLSSMEMKLRL LDLENIQIPEAPPPPIPKBPSSVDFVHYG |
| 6643 | 3049 | 2265 | SLHAPAEGRTRGRLAEPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSLVKYLEENNTCPTCRIVINHSHPLQYIG HDRTMQDIVYKLVPLGQBAEMRKQREFYHKLGMVEVPGDIKGETC SAQHLDSDHRNGETKADDSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKRLGLKRWIRCSAQATVLHLKKFIAKKNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKAPILLHYRPKMDLL |
| 6644 | 1489 | 290 | FRPLATEPRGSSPVQLVSSVTSLPLFLNLGGEMLYILDQR LRAQNI PGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDITKGFIRDSPTILQVQVDETLRQLTEIYGGLSAGEFQ LIRQTLTIFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPGWT EVPGLIRMFNNKGEVVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGMEIKKPSGPEPGFRLNLTDEEEQAALTRPEELSY EVINIQTQDQQRSEELARIMGEFEITEQPRLSSTSGDDLLAMM DEL |

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|------------|--|--|--|
| 6645 | 6530 | 4646 | FVEGLAGVYVYKAASEGKVLTLAALLNRSSEDIRYLLGYVSQOG GQRSTPLIIAARNGHAKVVRLLLEHYRVQQTQGTVRFDGYVID GATALWCAAGAGHFEVVKLLVSHGANVNHTTVNSTPLRAACFD GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRVYLE QRADPNKAHCGATALHFAEAGHIDIVKELIKWRAAIVVNGHG MTPLKVAESCKADVVELLLSHADCDRRSRIEALLEGASFAND RENYDIKTYHYLYLAMLERPDGDNIKEVLPPHAYGNRTE CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN YECNLYTFLYLVLCISTKTQCSBEDQCKINKQIYNLIHLDPRTE GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLDCGAEVNA VDNEGNSALHIIQYQNRPISDPLTLHSIIISLVEAGAHTDMTNK QNKTPLDKSTTGVS EILLKTQMKMSLKCLAAARAVRANDINYDQD IPRTLEEFVGFH |
| 6646 | 176 | 890 | PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLWIIELNVNGGIENL EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAPLLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLEL |
| 6647 | 176 | 890 | PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLWIIELNVNGGIENL EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAPLLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLEL |
| 6648 | 413 | 897 | RNCWNCFTKYFNSPPEIDHKDSYLI TRSMAEPDYIEDDNPEL IRPQKLINPVKTSRNHQLHRELLMNQKRGAPQNKPBQKVME KXKRDQVIKQKEEAQKKSDLEIELLKRQKLEQLELEKQKQKQ EEQENAPEFVKVGNLRRTGQEVAAQES |
| 6649 | 1357 | 832 | WIPRAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRLNEV SKRVRIPLPVSNIWEHCIRLANRTIVEGYANVKKCSNEGRALM QLDFQQFLMKLEKLTDIRPIPDKEFVETIYKAYLTENDMERWI KEHREYSTKQLTNLVNVLGSHINKKARQKLLAADDIDRPKR |
| 6650 | 32 | 765 | LVPLVFSLLVQSCQVYRSIAMKFVPCLLVLTSLGLTGQAPR QKQSGTGEEFHFQTGGRDSCMRPSSLGQAGAEVWL RVDCRNTD QTYWCEYRGQPSMCQAFADPKSYWNQALQELRRLHHACQGAPV LRFSVCREAGPQAHMQQVTS SLKGSPEPNQQPEAGTPSLRPKAT VKLTEATQLGKDSMEELGKAKPTRPTAKPTQPGPRPGGNEEAK KKAWHCWKPFQALCAFLISFFRG |
| 6651 | 3425 | 1353 | AKELLKVGDFSLCAGPYQNTADTMENLSKEFLASFVSESFDISA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSTYLRGSYTRKKDVPTDGYESSLNF HNNQEDWGCSSWVPGMETSLPPGHWA AVKKEEKCVPYVQIR DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFANCGLPSSW TSTWQVADDLTQNTLDLBYLRFHAKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSLLVTVVESDP RPQGGPRRGYTASSLDSSSSWRERC SHNRDLRNSQRNHTVS FHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFVVRTKNLLRKGHTEIEPQHFCAQFHR ENDTLIIIRNEDISSHLHQIPSLLLKLKHFPSVIFAGVDS PGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNNG RWKLLHYRENKCLKEDERVDS TAHKKNIMLKS PQSANIIELH YHQCDRSSTKAEILKCLNLQIQHIDARFAVLLTDKPTIPREV |

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|------------|--|--|--|
| | | | FENNGILVTDVNNFIENIEKIAAPFRSSYW |
| 6652 | 2 | 1343 | IPGSTISCSCHSRRLRGSSPAPRLSLGAASPRPRPSSLPLPLPLP PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI TCDSFKISWEMDSKSKDRITHYFIDLNNKENKNSNFKHKDVP KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVS WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHK YFDYVREHHGNAMQPSVKDNGSGSHGSPISGKLEGIFFCSTFN TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV ILVIAPVSGPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA QDVILEVIYTDVVDLSLGTVAEITGHQLMSLSTANAKKDPCKT CNISVGR |
| 6653 | 170 | 1910 | FPLEPRLRPFASRARFVPARTRPSPLHPCCFEGGGMSLSPO RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI LQDHIRDLDDVVVSVAAGAFRKGKSFILDFMLRYLSQKESGHS NWLGDPEEPLTGFSWRGSDPETTGIIQWSEVFTVEKPGGKKVA VVLMDTQGAQFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED DLQQLQLFTEYGRLAMDEIFQKPFQTLMPVLRDWSFPYYSYGL QGGMAFLDKRLQVKEHQHEEIQVNRNHIHSCFSDVTCFLPLPHG LQVATSPDFDGKLDIAGEFKEQLQALIPYVLNPSKLMKEKING SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAA SAKDIYNNMEVEVCGGEKPYLSPDILEEKHCEFKQALDHFCKT KKMGKDFSFYQQBLEEEIKELYENFCKHNGSKNVFSTFRTPA VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY IRYSGQYRELGGAI DFGAAYVLEQASSHIGNSTQATVRDAVVR PSMDKKAQ |
| 6654 | 1 | 705 | RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM WKVTAFIGNSIVVAQVWEGWMSCVVQSTQGMQCKVYDLSLLAL PDQLQAARALCVIALLVLFGLLVYLAGAKCTTCVEEKDSKARL VLTSGIVFVISGVLTLPVCWTAHAVIRDFYNPLVAEAQKREL ASLYLGWAASGLLLGGLLCCCTCPSGGSQGP SHYMARYSTSAP AISRGPSSEYPTKNYV |
| 6655 | 341 | 16 | KDAYMPKKGLLALALVFLPVFAAEHWIDVRVPEQYQEHVQGA INIPLKEVKERIAVAPDKNDTVKVYCNAGRQSGQAKEILSEMG YTHVENAGGLKDIA MPKVKG |
| 6656 | 2 | 1212 | TELPFRPANLAIQPPLSPLRALAPLPEKPGAVPPPKQKNAKVA DLNPGVKMSLGLQSQARGVACLGCKGTCSGFEPHSWRKICKSC KCSQEDHCLTSDLEDDRKIGRLMDSKYSTLTARVKGGDGIRIY KRNRIMTNPATGKDPTFDITITYEWAPPVGTQKLGLQYMEIIP KEKQPVGTGEGAFYRRRLMHQLPIYDQDPSRCRGLLENELKLM EEFVKQYKSEALGVGEVALPGQGGLPKEBGKQEKPEGAETAA TTNGSLSDPSKEVEYVCLCKGAAPPDSPVVYSDRAGYNKQWHP TCFVCAKCEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI IFAEDYQRVEDLAWHRKHVFCGCEQLLSGRAYIVTKGQLLCP CSKSKRS |
| 6657 | 830 | 2120 | LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLMEH HLEAHKNGHANGHLNIGVDIPTDGSFSIKIPNGMPNGYRKEM IKIPMEPELERSQYPMEWGKTFLAFLYALSCFVLTVMISVVHER VPPKEVQPPLEDFTFDHFNVRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRFFCIVGTLYLYRCITMYVTLPVPGMHFNCSK LFGDWEAQLRRIMKLIAGGGLSITGSHNMGDYL YSGHTVMTL TYLFIKEYSPRRLWYWHICWLLSVVGIFCILLADHXYTVDVVV AYYITTRLFWYHTMANQQVLKEASQMNLLARVWVYRPFQYFEK NVQGI VPRS YHWPFPWPVHL SRQVKYSRLVNDT |
| 6658 | 35 | 855 | HCCALGAPGSPYRGYFSSAAPCTAPRKAKHQSTLEGLTKRMLM |

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|------------|--|--|--|
| | | | FDPVPVKQEAMDVSVSYPSNYMESMKPNKYGVIIYSTPLPEKFF QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSSHRRA SPGLSMPSSSPPIKKYSPSPGVQPPGVPLSMPPVMAAALSRHG IRSPGILPVIQPVVQPVFFMYTSHLQQPLMVSLEEMENSSSS MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV SPPQALLQE |
| 6659 | 18 | 523 | EPQRGDCETWFQNCSLPKFVCFWGFWLWRAHMSNLHSLPGL RGLTSISRNLQCTNAMRVINNYQRRWKNQNTFLLATFANVNV CGNPTITCPHNRTLNNCHSGVQVPLMYCNLTTPSPQINISNCRY AQTTPANMFYIVACDNRDQRRDPPQYFVVPVHLHTII |
| 6660 | 514 | 1707 | CAASLDCRHHLCEDPMKLVWPSAKLLQAAAGASARACDSVTSNV LPLLEQFHKHSQSSQRRITILEMLLGLKLQKWSYEDKDQRL NGFKDQKCLSLVFMALTDPTQLQVLGIRTTLVLGAQPDLLSYED LELAVGHLYRLSFLKEDSQSCRVALEASGTLAALYPVAFSSHL VPKLAEEELRVGESNLITNGDEPTQCSRHLCCQLASAVSTHPSIV KETLPLLLQHLWQVNRGNMVAQSSDVIACQSLRQMAEKCCQDP ESCWYFHQTAIPCLLALAVQASMPKEKPSVLKVLLEDEVLAAM VSVIGTATTHLSPLAAQSVTHIVPLFLDGNVSLPENSFPSPRF QPFQDSSGQRRILALLMAFVCSLPRNVSEHIWEVLLFNLDKVT PG |
| 6661 | 179 | 430 | GVHAASGTLSATWLAEAKMFDLSLAKAGKYLGAAKLMIGMPDYD NYVEHMRVNHDPDQTPMTYEEFFRERQDARYGKGKGGARCC |
| 6662 | 185 | 423 | RSLPKPAPAQPASIHCFRSGVTPPTAKTAMSDGNTAFNALMYC GPKADDGNI FSACAPASSAVKASVSAQPPQAVIP |
| 6663 | 3 | 1005 | RPVLSRRVDDFVPLPETSGRRKKLERMYSVDRVSDDIPIRTWF PKENLFSFQTASTTMQATSNFRKHLRMVGSRRVKAQTFERRER SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWD T EKGLEAVACDTEGFVPPKVMILISSKVPKAEYIPTIIRDDPSII PILYDHEHATFEDILEEIERKLVYHKGAKIWKMLIFCQGGPGH LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGQMIET YFDFRLYRLWKSQRHSLKLLDFDDVL |
| 6664 | 58 | 968 | PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHVLVSVMA VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF LANHTNILLASSIWIYITFFCPHDLVSQGYSLPVQOLLASGMKEV TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL VKGDWKPEGDEWLKMSYPKAVTLLGSVITFTFQHTQHLAISKHL MFLYTI FIVATKIIMTTQTSTMTFAPFEDTSLNMLFGWQQPFS SCEKKSEAKSPSNGVGLASKFVDVSDNVKKKHTKKNE |
| 6665 | 171 | 1278 | DERRLACRQVVTTQQRSELYPGFQKRQRFPLPKAGEEAAAQGGRL PGRWLGPQGTQNPSCSVHTATGPEPRKLPLLPDPSNPGYPKEPA ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK TRLQNHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP EKAIKLAANDFFRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC PMMLKIQLDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS ATLIAWELLRTQGLAGLYRGLGATLLRDI PFSIIYFPLFANLNN LCFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK KGLGEDMYSGITDCAR |
| 6666 | 498 | 2868 | MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL WSPGCPQPIQKEGVGLWDIRKQSSLLRYGGNLSLQASAMSVRF NSNGTQLLALRRLLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC CFAGDRDQYILSGSDDFNLYMWRI PADPEAGGIGRVVNGAFMVL KGHRSIVNQVRFPNPTYMICSSGVEKIIKIWSPYKQPGCTGDL D GRIEDDSRCLYTHEEYISLVLSNGSGLSHDYANQSVQEDPRMMA FFDLSLVRREIEGWSSSDSDSSESTILQLHAGVRSERSGYTDS ES SASLPRSPPTVDESADNAFLGLPLRVTTTNTVASTPTPTCED |

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|------------|--|--|---|
| | | | AASRQQRLSALRRYQDKRLALSNESDSEENVCEVELDTDLFPR PRSPSPEDSSSSSSSSSEDEELNERRASTWQRNARRRQKT TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYNNKDGE TSLVTGEADGRAGTSHKDNAPAPSSSKEACLNIAAQRNQDLPP EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG SVEHPFETKKLNGKALSSRAEPPSPVPKASGSTLNSGSGNCP RTQSDDEERSLETICANHNNRRLHPRPFPHPNNGQNLGELEV AYSSPGHSDTDRDNSSLTGTLLHKDCGSEMACEPTNAGTREDP TDTPATDSSRAVHGHSGLKRQRIELEDTSSENSSEKKLKT |
| 6667 | 171 | 1310 | ABEERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPKWKRR KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI SNEEDSLENGQSLSSSLSLPALSEMEPVMPRPDPCSYEVLQPS DIMDGPDPGAPVKLPCLPVKLSPLPPKKVMICMPVGGPDLSLV SYTAQKSGQGGVAQHHTVLP SQIQHQLQYQSHGQHLPS TTGSL PMHPSGCRMIDELNKTAMTMQRLESSEQRVPCSTSYHSSGLHS GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL YTREEEEEEDEDDSSLYTSSLAMKVCCKDSLAIKPSNRPSKR ELEKNILFRQTDEERLELRQQIGTKL |
| 6668 | 714 | 358 | TLAVATGPALTLRCHVCTSSSNCKHSVVCFASSRFCKTTNTVEP LRGNLVKKDCAESCTPSYTLQGGVSSGTSSTQCCQEDLCNEKLH NAAPTRTALAHSAALSGLALSLLAVILAPSL |
| 6669 | 459 | 1207 | KDEETRKYDYMLDHPPEYYSHYYHYSSRRLLAPKVDVRVILVS VCAISVFQFFSWWNSYNKASISYLATVPKYRIQATEIAKQQGLLK KAKEKGKNNKSKKEIRDEEENIKNIIKSKIDIKGGYQKPKQICD LLLFQIILAPPFLCSYIVWYCRWYFNFIKGEYGEERLYIIR KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEELK KLELANDPRWKRYRRWMKNEGPGRLTFVDD |
| 6670 | 184 | 594 | VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA VMQPPPGMPLPPADIGPPPYEPGHPMPQPGFIIPPHMSADGTYM PPGFYPPGPHPPMGYYPGPYTPGPYPGPGGHTATVLPVSGAA TTVTV |
| 6671 | 1 | 763 | LPAEKPRSAAPNMAGGRCPQLTALLAAWIAVAATAGPEEAALP PEQSRVQPMASNWTLMVEGEWMLKFPYAPWCPCSQQTDEWEAF AKNGEILQISVGKVDVIEPGLSGRFFVTTLPAFFHAKDGIFRR YRGPGEFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL |
| 6672 | 304 | 1089 | APGSKPVQFMDFEKTSFGMSVFNLSNAIMGSGILGLAYAMAHT GVIFFLALLLCIALSSYSIHLLTLCAGLAGIRAYEQLGQRAFG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYSGLSLTCLMFF LVSVIYKFKQLGLCYRATMKQWESEALVGTPOPRDSTA AVKAQ MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFOAQD |
| 6673 | 1116 | 1963 | LQIQTHHTHIGARVTHLGSHQLLANAGTMLCRQSSSMAPAFSQ SVTCGFPSPVCRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPOAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSSGQERQS\WVLPVPVGEPLKLPGLPG*NK SFSRV/SGSKGWILPRQLM*AS*R\TPRFVPGTQWVPI TW/PL ITWH*SAPTPLKACPAPRESDPCCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG |
| 6674 | 1 | 440 | LEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ PTPC*IGTRVAFFLT |

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|------------|--|--|--|
| 6675 | 277 | 1678 | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE |
| 6676 | 277 | 1678 | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE |
| 6677 | 277 | 1678 | GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE |
| 6678 | 221 | 865 | GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRLVSSNFGRO*LR PFPCSQLPMSQGLWHLDCPCWPVYIPGQQRKGRQMRN*QS LLGSDQESVGLLEDLCVFNFLHVLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCLRLQTHDLEGSRN HHPLFLVVGWRDAVKHLETVQSGLASLGFVGQHTSHGPP |
| 6679 | 2 | 786 | LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLEKSGSFVSDL SSYCNKEVYNKENLFNLSLNYD/SCSQEEKEGHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFNRDLDFSTAILDSRRFNYV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLTYSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEPTPVTEESGLF |
| 6680 | 1498 | 2951 | PLCTPLMPSPALPGWAGERWEKQWPLA/PGPQTWQTPVGSISEE PARKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAIEQTS*ALP /NQVSPPPQM*GAENGDRQGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGQPP/SPLLPAS MQRSAQGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPTTCS SQF\PAPPGFTGLRPGGSSSGGHG*PGLPVGKV\GALGAAQD PQSQRGPTQGTGTGTEMLLSGLGSAKACPAARPAVP*LPSPDPA TIPKKGTRGFGGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVWGRHGPQV AQGCCPPGAGCWGQPRGSQRCPRTYTHSLPHGGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR FQGGGGG |

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|------------|--|--|---|
| 6681 | 1169 | 511 | INIIYYNQQRAPHELK\EKLSAPALGLPDLTKLFTLHVSERE KMTVGVLTTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH+LINARLTRYQ TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETS PAPVTPR S |
| 6682 | 109 | 1238 | TVLCGAMQVSSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKD VD VRRRIELIQDFEMPTVCTTIKVS KDGQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAGVTTTGQVLLY DLRS DKPLL VKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMMLTANETPKMGIYYIPVL GPAPRWCSFLDNLTELEENPESNE |
| 6683 | 109 | 1238 | TVLCGAMQVSSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKD VD VRRRIELIQDFEMPTVCTTIKVS KDGQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAGVTTTGQVLLY DLRS DKPLL VKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMMLTANETPKMGIYYIPVL GPAPRWCSFLDNLTELEENPESNE |
| 6684 | 111 | 527 | GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA PP\SGRRHA+RPA*WLGPGGDSGGREEGGS/GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFTVTDPRNLLLSGAQLEAS RNIVQNYR |
| 6685 | 258 | 1473 | KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPPDPQKVL QGVIDMKNAVIGNNKQKANLIVIGAVPRLLYLQQTSSSTELKT ECAVVLGSLAMGTENNVSLLDCHIIPALLQGLLSPDLKFIEAC LRCLRTIFTSPVTPPELLYTDATVIPHLMALLSRSRYTQYVICQ IFSHCCCKGPDHQTILFNHGAVQNIHLLTSLSYKVRMQALKCFS VLAFFENPVQSMTLVNVLDGELLFPQIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELQAAPFKLYASLGANDEDIRKKVSLGEGRPVVL TASRQGVST |
| 6686 | 310 | 927 | DSVTFDDLAVDFTPKWTLTDPTQRLNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEEERTVQRGDFQASEWKVQLKTKEALQQDV LGPTSSGIQMIQSHNGGEVSDVKQCGDVSSEHSCCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSSTGEQSRVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT |
| 6687 | 181 | 915 | EAMLEAPYKKEDEQQRKEVKDYPSNTTSSSTNSGNETSGSST IGETSNRSDRDRYRRNRSRSPGRQCRHRSRSDRRHGSER SRDHRREDRVHYRSPPLATGEVDNLSPEERDARTVFCMLAAR IRPDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLGVPIIVQASQAEKNRLAAMANNLQKNGGPMR LYVGS LHFNITDMLRGIFEPFGKV |
| 6688 | 1025 | 1 | AEVNPYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPLPR/SATARMATAAAPNNSIDLPSDSGMGFI SPAGDSLD LPDGGTGFFSLAGDSSSTRLSLAFISFSLSSVSGSAGTTS STSVGSVVAAPTSSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFTC TMSELEELFSLFSPAPLLSKLFTSSGSAICQDQSGPSDTGRLS VCQLWLADSDTGKLSDCQEVVTVGDSGGTLCPELSLGRM*MSLL |

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|------------|--|--|---|
| | | | SSAIVIPGYSSSSDSRLNTVPTVDLLCPPTKSST |
| 6689 | 640 | 1299 | SSSASYATSATISISDTAFSGSLKLKHGLLSALDSSSRST*STSS AEDSTFRICSPSVSDTSSDSSGSKDNVILFASKVSI*SCFSLSS FFSDSISFCFSSSSFCR*FVSSKVSQNALSSRLSNGPGSSK QRNSLTARQLAMSL*ATKF*RNACNPCLSSKKSAL*LSLNQRF GGSASRKPGNISFNSQKCSALSCCNFVFKPREVSVSSENYPAF |
| 6690 | 1 | 442 | GTRGKMAATLGLGSGWQWRRLSARDGSRMLLLLLLLGGSGQP QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFQKHGQKKNL\H GDGLAIWYTKDRMQP |
| 6691 | 287 | 1401 | LKTETSEEKARRYKDRPSQLNAVFOEQKKMIQAQESITLEDVAV DFTWEEWQLLGAQAQDLYRDVMLENYSNLVAVGYQASKPDALFK LEQGEQLWTIEDGIHSGACSDIWKVDHVLRLQSESLVNRKPC HEHDAFENIVHCSKSKQFLLGQNHDFDLRGKSLKSNLTLVNQSK GYELKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLSTKSQF ISPKHQKTRKLEKHVCSECGKAFIKKSWLTDHQMHTGEKPHR CSLCEKAFSRKFMTEHQRTHTGEKPYECPEGKAFLLKKSRLNI HQKTHTEKPYICSECGKGFIOKGNLIVHQRIHTGEKPYICNEC /GKGFIQKTCIAHQRFHTER |
| 6692 | 178 | 939 | WKEGELSLWERFCANI IKAGPMPKHIAFIMDGNRRYAKKQVE RQEGHSQGFNKLAEFLRWCLNLGILEVTVYAFSIEFNRKSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL DPSDISESLDKCLYTNRS PHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVWLWPEYTFWNLFMAILQFQMNHSLVQK |
| 6693 | 178 | 939 | WKEGELSLWERFCANI IKAGPMPKHIAFIMDGNRRYAKKQVE RQEGHSQGFNKLAEFLRWCLNLGILEVTVYAFSIEFNRKSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL DPSDISESLDKCLYTNRS PHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVWLWPEYTFWNLFMAILQFQMNHSLVQK |
| 6694 | 292 | 813 | SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPRV EVHSLGQILPDGLTAEAGPPEAQDPWGPSGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDYAADKSKLIQLGITHV NAAAGKFQVDTGAKFYRGMSLEYGIEADDNPFDFLSVYFLP |
| 6695 | 292 | 813 | SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPRV EVHSLGQILPDGLTAEAGPPEAQDPWGPSGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDYAADKSKLIQLGITHV NAAAGKFQVDTGAKFYRGMSLEYGIEADDNPFDFLSVYFLP |
| 6696 | 1 | 782 | PRVRGRVGERWAFSLVPAAMSSEMEPLLLAWSYFRRRKFQCAD LCTQMLESPPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML DENAIQVPRPGTSLKLPGTNOTGGPSQAVRPITQAGRPIGTGFL RPSTQSGRPGTMEQAIPTPTATYARPTITSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWK/DQIEKCYRVGMRYAEKQIKSS |
| 6697 | 3 | 782 | PPLFLRLNSRALRPGSRKVMVVPASLSGQDVGFSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGEGVEAEKKAISLLSKLRNE LQTDKPFIPLEKFDVDIWNQYLEYQSSLLNESDGKSRWFYSP WLLV\ECYMYRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSQNTNVLNLSLEDLKPFI LLNDMEHLWLSLSNCK |
| 6698 | 668 | 754 | VGSCACAGSCKCKECKCTSCCKSECRAFP |
| 6699 | 325 | 492 | EGELF/PARRVLPRAMTASAQPRRRPGVGVVVTSCKHPRCV LLGKRKGSVAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK NVHFASVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN |

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|------------|--|--|---|
| | | | ESKRIIYNHAFFFQESKWSGGILQ |
| 6700 | 1098 | 1392 | TQCWRSSSTPGMRTHFRTQF/RLECGQGFSSQENGHCMDTNECIQ FPFVCPDRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT LLGLCNLLGK |
| 6701 | 2 | 1485 | AAAGPRTRVRRAAFEGQPSPSPLGPTSDKAAAPRTPKRRRLW RQRQ/HPAMLCYVTRPDVLMVEVEVEAKANGEDCLNQVCRRLLGI IEVDYFGLQFTGSKGESLWNLNRNRI SQMDGLAPYRLKLRVKF FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ ASAELYQLQIVSAMENYGIWHSVRDSEGGQLLIGVGPBGISIC KDDFSPINRIAYPVVQMATQSGKNVYLTVTKEGNSIVLLFKMI STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHASLF LNENINLGGKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRRNQ SPSHSPLKSSSSMNCSSCEGLSCQQT RVLQEKLRKLKEMLCM VCCCEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL LLTGSRSQVLAR |
| 6702 | 397 | 1971 | PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK RAEALLCSRKATVVRLDVAVRMAEEQEFTQLCKLPAQPSHPHCV NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL LAASCDYFKGMFAGGLKEMEQUEVLIHGVSYNAMCQILHFIYTS ELELSLSNVQETLVAAQCLQIPEIIHFCCDFLMSWVDEENILDV YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL LSSNRLEVSCETEVEGALLYHYSLEQVQADQISLHEPPKLLLET VRFPLEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ SPQTELRSDFCVVGFGGIHSTPS\MSSATRPKYLNPPLGEWKH FTASLAPRMSNQGIAVLNNFVYLIGDNNVQGFRAESRCWRYDP RHNRFQIQSLQQEHADLSVCVVGRIYIYAVAGRDIYHNDLNAVER YDPATNSWAYVAPLKREYVAHAGATLEGKMYITCGRKGRIT |
| 6703 | 45 | 1244 | GVGFRAAAMPLELELCPRGWVGQHPCFIIAEIGQNHQGDLDVA KRMIRMAKECGADCAKFOKSELEFKFNKALERPYSKHSWGKT YGEHKKHLEFSDHQYRELQRYAEVGIFFTASGMDMAVEFLHE LNVFFFKVSGDNTNFPYLEKTAK/TRGWHSVLRDVCVQQLNDE TSSWDVLGRVRSKEKVLMLVLDYSGRPMVISSGMQSMQMDTMKQ VYQIVKPLNPNFCFLQCTSAIPLQPEDVNLRVISEYQKLPDIP IGYSGHETGIAISVAALGAKVLERHITLDTKWGSDHSASLE PGELAEVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV KIPEGTILTMDLTVKVGEPKGYPPEDIFNLVGKVLVTVEEDD TIMEE |
| 6704 | 82 | 1007 | TMNTRNRVVNSGLGASPASRPTDRPDPSGRQGELESPVEDQREG LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIAEQE LANLEKWKQNRAPVHLVPRRLGGSQSETEVRQKQQLQLMQSK YKQKLKREESVRIKKEAEAEALQKMKAIQREKSNKLEKKRLQE NLRREAFREHQYKTAEFL/ROTEHRIARQKCLSKCCLWPTILN MGQKLGLO\DSLKAEENRKLQKMKDEQHOKSELLELKRQQQE RAKIHQTEHRRVNNAFDLRLQGKSQPGGLEQSGGCWNMNSGNSW GI |
| 6705 | 2 | 786 | RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT SYKRKGGIMSTIAAFYGGKSLITVATGFLGKELMEKLFRTSPD LKVIYILVRPKAQTLQHRVFQILDSKLFKVI EVRPNVHEKIR AIYADLNQNDFAISKEDMOELLSCTNII FHCAATVRFDDTLRHA VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK |
| 6706 | 130 | 531 | PTHSSSSHSQEMGLKLNMLRNDGHFCDDITIRVQDKIPRAHKVVL AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPPLEYATAT LSINTENIIDVLAASYMOMFSVASTCSEFMKSSILWNTPNPSQP EK |

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|------------|--|--|--|
| 6707 | 2233 | 1343 | YWSGIGYELQHFHWRKFHFEKKGPPSTCQERLYESRSRWPCIS* GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQASKCHS FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH TD*LPK*GPGYIQHFHCDNLCILYNISFNLFYSYF*GVARYA C*RWYFEWLLYNHCGDILVACL*RRQL*SSQ |
| 6708 | 115 | 1729 | TVGSWSRSGRSPPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT GEIIRVVPHRPPCKLALGSDGVRVTMESALTARDRVGVQDFVLL ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVPYRDLQIYYSR QHMERYRGVSFYEEPPLLAVADTVYRALRTERRDQAVMISVES GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLQSNPVLEAFGN AKTLRNDNSSRFGKYMDVQDFDKGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEEETLRLGLERNPQSYLYLVKGQCAK VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNH FAANESNAQVTENQLKYLTRLSSVEGSTLREALTHRKIIAKG EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV ESPSWRSTTVLGLLDIYGFVFOHNSFEQFCINYNCKLQQLFI ELTLKSEQEEYEAGIAWEPVQYFNNKIICDLVEEKFKGIT\SI LDE\ECRLPGE |
| 6709 | 3 | 894 | PPHEHLFPSEGERGPFSSFLVSRRLGPGKMGKKGKKEKKGRAEK TAAMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCFP PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK DTWTKVDIPSPPPRRCAHQAQVVPQGGGQLWVFGGEFASPNGEQ FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAVKROLILF GGFHSTRDYIYNDVYAFNLDFTTWSKLSPSGTGPTPRSGCQ\ IPSPRAASSVYGGYSKQVRKDVCKGTRHSDMF |
| 6710 | 158 | 980 | RHKMTNYRVESSSGRAARKMRLALMGPAFLAAIGYIDPCNFATN IQAGASFGYQLLWVWVANLMAMLIQILSAKLGATGKNLAEQI RDHYPRPVVWFYVWQAEIIAMATDLAEFIGAAIGFKLILGVSL QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLFLVAAAYIVELI FSQPNLAQLGKGMVIPSLLPTSEAVFLAAGVL\GATIMPHVI/YI WHSSLTQHLHGSRQORYSATKWDVAIAMTIAGFVNLAIMATAA SELNFYGHGTGVA |
| 6711 | 3 | 347 | VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDITNAHQIIFKELIML MAMLTWSYHDNMHDADYGPQQHRPG |
| 6712 | 118 | 578 | PHGQKRTRYQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLLPGENIDDWIAVHV VDFFNRIINLIYGTMAERCS*TSFVPMAGGPRIEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI |
| 6713 | 2485 | 3 | QARGSDSEGEFEIQAEDDARARKLGPGRPLPTFPPTSECTSDVE PDREMVRQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPIVILDGKDVVAMARTGSGKTACFLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIATPGRLVHVAVEMSLKLSVEYVVFDEADRLPE MGFAEQLOEIIARLPGGHQTVLFSATLPKLLVEPARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHAEYLTTELLTQTVSCAHIYSALDPTARKINLAKFTL GKCSLTIVTDLAAGLDIPLDNVINYSFPAKGKFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVDDEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESI KRAKEMDLVGLGLHPLFSSRFEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAAPSRPALQEKQPEKEEEEEEAGESVEDIFS EVVGRKQRSGPNRGAKRREEARQRDQEFYIPYRPKDFDSESG |

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|------------|--|--|---|
| | | | LSISGEGGAFFQQAAGAVLDLMGDEAQNLTGRQQLKWRDKKKR FVGSGQEDKKIKTESGRYISSYKRDLYQKWKQKQKID*S*L GRRRGILTRRRPRTBEVGEARPLAQAGCIPGPHAPRHPLQAESA LELKTQKQILKQRRRAQKAALSQRWWPQAALCPQ |
| 6714 | 169 | 1416 | NNCQELLPPPPAPMAHIPSGGAPAAAGAPMGPOVCCKVELSVS GQNLDDRDTVSKSDPFCVLTENNNGRWIEYDRTETAINNLNPAF SKKFVLDYHFEEVQKLKFAFDQDKSSMRLEHDFLGQFSCSLG TIVSSKKITRPLLLNDKPAKGGLITIAAQELSDNRVITLSLAG RRLDKKDLFGKSDPFLEFYKPGDDGKMWLVHRTVIKYITLDPVW KPFTVPLVSLCDGDMCKPIQVMCYDYDNDGGHDFIGEFQTSVSQ MCEARDSVPLEFECINPKKQKQKKNYKNSGIIILRSCKINRDYS FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP TNPPFCSGVDGIAQAYSACLP |
| 6715 | 32 | 493 | GPAGAESGSLHCLPATVQALAGAAHS PHGGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTGPOGQGEGRGSSLSIHS PSGPSSFPPTTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS AENVTFWKACERFQQIPASDT |
| 6716 | 1 | 176 | GAGGPAPRSFGSEEPRAALERDKMSARAAAAXSTAMEETAWEQ HTVTLHRVSLCCSK |
| 6717 | 115 | 896 | LFAMSGFENLNTDFYQTSYSIDDSQQSYDYGGSGGPYSKQYAG YDYSQOGRFVPPDMMQPOQPYTGQIYQPTQAYTPASPOPFYGN FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLG PMVFCIAFGATLLLAGKIQFGYVYGISAGICLGMFCLLNLSMT GVSFGCVASVLGYCLLPILLSSFAVIFSLQGMVGIIITAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF |
| 6718 | 290 | 599 | KQSTVPGTILPSLKHNSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEELGLLDVQNRNLYQDVMLENFRNLLSVGHHPFKHDFVL LEKEKKLDIMKTATQ |
| 6719 | 1 | 691 | PTREEQDREDGKCHKMEMNPISGNLNCPIAMSCSSDHGCET DLSDDDDKIEKPNFMKDSASQDNGLSRKISRKRVSSDSDSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLNVHT RSKNGRKKPLHLACTAKKLSDCGESHVCEVPSEQYACBGKPP DPDSEGSTKVLSQALNGDSSEDMLNSEKHRTNIHKIDAPSK RKSSSVTSSG |
| 6720 | 3 | 822 | HEVAEEAGGTVPQRGTMPGTRFQHVITPEPGKWELTGVEAA VPITEKSNPLTQDLDDKADAENIVRLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLSSGGTSGRMAF LMSVSFNQMLKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFPNPMARHPFPFPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE |
| 6721 | 3 | 822 | HEVAEEAGGTVPQRGTMPGTRFQHVITPEPGKWELTGVEAA VPITEKSNPLTQDLDDKADAENIVRLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLSSGGTSGRMAF LMSVSFNQMLKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFPNPMARHPFPFPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE |
| 6722 | 1 | 390 | RSWSKRTWQALPMAVLFLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPADDPGK PGRESRLRLGNYSWLLEGSKEEDAGRYWCAVLGQHNYQNW |
| 6723 | 173 | 659 | VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKQLALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL |

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|------------|--|--|--|
| | | | VEVKELQREPLTPBEVQSVREHLGHESDNL |
| 6724 | 173 | 659 | VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLSAHKESSFDIILSLGVPGSTTLHSABEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL VEVKELQREPLTPBEVQSVREHLGHESDNL |
| 6725 | 356 | 722 | RRRTFPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD ASWELVDPTPDQLALFVQFNDQFFWGQLRAVEVKWSVRMTLCAG ICSYEGKGGMCSIRLSEPLLLKLRPRKDLVEVFFV |
| 6726 | 98 | 714 | HLQKMERKINRREKEKEYEGKHNSLEDTDQGNCKNSTLMTLVNG GYLYITQKQTLTKYPTDFLEGIVNGKILCPFDADGHYFIDRDGL LFRHVLNPLRNGELLPEGFRENQLLAQEAFFQLKGLAEVKS RWEKEQLTPRETTFLEITDNHDSQGLRIFCNAPDFISKSI VLVSKSRDLGFPEEFSISSNIIQFKYFIK |
| 6727 | 1 | 831 | FRGMGDERPHYYGKHTPQKYDPTFKGPIYNRGCTDIICCVFLL LAIVGYVAVGIIAWTHGDPKVIYPTDSRGFCGQKGTKNENKP YLFYFNIVKCAPLVLLLEFQCPTPQICVEKCPDRYLYTLNARSS RDFEYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLFILLRFLAGIMG RGMIMGILVLGY |
| 6728 | 486 | 935 | FCSSWLRLSLADSSLSWKMLFVLGTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVPQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRRQLLNATHPEIRKEMMKETFKYFLREPTSPRGKK HVPSSALKEADSLMRRDT |
| 6729 | 259 | 1191 | VGLTGAQSGRTASMGDRQRAVAGPALRRWLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGVGPQGYNGPP GLQGFPGQLGRKGDKGERGAPGVTPKGDVGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCNGTQGDSPGQPPGSEGFTGPPGPGG PKGQKGEPYALPKEERDRYRGEPEPGLVGFQGPGRPGHVQGM GPVGPAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGESEGEPIRGISLKGEE GIM |
| 6730 | 784 | 1015 | NMVDYEVVLGLQRYASPEDIKKAYHKVALKWHPKNPNENKEEAE RKPFKEVAEAYEVLNDEKRDIDYKYGTEGLNEF |
| 6731 | 1 | 446 | GIRKRLHGAUVVPRVEVGCFWETRESEGVHLERPTSFLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCCLDLYEILTBEGTAKEATY NDLQVEYGGKQLQMKELMKKFKIEIQTNFSLINENQSLKKNISA LIKRTARVEINRKDEEI |
| 6732 | 102 | 1205 | GRWQRRPPPPSPPLWCLQPGGSDPQQLTLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPSRHRHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSDAPAYRTPPSRQGRREVRFSDPEPEVYGDFE PLVAKERSVPVGRTRLEEFRRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSFVMTRRGLRDSHSSSE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFESEGETEEDDQSSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW |
| 6733 | 613 | 1311 | RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRLKTSCECERKTKKSLELSKEDLI QLLSIMEGELQAREDVHMLKTEKTKFVLEAHYGSAAEPEKVL VLHRDAILAQEKSIGEDVYEKPISELDRLLEEKQKETYRMLLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDFTNLLEQERERLKK LLEQEKAYQARKE |
| 6734 | 189 | 551 | SAAMFFVFGSCFQELQEKNSLELVSFEEVAVHFTWEEWQDLDD AQRTLYRDMLETYSLSVSLGHCITKPEMIFKLEQGAEPWIVBEE |

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|------------|--|--|---|
| | | | TLNLRSLSGGSKKQVFSGICHRSLSLVEQLQEVHLV |
| 6735 | 280 | 558 | KSRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLITYGTI XDGCT |
| 6736 | 195 | 808 | MNYELNFKREMPNISKGLTNLNLFLKRLSSVLEPLITDYVYPEN SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRDISNTLIMLAD KHAKEIEBESETTVEADLTQKQKHLKRELFSLRQYESLPATH IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG EIRVGPRYQADIPEMLEGTFFCFVFAVL |
| 6737 | 150 | 1209 | PVIMPLHFSFGDIVRPSCCVSSSPKLRNNAHSRLSEYRPTDLS REDTGCNLQHSIDRENIDDLNMEFNPSPDHPRASTIFLSKQSQTVD REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP ANWKRIVLGAILLASKVWDDQAVWNVYDQCILKIDITVEDMNELE RQFLELLQFNINVPSSVYAKYFDFLRSLARANNLSFPLEPLSRE RAHLEAISRLCEDKYKDLRRSARKRSASADNLTLPWSPAIIS |
| 6738 | 148 | 653 | CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLL WGAPWTHGRRSNVRVITDENWRELLEGDWMEFYAPWCPACQNL QPEWESFABWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC KDGEFRRYQGPRTKKDFINFISDKWKSIIEPVSSWF |
| 6739 | 3 | 631 | SWPDMAEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKSSSSSFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSKELDLSANPEVMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEI IASHWVSEVEGVNKAL |
| 6740 | 3 | 631 | SWPDMAEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKSSSSSFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSKELDLSANPEVMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEI IASHWVSEVEGVNKAL |
| 6741 | 141 | 960 | PLTLFFSSRARAGHTMNTSPGTVGSDPVILATAGDYHTVRFWQA HSGICTRTVQHQSQVNALEVTTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIIHW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVFFSCLL PLAIGILQEGEFESLARRGLLFLACQGNVCVWNLTTGGIGDEVTO LIPKTKIP |
| 6742 | 141 | 960 | PLTLFFSSRARAGHTMNTSPGTVGSDPVILATAGDYHTVRFWQA HSGICTRTVQHQSQVNALEVTTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIIHW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVFFSCLL PLAIGILQEGEFESLARRGLLFLACQGNVCVWNLTTGGIGDEVTO LIPKTKIP |
| 6743 | 1 | 412 | MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPPKRISISKQLASVK ALRKCSDLKAIATTALIFRNSSDSGKLEKAIKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDDEFDMILLLSITVMSDL LQNIR |
| 6744 | 95 | 1343 | RTPARNRCAGCEVLSRFSSPNKASSPALQSAAGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHRARLKELFDSFDTTGTGSLGQBELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAPKPYVRGGKRYGRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEYEAEQGRLRFWNP DDNLNASQSGSSPPQDWIEKIQEVCELDLITRDGHLNRKKLVSI |

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|------------|--|--|---|
| | | | CEQYGLQNVGDGEMLEEVFHNLDPPDGTMSEVDFYGLFKNGKSLT PSASTPYRQLKRHLMSQSFDESGRRTTSSAMTSTIGFRVFSCL DDGMGHASVERILDWQEEGIENSQELKALDFGLDGNINLTEL TLALENELLVTKNSIHQACI |
| 6745 | 1 | 588 | TFRDQGWQRRRWLLGCASWESWEAAIAAGPLPSSTARQNNP AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP ELPVTSDCAVCLEVLHQPVTRCGHVFCRSCIATSLKNNKWTC PYCRAYLPSEGVPATDVAKRMSYKNCACEDTLVCLSEMAHI RTCQKYIDKYGPLQLEETA |
| 6746 | 110 | 492 | GATGAMAESAPARHRRRRSTPLTSSTLPSQATEKSSYFQTTEI SLWTVVAAIQAVEKKMESQAARLQSLGRTGTAEKKLADCEKMA VEFGNQLGKQWAVLGTLLQYGLLQRRLENVENLLRN |
| 6747 | 247 | 484 | EAVTFKDVAVVFTEEBGLLLDLAQRKLYRDVMLENFRNLLSVGH QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC |
| 6748 | 201 | 665 | MTTFKEAVTFKDVAVVFTEEBGLLLDPAQRKLYRDVMLENFRNL LSVGNQPFHQDTFHFLGKEKFWKMKTTTSQREGNSGGKIQIEMET VPEAGPHEEWSQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC QTEARLSISXVQXQPYRCNECKQ |
| 6749 | 95 | 719 | RREVKGDDGVCPRARGSPQSQFPSCAGGEGGLQSGEALDGAM SAGGPGCPAAAGGGPGGASCSSVGAPGGVSMFRWLEVEKEFDKAF VDVDLLLGELDPQADITYEGRQKMTSLSSCFQLCHKAQSVSQ INHLEAQLVDLKSBLTETQAEKVLEKEVHDQLQLLHSIQLQL HAKTGQSADSGTIKAKLSGSPSEELERELKAN |
| 6750 | 3 | 428 | SCESRRPGAKWVWASGALPRDITGLGSEQPSGDVAQSNRATMGT TAPGPIHLLLECDQKLMFLCNMDNLDLVWLEEQEAEARMFTR BFSKEPELMPKTPSQKNRRKKRIRISYVQDENRDPIRRRLSRKS RSSQLSSRR |
| 6751 | 152 | 1417 | PTKATEMAGASVKVAVRVPFNSREMSRDSKCI IQMSGSTTTIV NPKQPKETPKSFSFDYSWHTSPEDINYASQKQVYRDIGEEML QHAFEGYNVCI FAYGQTGAGKSYTMMGKQEKDQGGII PQLCEDL FSRINDTTNDNMSYSVBVS YMEIYCERVRDLLNPKNGNLVRVRE HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS SRSHAVFNI IFTQKRHDAETNITTEKVKISLVDLAGSERADST GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNNKKKKT FIPYRDSVLTWLLRENLGGSRTAMVAALSPADINYDETSLTLR YADRAKQIRCNVINEDPNNKLIRELKDEVTRLRDLLEYAQLGLD ITDMTNALVGMSPSSSLSALSSRN |
| 6752 | 24 | 1834 | RNCVPLGCRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL CDCTIVIGEFQFKAHRNVLASFSEYFGAI YRSTSENNVFLDQSQ VKADGFKLLEFIYTGTLNLD SWNVKEI HQAADYLVKEBVVTKC KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK SEVSTDLIOANPKQALAKKSSQTKKKKAFNSPKTGQNKTVQY PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDI VHTVTVKRKGKSPNCALKEHSMNSIASVKSPEYAE NSGEELDQRYSKAPMCNTCGKVFSEASSLRHRMIRIHKGVKPYV CHLCGKRAFTQCNQLKTHVRTHTEKPYKCELCGKFAQKQCLVF HSRMHGHGEEKPYKCDVNLQFATSSNLKI HARKHSGEKPYPVCDR CGQRFQAQASTLT YHVRRTGEKPYVCDTCGKAFVSSSLI THSR KHTGEKPFICELGNSYTDIKNLKKHKT KVHSGADKTL DSSAED HTLSEQDSIQKSP LSETMDVKPSPDMTLPLALPLGTEDHMLLPV TDTQSPSTDTLLRSTVNGYSEPLIFLQQLY |
| 6753 | 2 | 1305 | VPSPYPYPQKVVVAHTEFTTSSDSETANGIAKPDVPMPGGEEKAS PPGIKLRRTNYSRLFNCDQQAQKQKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRDRSAEPSSSRSPV AHFGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSTPPAS |

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|------------|--|--|---|
| | | | PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRPPSPFP GPEERKGGQRDEEEETERKPASPPLPATQQEKPSQTPEAGRKE KPMQLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE VSKRFSSPDDAPVSSPEAWLALAKRKAKAWSDCPLIIK |
| 6754 | 2 | 413 | FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE LSFSGGIPCEGGRLCLCWKILLNYLPLERASWTSILAKQRELYAQ FLREMIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD NEVLL |
| 6755 | 298 | 1343 | PGLQLQVALEADWFLDMPGGRGRRQQLSRALPSLQTLVGGG CGNGTGLRNRNGSAIGLPVPPITALITPGFVRHCQIPDLVDGS LLFEFLFFIYLLVALFIQYINIIYKTVMWYPYNHPASCTSLNFHL IDYHLAAFTVLMARRLVWALISEATKAGAASMIHYMVLISARL VLLTLCGWVLCWTLVNLFRSHSVLNLFLGYFPFVGVVPLCCFHQ DSRAHLLLTIDYNYVQHEAVESASTVGGAKSKDFLSLLES KEQFNNAFPIPTHSCPLSPDLIRNEVECLKADFNRHRIKEVLFNS LFSAYYVAFPLCFVKVSGYLTFCFLDLCVNIWVFLV |
| 6756 | 180 | 754 | IERALGSLPLSIPVSWGSLRTLKYQQQLRPKVLLCQTRVQCHD LRSLOPQPPLKQSFCLRVLGLQTGATTGRLDLCCKELIILTE REAQKRKKRKEKESGMALTQGLTPTRDVAIEFSQEWSKSLDPVQ KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSW PFHYLTETETALLTHK |
| 6757 | 2 | 459 | NSRVEAPEAHSRESQSDAMRKHLSWWLATVCMLLFSLHSAVQ TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID FGAEGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQQVLW |
| 6758 | 1 | 1008 | ASGFELPGRFRDRAFWLPARLLRGVLAVVWSLSALGPGSFCRR RVPSLAQLGHSEAPSPDDVRWSRVPDRCPEDRDRAWPPPPPS LPPSFRNMANNSPALTGNSQPQHQAQAAAAQQQQCGGGGATK PAVSGKQGNVLPWGNKTMNLNPMILTNILSSPYFKVQLYELK TYHEVVDEIYFKVTHVEPWEKGSRTAGQTGCGGVRGVGTGGI VSTAFCLLYKLFITLKLTRKQVMGLITHTDSPIRALGFMYIRYT QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSLFTKLE WFSTLFPRIIPVPVQKNIDQDIKTRPRKI |
| 6759 | 1 | 513 | RKHNHSLDGTSTRAHPQTGLPLLSSPVPQRKTQSGCFDLDSS LLHLKSFSSRSRPRCLNIEDDPDIHEKPLSSAPPITSLSLLG NFEESVLNYRFDPLGIVDGFTEVVGASGAFCPHTLTPVEVSFY SVSDDNAPSPYMGVITLES LGKRGYRVPSPGTIQVVCVL |
| 6760 | 239 | 606 | VLSKKKGLSAEEKRTRMMEIFSETKDVFPQLKDLEKIAPKEGIT AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKL VLESQSLSEGSQKHSALQKSIKAKIGRCETEERT |
| 6761 | 29 | 1733 | ERTLRGLREVAAPSDVADAASRRGRCCCLHCTQTQVAQDCPS SSSSVQRCESLFLQSLHTMTSKKLVSNSVAGCADDALAGLVACNP NLQLLQGHVLRSDLSLKGRRVALLSGGGSGHEPAHAGFIGKG MLTGVLAGAVFTSPAVGSILAAIRAVAQAGTVGTLIVKNYTG RLNFGIAREQARAEGIPVEMVIGDDSAFTVLKAGRRGLCGTV LIHKVAGALAEAGVGLEEIAKQVNVVKAMGTLGVSLSSCSVPG SKPTFELSADVELGLGIHGEAGVRRIKMATDEIVKLMMLDHMT NTTNASHVPVQPGSSVVMVNNLGLSLFLELGIADATVRSLEG RGVKIARALVGTFSALEMPGISLTLVDEPLKLLIDAETTA AWPNVAASVITGRKRSRVAPAEAPDSTAAGGSASKRMALVL BRVCSTLLGLEEHLNLDRAAGDGDGCTHRSRAARAIQEWLKEG PPPAPQALLSKLSVLLLEKMGSSGALYGLFLTAQAQPLKAKT SLPAWSAAMDAGLEAMQKYGKAAPGDRMTLDSLWAAGQEL |

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|------------|--|--|---|
| 6762 | 3 | 613 | ASTISWRLCVAGAEARRFPVAGERAGGGAMWFMVLLSWLSLFI QVAFITLAVAAGLYLAELIEBYTVATSRIIKYMIWFSTAVLIG LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG LVVVNHYLAFQFFABEYYPFSEVLAYFTFCLWIIFFAFVVSLSA GENVLPSTMQPGDDVVSNYFTKGRKG |
| 6763 | 2 | 760 | SGPDFPGRRRFRGCCVRRPPAGAGMELGGHWMNSAPRLVSETAE RKQEQTGTAEAAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP LLSLHVKSLSGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR SLLACILLSALGYLLGAATNVFLFVLARVPAGIFKHTLSISR ALLSDVVPEKERPLVIGHFNTASGVGFIILGPVVGGLTELEDGF YLTAFICFLVFIINAGLVWFFPRREAKPGSTE |
| 6764 | 80 | 438 | LKKMDTMMLSVRNLFQVLVRRVEILSEGNEVQFIQLAKDFEDFR KKWQRTDHELKGYKDLLMKAETERSALDVKLKHARNQVDVEIKR QRRAEADCEKLERQQLIREMLMCDTSGSIQ |
| 6765 | 3 | 550 | ARYSRVDHFCRRRCRAVARAPRFLLOFPFSGPSRHFACVARWL RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDLLSGSVLSSPNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGVETETE VIAIGLPFGKVTNIMLMKGKNQAFLELATEEAAITNGNYYSAVT PHLRNQ |
| 6766 | 1 | 1287 | EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGV RAVLSLCCQTSRSQPPVAFRLLISTLKDCKRGTRYELRENIEQFFT KPFDEGKATVRLKEPPVDICLSKANSSSLKGLFSAMRLAHRGN VDTVPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFFYSLEHL QTSYCGLVVRDMRLCLKSLRKLDSLHNHKKLPATIGDLIHLQ ELNLDNHLBSFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQBLKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSF RNLSEYLDLFGNTFEQPKVLPVIKLAQPLTLESSARTILHNR IPYGSIIIPPHLCQDLDTAKICVGRFCLNSFIQGTTIMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI |
| 6767 | 336 | 919 | APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDFRMKHLNV GRLOQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLOSDVKYKSDNLNLRGVGWT PPGSYKVMARRAAELANARGLGLQGAIRGAEEAVEAGDHQSGEV NPDATEILHVKKKKALLL |
| 6768 | 2 | 363 | PGSTISCYLLSEGLPLCMQVACGEEKHRAPTMTKLRLARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLOAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL |
| 6769 | 284 | 396 | MSTPDFSTAENNQELANEVSCLKAMLTMLQAMGQAD |
| 6770 | 1 | 397 | QRNYQVIWSSSTMAKLHDYKDEVVKLWTEFNYSVMQVPRVEK ITLNMVGGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDPRGLSAKS |
| 6771 | 3 | 378 | APAGTLAMTGRSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNKANRLYEAYLPETFRFPQIDPYLFWNSLEG |
| 6772 | 1 | 1400 | AAAFLOQMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYPFGSG\HKPRWLWGR\VLMTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMGLQFL HGVGATPLYTLGVTYLDENVKSSCSPYIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRTELTTESPLWVGAWVWVFLGSGAAFFT AVPIILGYPRQLPGSQRYAVMRAAEMHQLKDSRGEASNPDGKT IRLPLSIWLLKNPTFILLCLAGATEATLITGMTSTFSPKFLES QFSLASEAATLFGYLVVPAGGGGTFLGGPFVNKLRLRGSVAVIK FCLFCTVVSLLGILVFSLHCPSPVMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG QKYVRDCSIPQNLSSGFGHATAGKCTST |

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|------------|--|--|---|
| 6773 | 1 | 630 | PWEAPKEHKYKAEHTVVLTVTGEPCHFFQYHRQLYHKCTHKG RPGPQPCATTNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT CVNMPSPGPHCLCPQHLTGNNHCQKEKCFEPQLLRFFHKNEIWYRT EQAAVARCQCKGPDHACQRLASQACRTNPFCLHGGRCLEVEGHRLL CHCPVGYTGPPCDVGE*GSGASRRPAPRWDLAR |
| 6774 | 146 | 389 | LTELSDQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIIS GLRIGFLTGPPLIERVILHIQVSTLHPSTFNQLMISQ |
| 6775 | 104 | 614 | TCPSQLRVLTARGGRAPSPQLWTLVLALIEEKWRSHRILRMNS GRPETMENLPALYITIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT HMSSCRVDKPEIVDVGDKVWVKLIGREMKNDRIVSLSMKVVN QGTGKDLDPNNV\SLSKKRGGGDPSPRITLGRSPRLRLS |
| 6776 | 3 | 1108 | HERHERHEGALSQDALLRISIFLDSNMRPEKCRRFVHPQWQLLH LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSSQL TSVAKFVFMAGMMVGGILGGHLSDFRGRFVLRWCYLQVAIVGT CAALAPTFLIYCSLRFSLGIAAMSLITNTIMLTAEWATHRFQAM GITLGMCPSGIAFMTLAGLAFIRDWHILQLVVSVPYFVIFLTS SWLLESARWLIINNKPPEGLKELRKAHRSGMKNARDTLTLEIL KSTMKELEAAQKKKPFLEGRHMPNICKRISLLPFTKFANFMA YFGLNLHG/LKHLGNVFLQLTLPFQAV/TPPGQLVLHLGHWSG RVSSRGVNCGLFLVLQVW |
| 6777 | 779 | 63 | CFHGPAPWRDCEVRATFAKKQGGSGIISCIAPSPAQPLYACGSY GRSLGLYAWDDGSPALALLGGHQQGITHLCFHPDGNRFFSGARKD AELLCDLRLQSGYPLWSLGREVTNQRIFYDLDPQTGQFLVSGST SGAVSVWDTDGPNDGKPEPVLSFLPQKDCNTGVSLLHPSLPLLG HCLPVSVCFSLSPTESGGRRRGAGPSLGSPPRHVHLECRLLQLWWC GGGARLQHP**SPRARKGR |
| 6778 | 311 | 805 | IQSITDESRSIRRNKPANTRLRLNVP\ETAGDSE/ERSPEER VQADPRIASAPKCPSTSPFPKGRSPEGEGET\DPEKVHFPHPG KDKSVAEK\KGP\SPVSSSEGIKDFFSMKPEWENLQSNVRRMH T\AVRLNEVIVKSRDAKLVLNMPGPPRRNRNGDENV |
| 6779 | 2 | 535 | RALRRQPRLLAANGIEPESMAISEPIKGRKPCVNKEELAKKP MAKCAWKGPREPQDARAEAESPGGASESDQDGGHESPPKKKAV AWVSANPAPMRKKKVSIGPVSYVLVDSBDGRKKPVMPPKGGP SRREASDQKAPRQQAETASTSRGPKAKPEGSPPRATNESRK V |
| 6780 | 3 | 403 | HEVNDNKPBININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD SGLNGEIVCKLHGHHFKLQKTYENNYLILTNATLDREKRSEYS LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE K |
| 6781 | 1 | 1269 | AFTRPVFPFTLQDLSSSKEPSNSINLPHSNELCSSLVHPSELSEVS SNVAPSIIPVMSRPVSSSSISTPLPPNQITVFTSNPITTSANT SAALPTHLSALMSTVVTMPNAGSKVMVSEGGQSAQAQSNARQFI TFVFINSSSI IQVMKGSQPSTIPAAPLTNLSGLMPPSVAVVGLP HIPQNIKFSAPVPPNALSSSPAPNIQTGRPLVLSRATPVQLP SPPCTSSPVVPSHPPVQVVELNPDEASQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKQKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVPGGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG |
| 6782 | 3 | 1327 | RKPTVIRIPAKPGKCLHEDPQSPPLPAEKPIGNTFTSVSGKLS NVERTNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK VPPERPPPKLSATRRSNKKLPFNRSSDMDLQKKQSNLATGLS KAKSQVFKNQDPVLPKPKPGHPLYSKYMLSVPHGIANEDIVSQ NPGELSCKRGDVLVMLKQTENNYLCQKGEDTGRVHLSOMKLIT PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV |

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|------------|--|--|--|
| | | | DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGNGKRECVSSHCVKGSRCVARFEYIGEQLDELFSFEGEIII LKEVYNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV PLKTKKEDSGSNSQVNSLPAEWCEALHSPTAETSDDLFSFKRGDR I |
| 6783 | 3 | 1750 | SYHHHHAQQSAAASPNTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQAVALSDVQNTPVNLQTSSKVT GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDHLLEIQSKRQERKRRTANPVYSGAVFE PERKKSAVTYLNMHPGTRKGRPPKYNVAVLGFGALTPTSPQS SHPDSENEKTEFTTFFPAPVQVSLPSPSTSDGDIHEDFCSVC RKSGQLLMCDTCSR VYHLDCLDPPLKTIKGMWICPRCQDQMLK KEEAIWPWGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVQKLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSSEATVGAI SNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK |
| 6784 | 3 | 1750 | SYHHHHAQQSAAASPNTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQAVALSDVQNTPVNLQTSSKVT GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDHLLEIQSKRQERKRRTANPVYSGAVFE PERKKSAVTYLNMHPGTRKGRPPKYNVAVLGFGALTPTSPQS SHPDSENEKTEFTTFFPAPVQVSLPSPSTSDGDIHEDFCSVC RKSGQLLMCDTCSR VYHLDCLDPPLKTIKGMWICPRCQDQMLK KEEAIWPWGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVQKLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSSEATVGAI SNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK |
| 6785 | 1 | 528 | LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR LKAQCEDDLSSQAKSGKFNPHVHVEYEWNLQREEIDESDDDDDD KPSVPKKERSPRPQSFCSSSISPQDKLALPGFSTPRDKQRLSY GAFTNQIFVSTSDSPTSPTTEAPPLPPRNAGKGTGPPITPHR |
| 6786 | 1820 | 1397 | RSPKVLVLAPTRELANHVSRDFKDI\TRKLTUARFVGGTSVQSQ INHNRNGIDILVGTGRIKDHLSQGRDLKSLRHVVLDDEVQML DLGFAEQVEDIIHESYKTDSEDNPTLLFSATCPQWVYTTVA\KK YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPVIGDVLQ VYSGSEGRAIIFCETKKNVTAMAMNPHIKQNAQCCLHGDIASQR EITLKGFFREGSPKVLVATNVAARGLDIPVDLVIQSSPPQDVES YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFRVG VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQLRIEEKGAV DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC ANKELNRKLSSNAVSIITRMCLLKGNMGVCFDVPTTESERLQAE WHDSDWILSVPAKLPEIEEYDGNSTSSNSRQRSGWSSGRSGRSG RSGGRSGRSGRQSRQSRSGRQDGRRRSGNRNRSRSGGHKRS FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS SVWN |
| 6787 | 2646 | 2270 | PSSFKNVPLEELEPPK*KRSGLSLTPKSIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI LVFLVEMGFHHVQAGLKLLTL\VIHPPWPKVLGLQT |
| 6788 | 16 | 936 | GGTVDLR\DM LAVSVLA AVRRGR\ATVRRVRESNVLHEKSKGKT REGAEDKMTSGDVLNRMFYLLKTAFFSVQINTEEHVD\ELDQ |

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|------------|--|--|---|
| | | | EVILWGS*DS*GYPKKG*LLPKEVPSR/RVLLSGLTPLDATQE\FTEDLSK\YVTTMVCVAVNGKPMGLVVIHKPFSEYTAWAMVDGGS NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG AGYKVLALLDVPDKSQEKADLYIHVYTIKKWDICAGNAILKALG GHMTTSLSGEEISYTGSDGIEGGLLASIRMNHQLVRKLPDLEKT GHK |
| 6789 | 2 | 678 | GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA GSLAGAIQAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE GVAIFYKGYVPNMLGIIPIYAGIDLAVYETLKNALQHYAVNSAD PGVFWLLACGTMSSTCGQLASYPLALVTRMQAQASIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVYENLKI TLGVQSR |
| 6790 | 2 | 4068 | APPAGRRRRQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD EPLVSGPLPHVAFSSSSSSISGSYSPGYAKINKRGAGGWSPSDS HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSIDTGRNW KPYHQDGNIAWAPGNINSDGVVRHELQHPHIIARYVRIVPLDWN EGRIGLRIEVYGCSYADVINFDGHVVLPRFRNKKMKTLDKDI ALNFKTSESEGVILHGEQQQDYITLKLKAKLVLSNLGSLNQL GPIYGHSTVMTGSLDDHHHWSVVIERQGRSINLTLDISMQHFR TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG RLNQDLFSVSFQFRTWNPNGLLVFSPHADNLGNVEIDLTESKVG VHINITQTKMSQIDISSGSLNDGQWHEVRFLAKENFAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNQMNSSSHSVLQPSFQGC MQLIQVDDQLVNLVEVAQRKPGSFANVSIDMCALIDRCVPNHCE HGGKCSQTWDSFKCTCDEGTGSGATCHNSIYEPSCEAYKHLGQT SNYYWIDPDGSGPLGPKVYCNMTEDKVTIVSHDLQMOTPVVG YNPEKYSVTQLVYSASMDQISAITDSABYCEQYVSFYCKMSRL NTPDGSPTTWVWGKANEKHYYWGGSGPGIQKACGIERNCTDPK YYCNCADADYKQWRKQDAGFLSYKDHLVPSQVVGDTDRQGSEAKL SVGPLRCQGDNRNYNAASFNPSSYLHFSFTQGETSADISFYFK TLTPWGVFLENMGKEDFIKLELKSATEVSFSDVGNPVEIIVR SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL ELYSQLFVGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI SGCSGHCTS YGTNCENGKCLERYHGYSCDCSNTAYDGTFCNKD VGAFEEGMWLRNFPQAPATNARDSSSRVDNAPDQNSHPDLAQ EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG GTREPYNIDVDHRNMANGQPHSVNITRHEKTI FLKLDHYPSVSY HLPSSSDTLFNSPKSLFLGKVIETGKIDQBIHKYNTPGFTGCLS RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM SSATDPWHLHLDSASADFPYNGPQQQAIRNGVNRNSAIIIGGVI A\VVIFTPLCTP\VLP*SR*HVS PHKGTLP IPNEAKGAGSRQK KPGRRPSMNDPPTSQRPIDESKKEWPHLRGGYLAG |
| 6791 | 1801 | 1193 | TGHEGAKGEKGDGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW SAVV*SWLTAATKVAIILLPQPLE*LGLQIAFMASLATHFSNQ NSGIIFSSVETNIGNFFDVMTRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW LRMNGALHGDHQRFTFAGFLLFETK |
| 6792 | 33 | 1073 | VRHTNWGVDMYLFSLGSES PKGAIGHIVSTEKTILAVERNKVLL PPLWNRTFSWGDDFSCCLGSYGSDKVLMTFENLAAGRCLCAV CPSPTTIIVTSGTSTVVCWELSMTKGRPRGLRLRQALYGHQAV TCLAAVTFSLVSGSQDCTCILWDLHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDEVCSWTASRRG APGSASKPKRPQVGEEPLESRAGR*HCFDREAQQNQF\ PVTAL AVSRNHTKLLVGDERGRIFCWSADG*EEGRSGSGTIVPG |

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|------------|--|--|--|
| 6793 | 2340 | 805 | GRKEANY\YGS LTQAGTVSLGLDAEGQEVFPVFSAVLPMVAFND LVFDGWDISSLNLAEMRRRAKVLWDGLQEQWLPHMEALRPSPSV YIPEFIAANQSARADNLIPGSRAQQLQIRRDIDFRSSAGLDK VIVLWTANTERFCEVIPGLNDAENLLRTIELGLEVSPSTLFAV ASILEGCAFLNGSPQNTLVPGALELAWQHRVFGGDDFKSGQTK VKSVLVDFLIGSGLKTSIVSYNHLGNNDGENSELAPLQFRSKEV SKSNVDDMVQSNPVLYTPGEEPDCVVIKYVPYVGD SKRALDE YTSELMGLGTNTLVLHNTCEDSLLAAPIMLDLALLTELQCRVSF CTMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVNNALFRQRSCI ENILRACVGLPPQNHMLLEHKMERPGPSLKRVPVAAATYPMLNK KGPVPAATNGCTGDANGHLQEPPMPTT*GPGHTVSRFLPAAP HDPTLKAFTNKGRCHFSPPTWGSWGL |
| 6794 | 169 | 1349 | DDVKKRKEASAH*EKPGPPSRPGVRRGRERAGRGSHGARSCR\ EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGKTYTQRCRLFVG NLPTDITBEDFKRLFERYGEPSEVF INDRGFGFIRLESRTLAE TAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELEQA FSQFGPVEKAVVVDDRRGRATGKGFVEFAAKPPARKALERCQGD AFLLTTPRPVIVEPMEQFDDDEDGLPEKLMQKTQQYHKEREQPP RFAQPGTFEFYASRWKALDEMEKQOREQVDRNIREAKEKLEAE MEAARHEHQLMLMRQDLMRQEEELRLLEELRNQELQKRKQIQLR HEEHRRREEMIRHREQEELRRQEGFKPNYMENYVCHFLR |
| 6795 | 1740 | 1010 | GPRRQTQVRDHELDSE*DWAAQETDCAQNSGERL* KGV/LENFS TMSKSAVKISLDLNSNPLCEQDQDLDLNMVLTALDTAMKRMDAFNQ EKVNIQKTVEIPLKKFGSVFPSLNMVAKRREQUALQDYRRLQAK VEKYEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEMPR FYGSRLDYFQPSFESLIRAQVYVYSEMHKIFGDLSHQLDQPGHS DEQREERENEAKLSELRLSIVADD |
| 6796 | 48 | 683 | GKEIQIPTIKLAWLLFGL*PVGALGKGVVSF**SHVALGQLGW LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGCPSLNPPET SVQBGDRDCWQR*LPRLFSAVVGQPGCWPGAPPERCV*PGRCKW HLQSQVLR*ERRRCCRLPRFA*GWRRRHQRGLGLIHAPLPGST SPHPPEGNSQQCR*GWAAELRLPSSVVL*GKLGK* |
| 6797 | 1620 | 211 | TERMTPSQPTRGSSCTRFSSMLWTSTWRCLTCHWAGMRMSVVG V TLGPMAGLLSASGTTTTEATWTRPTHTLIRWLLTASRVDP ERPPPPPSDDLTLLESSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPAS*SRLTTKHTVGGSPSAWRPRPTSRS VSTPVSSSTETTASGSCLTWWSPPAPCPSSSAPAHSEASCK TSLWGS CGSGDGSACGSGWNLSMAGTSCSSPAMCSPSRAPS* RSASRPRTWRATTSAASSWAPRRWCWGA*SAT*PSSTTTISS PHCGWPCPASCASAAWLSSTWATASVAGSCWGPIM*SSAHS PW CLSACSRSSMGTTC*RSPP\SGASRAAAWCGSSPSSTFTPS ASSSTWCSASSRSPAPTTTPSSI PAAQAQRASCRPTSHSART APPPASSAAGAARPAAFSAAEGTPRRSIRCW |
| 6798 | 3894 | 1696 | STISWESLESWLNKATNPSNRQEDWEYIIGFCQINKLEGG*VS ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ/PQIA VRLLAHKIQSPQEWELQALTYLGDVSEKVKTKVIELLYSWT ALPEEAKIKDAYHMLKRQGIQSDPPIPVDRTLIPSPPPRPKNP VFDDEEKSKLLAKLLKSKNPDDLQEBANKLIKSMVREDEARIQV TKRLHTLEEYNNVRLLEMLLHYSQEDSSDGDRELMKELPDQC ENKRRTLFKLASETEDNDNSLGDILQASDNLRSVINSYKTIIEG QVINGEVATLTPDSEGNSSQCSNQGTLDLAELEDTTNSLSSVLA PAPTTPSSGIPILPPPPQASGPPRSRSSQAEATLGPSSSTSNAL SWLDEBLLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPPFAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLEEAQVTSGLVKPTTSPLIPTTTTPARPLLPSTGPGSPFLQ |

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|------------|--|--|--|
| | | | PLSFQSQGSPFKGPELSLASHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPPGRPDVLLVVVSMNLNTAPLVKSIVLQAAPVKS MKVKLQPPSGTELSPPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVGEVDQFPFVEQWGNL |
| 6799 | 3894 | 1696 | STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS ALWQQLRGSGLRGRTTMAKEGQPGSPRLSALECVLLVPQ\POIA VRLLAHKIQSPQEWELQALTYLGRVSEKVKTKVIELLYSWTM ALPEEAKIKDAYHMLKRGIVQSDPPIPVDRTLIPSPPRPKNP VFDDEEKSKLLAKLLKSNPDDLQEAANKLIKSMVREDEARIQKV TKRLHTLEEVMNNVRLLEMLLHYSQEDSSDGDRELMKELFDQC ENKRRTLFKLASETEDNDSNLGDILQASDNLRSVINSYKTIIEG QVINGEVATLTLPDSEGSQCSNQGTLIDLAEELDTNSLSSVLA PAPTPPSSGIPILPPPQASGPPSRSSSQAEATLGPSSSTSNAL SWLDEELLCLGLADPAPNVPPKESAGNSQWHLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPFPAPVVPASVP APSAGSSSLFTGTGAPALAPKVEPAVPGHGLALGNSALHHLDAL DQLEERAKVTSGLVKPTTSPLIPTTTPARLLPFSTGPGSPLEFQ PLSFQSQGSPFKGPELSLASHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPPGRPDVLLVVVSMNLNTAPLVKSIVLQAAPVKS MKVKLQPPSGTELSPPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVGEVDQFPFVEQWGNL |
| 6800 | 404 | 1646 | RRSPSTGLSPVPQSPSSPSLSDYSIPWSLLSGTIAWATPGK*AG *PQAW*LGLAPAIIFI/GLTRGRKQNKKEKMAEGSGDVEDDAGDC SGARYNDWSDDDSDNESKSIWYPPWARIGTEAGTRARARARA RATRARRAVQKRASPNSDDTVLSPOELQKVLCLVEMSEKPYILE AALIALGNNAAYAFNRDIIRDGLGLPIVAKILNTRDPIVKEKAL IVLNNLSVNAENQRRLKVYMNQVCDTITSLNSSVQLAGRLRL TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLNLAE NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN FKWEENEPTQNGFEGGSLFFFLKEFQVCADKVLGIESHHDFLVK VKVGKFMAKLAHEHMFPSQE |
| 6801 | 2 | 1755 | SAEEFESQQAQSVTMHVDVAESFEVLVDVYCTGRVSLSEANVERL YAASDMLQLEYVREACASFLARRDLTNCTAILKFADAFGHRKL RSQAQSYIAQNFQQLSHMGSIREETLADLTLAQLLAVLRDLSDL VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTBEDQD YLEGLLTKEPIVKKYCLDVIEGALQMRYGDLLYKSLVPVNSSSS /R*QQQLSCICSRKSTPETGYVCQGDGDLWTQPSLS\RYDPY SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDYLAAPRKLW VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPIITGVK LKEVECYSVQRNQWALVAPVEHSFYSEFELIVVQNYLYAVNSKRM LCYDP SHNMWLN CASLKRSDFEACVFNDIYICIDI PVMKVYN PARGWRRISNIPLDSETHNYQIVNHDQKLLITSTTPQWKQNR VTVEYDTRDQWINIGTMLQLQFDSGFICLCARVYPSCLPEPG QS FITEEDDARSESTEWDLDFSELDSESGSSSSSFSDDEVWVQ VAPQRNAQDQGS |
| 6802 | 157 | 1341 | ETFFLFFFLSKTPGKTASMAHFVQGTSMIAAESSTEHEKCAE PSTRKNLMNSLEQKIRCLEKQKRELLEVNQQWQQFRSMKELYE RKVAELKTKLDAAEFLSTREKDPHQQRKDDRRQREDDRRDLT RDRLOREBEKEKERLNEELHELKEENKLLKGKNTLANKEHEYEC EIKRLNKALQDALNICKSFSEDCLRKSRVBFCHHEMRTEMEVLK QQVQIYEEDFKKERSDRERLNQEKEELQINETSQSQNLRLNSQ IKACQMEKEKLEKQLQMYCPCNCGLVFHLQDPWVPTGPGAVQ KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRE G |
| 6803 | 1 | 2203 | KLSGRPYRHMGLVGTSKLYDIRKTIFFTFPOFIDQQQFYLALDN |

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|------------|--|--|---|
| | | | <p>KMIVEMLRITDLSYLCRWRTGQPTITFPISHSMLDEDEGTSINS SILAALRKMQDGYFGGARVQTGKLEFLTSCCTHLSFMDPGPE GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL AHTAPHKPLAPTSQKGLDRFQAQVQTTCDLMSLVTKAKELHVQ NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD QSSEVDFKALVLQKETSLSLQEQADILYMLYTMKGPDWNTLYN ERSATVRELLTELYGKVGIEIRHWGLIRYISGILRKKVEALDEAC TDLLSHQKHLTVGLPPEPREKTI SAPLPYEALTQLIDEASEGDM SISILTQEIIMVYLAMYMTQPGLFAEMFRLRIGLIQVMATELA HSLRCSAEAEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR PTDSNVSPAISIHEIGAVGATKTERGTGIMQLKSEIKQVEFRRLS ISAESQSPGTSMTSPSGSFPSAYDQSSKDSRQSQWQRRRLDG ALNRVPVGFYQKWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK FSVHVES\VLNVLRLPEYRQLLVEAILVLTMLADIEIHSIGSII AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD SAPSGRFGTMTYLS\RAA\ATYVQEFPL\HSICAMQ</p> |
| 6804 | 1 | 951 | <p>GSFGKKEEKAKNKESELCMENSSNSSSDEDEETKAKMTPTKKYN GLEEKRSRLRTTGFYSGFSEVAEKRIKLNNSDERLQNSRAKDR KDVWSSIQQWPKKTLKELFSDSDTEAAASP PHPAPEEGVAEES LQTVAEESCSPPSVELEKPPFVNVDKPIEKTVEVNDRAEFP SSGSNFS* IPLPYLHLNRLHQS* KQGSRQSSVTVSEPLAPN QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF* CQCEL KQ**SARTRTS* KSLYRSEKSEKSGRRKFIKKAEEKP* SNSGK QQKEGKRHK</p> |
| 6805 | 1539 | 206 | <p>RQPDLYFGKSFDFVSSESSSLNSNDLPKPADGIKARNRNQNYL VPSPLRILDHAFSTEKSADIVICDEECDSPEVNVQQTQEESE IEVHTAEDVPIAVEVHAISEDYDIETENSSSESLQDQDEEPPA KLCKILDKSQALNVTAQKQWPLLRANSSGLYKCELFNSKYP DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSELY LHFQEHSCDEQYLQCFCEHETNDPEDLHSHVNEHACKLIELSD KYNGEHGQYSLSLKITFDKCKNFVFCVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSGIIYLCQYW EYSTGQIEDLKIHLDFKHSADLPKCSDCMLRFGNERELISHLP VHETT</p> |
| 6806 | 272 | 3794 | <p>VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLGSGVFLALTTDACQKGLPKAQTGEVAAPKGWPPLSWLVI DGKHLAKPPKDWHLAQTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEATLTNVLDFKRDAGLWHGVLTSMVNR MHVSVVPYALMKANPLSWIQKVCIFYKARAALVKSMDHWSLLAQ RGQRDVSLSSRLMIVADGANPWSISSCDAPLNVFQSRGLRPEV ICPCASSPEALTVAIRRPDLGGPPPRKAVLSMNGLSYGVIRVD TEBKLSVLTVQDVGQVMPGANVCVVKLEGTPYCKTDEVGEICV SSSATGTAYYGLGITKNVFEAVPVTGGAPIFDRPFTRTGLLG FIGPDHLVFIGKLDGLMVTGVRHNDVATALAVEPMKFVY RGRIVFVSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLPCHN VLMCPHTCVTNLPKPRQKQPEVGPASMI VGNLVAGKRIAQASGR ELAHLEDSQARKFLFLADVLQWRAHTTDPHPLFLLNAGTGT STATCVQLHKRAERVAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPTVRPPHQNLTTLPTVKMIVEVSKSACVLT QAVTRLLRSKEAAAVIDRTWPTILDITDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRS IKLQCELYPSRQ IAICLDPYCGLGFLWCLCSVYSGHQSVLPPELESNVSLWLS AVSQYKARVTFCCYSVMECTKGLGAQTGVLRMKGVNLSCVRTC MVVAERP\RIALTQSFSLFKDLGLPARAVSTTFGCRVNVIAIC</p> |

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|------------|--|--|--|
| | | | LQGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL PGVKVIIAHTETKGPLGDSHLGEIWSVSPHNATGYTVYVYGEAL HADHFSARLSFGDTQTIWARTGYLGFLRTELTDASGGRHADLY VVGSLEDTLELRGMRYHPIDIETSVIRAHRSIAECAVFTWNL VVVVELDGLQDALDLVALVTNVVLEEHLVVGVVVIVDPGVIP INSRGEKQRMHLRDGFLADQLDPIYVAYNM |
| 6807 | 1444 | 606 | VGHDTVHAMFTCFPKCLGFSFPVNVTVSPRSESHTTTVSGGNG SVFQAGPQLQALANLEARRGSIGAAALSSRDVSGLPVYAQSCEPR RLTAQQAFAAPGENALEHSSDQDTWDSLRSPGFCSPSSGGGAE SLPPGGPGHAEAGHLGKVCDFHLNHQQSPSTSVLPTEVAAPPLE KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTGECRLSLSGDLN RFPCEMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLDRSR FLFRLPMGLSCPLQVQ |
| 6808 | 2063 | 737 | GVGGAASALARSRLASRLSSRRRTRAPRSGAMQRLAMDRLML SRELSLYLEHQVRVGFSGVGLSLILGFSVAYAFYLLSSIAKK PQLVTGGESFSRFLQDHCPUVTETYYPTVWCWEGRGQTLRPF\ ITSKEPPVQYRNELIKTAGGQISLDWFDNDNSTCYMDASTRPTI LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGMLLLNLYL GKIGSKTFLMAAATFSVGWNTFACSESLKPLNWLFFNYLLTTC LQSSVNHHRMFVKQVMDHVMKAKSIREFDKRFTSVMFYQTI DDYYTDAASPRLKSVGIPVLCNSVDDVFSHPHAIP IETAKQN PNVALVLTSGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH ELS |
| 6809 | 939 | 65 | DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTKQPKRLHVSNI PFRFRDPLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGLTIV EGRKIEVNNATARVMTNKKTGPNYTNWGLNPNVVGAVYGFPEFYA VTGFPYPTTGTAAYRGALHGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRLFLGP |
| 6810 | 939 | 65 | DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTKQPKRLHVSNI PFRFRDPLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGLTIV EGRKIEVNNATARVMTNKKTGPNYTNWGLNPNVVGAVYGFPEFYA VTGFPYPTTGTAAYRGALHGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRLFLGP |
| 6811 | 1522 | 658 | DLVTVVSFVDCRVIASTHGH\KSWVSVAFDPTYTSVEEGDPME FSGSDEDFQDLLHFGDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHNVNMNATSPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDKRKHHEKDKHNRHSMGHISKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLEPLICKIAHERLTVLIFLEDICI VTACQEGFICTWGRPGKVVSFNP |
| 6812 | 4001 | 1682 | EDAVFSLDLSSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLLIHAVKHQDSGALVGFSVCPGVQDSAAITIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTGVSFAFGVTVDPPV HIVDPREHVFVHAITSECVMACEV\DR\EDAPVRWYKDGQVEVE ESDPVLLENEGPHRRLLVLPATQPSDGGEFQCVAGDECAFTVTI TDVSSWIVYPSGKVYVAARLVRVLTCELCRPWAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPVQLEDSEYLCIEDDESASFV VTVBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVEESEALVLERDGPRLVLPAAQPEDGGEFVCDAGDDSA FFTVTVTEPPVQFLAETTPSPLCVAPGEPVVLSCELSRAGAPV |

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|------------|--|--|---|
| | | | VSHNGRPVQEGEGLELHAEGPRRVLCIQAGPAHAGLYTCQSG AAPGAPSLSTFTVQVAEPFVRVVAPEAAQTRVRSTPGGDLELVVH LSGPGGPVRWYKDGGERLASQGRVQLEQAGARQVLRVQGARSGDA GEYLCDAPQDSRIFLVSVVEPLLVLKLVSDLTPLTVHEGDDATFR CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART CVSKWRQAEWVQRGPCAGCEVGSPPCTTLACPWFRMGSTSTASS MVSYWPTRAPTAARATTIAPWPGSA |
| 6813 | 9 | 836 | SSTQQRPGVPAGPRPLDGYLGVDHKLPMHCRDCALVTSSGHL LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRSTSLRVIAHSSI QRILNRHDLNLSVQGTVFIFWGPSSYMRRDGKQVYNNLHLLS QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYEYFPGPDEC TMYLSHERGRKGSXHRFITEKRVFKNWARTFNIHFFQPDWKPEPES LAINHPENKPVF |
| 6814 | 3 | 737 | KFRROEAN/ARENRMHGLNDALDNLKRVVPCYSKTQKLSKIET LRLAKNYIWAELSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG CLQLNARSFLMGQGEAAHTRSPYSTFYPPYHSPELTTPPGHG TLDNSKSMKPYNYCSAYESFYESTSPECASQFEGPLSPPPINY NGIFSLKQEBTLDYGNYNMGMYCAVPPRGLGQAMFRLPTD SHFPYDLHLRSQSLTMQDELNAVPHN |
| 6815 | 906 | 553 | QGLDPASQTKVVELLDKDGSGRRGDRSRSDMAGGAGPRSESDLE DVGPATAEWNGDGSGLRRSGSGFKLRDALRRSSEMLVKLQGGT PQEPNPRMKRASSLNFLNKSVEEPTQPGG |
| 6816 | 1 | 803 | NLLKTHKF\LLGQDEDSLHSVPVQMGNYQBYLKTLASPLREID PDQPKRLHTFGNPFKQDKKGMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMSLLLRKPQTPTVTNHHVGGKPPSASWFPSPYN LIKPTLVHTDATIIHDGHEEKMEGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDFTSLSKDGLIQKPGSNAFVGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK |
| 6817 | 172 | 3457 | LGMMDSPKIGNGLFVIGPGTDIGISSLHMVGLGNFDSAKVPS DEYCPACKEKGLKALKTYRISFQESI\FLCEDLQCIYPLGSKSL NNLISPDL EECHTPHKPQKRKSLESSYKDSLLANSKKTNYIA IDGGKVLNSKHNGEVDYDETSNLPDSSGQNP IRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSQNEGCTSKLEMPLESKE TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYSQLSGVKDGDCCKLTSEIFAEIET CLNEVRDEIFISLQPLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSDWFECSQCGHQYQNRHMSLVTFNTVPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFTWILDADGSWLECDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPKKTNDQHALSNE KPVSLTSCSVGDAASAEASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNLPPLTLEETIQKTASVSQLSNEAFL\LENKPV AENTGILKTNLLSQESLMASVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKETTADSQTTSKSLQNO SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKASKPPPI SKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSYNGGISSANH EDLVBGGQIHKRLKRLKRLKAEKKLAALMSSPQSRTVRSNLE QVPQDGS PNDCEI EDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNVCSPTKKNPCVQPDLSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY |
| 6818 | 2 | 240 | RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTTYTL |

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|------------|--|--|---|
| | | | DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI |
| 6819 | 1 | 961 | GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY GEEKKKKCNPYVKTYLLPDRSSQGRKRTGVQRNTVDPTFQETLK YQVAPQLVTRQLQVSVVHLGTLARRVFLGEVVIPLATWDFEDS TTQSFWRHPLRAKADKYEDSVQSNGLTVRAKLVLPSPRPRKIQ EAQEGTDQPSLHGQLCLVVLGAKNLVPRPDGTLNSFVKGLCTLP DQQLRLKSPVLRKQACPOWKHSFVFSGVTFAQLRQSSLELTVM DQALFGMNDRLGGT\RLGSKGDTAVGGDACSQSKLQWKVLSS PNLWTDMTLVHL |
| 6820 | 1014 | 340 | GDMVYIVGHVPPGFFFEKTQNKAWFREGFNEKYLKVRKHHRVIA GQFFGHHTDSFRMLYDDAGVPIISAMFITPGVTPWKTTLPGVVN GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMTVLDRIDAGDQSTLQRYVYVNSVSYSAG VCDEACSMQHVCMARQVIDDAYTTCLYASGTTFPVQPLPLLMAL LGLCT |
| 6821 | 1088 | 518 | EFDIYR/EVGGEFVFPVTRDDSSNGFPRTQHGFSPTVHPIQSPQN RFCVLTLDPELPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHALVPEDGI GSVIEVLQRRQEGLAS |
| 6822 | 1088 | 518 | EFDIYR/EVGGEFVFPVTRDDSSNGFPRTQHGFSPTVHPIQSPQN RFCVLTLDPELPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHALVPEDGI GSVIEVLQRRQEGLAS |
| 6823 | 654 | 221 | PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFVAVTGETALYGNL ILRKGVLALNPLL |
| 6824 | 858 | 104 | LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFLALTLAHLTLLLFALCRWHRGTGESILS LLRDPSKRKVPVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPPKSTQHSKKAH |
| 6825 | 3 | 1173 | SSGEFGLQASDIMWTISDTGNWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPKSMGAPIVYRMLLQDLSSYKFPHLQ NCLAGGESILLPETLENWRAQTGLDIREFYQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPTGTEGIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGKDEBGYPQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDVPRGEVVKAF VILALQFLSHDPEQLTKELQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLDRKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF PFGPLALPMDGYGDSLWEEHEYKFCIALVISTKLYHVR |
| 6826 | 2304 | 954 | LKTESFKPW/VNIALAFHLLGERASPNSFWQFYIQTLPREYDTP LYFEEDDEVRLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA NKLPLKDSPTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPW DMCNHTNGLITTGYNLEDDRCECVLQDFRAGEQIYIFYGTRSN AEFVIHSGFFFDNNSHDRVKIKLGVS KSDRLYAMKA EVLARAGI PTSSVFALHFTPEPISAQLLAFLRVFCMTEEBELKEHLGDS AID RIFTLGNSEFPVSWDNEVKLWTFLEDRA SLLKTYKTTIERDKS VLKNHDL SVRAKMAIKLRLGEKEILEKAVKSAVNREYRQOME EKAPLPKYESNLGLLESSVGD SRLPLVLRNLEEEAGVQDALNI REAIKAKATENGLVNGENSI PNGTRSENE SLNQBSKRAVEDAK GSSSDSTAGVKE |

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|------------|--|--|---|
| 6827 | 1 | 779 | SSVVEFGLSVLGGFLFLFVLENMGLLRHRLRPRCCRRKRRL ETRNLDPENGSGMALQPLQAAPEPGAQGGREKNSQHPALAPPG HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG LSTTLAVFCHLPHLPHLGDFAMLLQSGLSFRRLLLSLVSGALGL GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVMDLPAFPSS GAPAYA\HVLLQGLGLLGGCLMLAITLEERLLPVTTTEG |
| 6828 | 3 | 1654 | KSQHG/WILQLMHSCKEGYVKDLKGNPGLRAMLDDLNGTRPSE LQHLSTASLKRGSFQSGRDDTWRYKTPHRVAFVEKLTKLVL S QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDPKKM IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVCVMATLQH TAEIIRLAEKEDWIVDNEGLTSLPCQPEQCIVCSLQSLKGVLE CKPGEASVFQPKTQEEVCQLSINIMQVPIYCLEQLSTKPDADI DTHLSVDVSSPDLFSGIHEDFSLTSEQRLILVLSNCCYLERHT FLNIAEHFEKHNFQGIKTIQVSMASLKBELDQRLFENYIELKAD PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNI IAVHAEV FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE ICALRDTAVVYLTPEKSSSFQKALEALPQLSSGADKKLLEELLN KFKSSMHLQLTCTFQAASSTMMKT |
| 6829 | 1 | 782 | MRMEAGEAAPAGAGGAGGAGGKWRVRLNVGGTVFLTRQTLCR EQKSLFSLRCQGEELQSDRDETGAYLIDRDPYFGPIILNFRHKG KLVLDKDMAEGVLBEAEFYNIQPLIRIKDRMEEDYTVTQVP PKHVVYRVLQCCQEEELTQMVSTMSDGRFEQLVNIGSSYNYGSED QAEFLCVSKELHSTPNGLSSSESSRKTSTEEQLEEQQQQEEEV EBEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI |
| 6830 | 1 | 939 | MRPGSVENLSIVYRSRDFLVVNKHWDVRIKAWRETLTLQKQL RYRFPPELADPDTCYGFRFCHQDLDFSTSGALCVALNKAAGSAYR CFKERRVTKAYLALLRGIHQESRVTISHAIGRNSTEGRAHTMCI EGSGQCENPKPSLTDLVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFMRMLHAFYLRIPDTT ECEVECTPDPLPSLDACWSPHTLLQSLDQLVQALRATPDPPDE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPTS |
| 6831 | 3 | 1087 | SLFFGSSTPDNKNVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVLKTADEPRGTLVKSGDQGNVKEKSMILSN VEDLQQPKFISEVSRDYGKKEISGDSEEMNINSVVTADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPKWN I SIFKEEPRSDQKQKSLSDVVDKVPQQPKSASSNFASKNITKE SEKPEIILPVEESKGLIDFSEDRLKKEQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRTSELKESKADAMPQHfyQNE DYNERPKIIVG SEKEKDEKKKK |
| 6832 | 1809 | 412 | MGSGLISGFPQDNGEALKEPERAQEHSLENFAGGQHFPBYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQEEERLLKAIPLF CFPDGNWASLTYEPRTFSFVLTNVDGSRKIGYCRRLPAGPG PRLPKVYCIISGICGFLFSKILDEVEKRHQISMAYIYPFMQGL REAFAFPAGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFFSL LHCLSFQILQIFASAVLERKIIFLAEGSLTSLQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRQQEVMDSMPME EVLLVNLCEGTFILMSVGEKIDILPFLQDDILDLSLGGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKFKVTQLFSLFIQAEKSKNPPAGFYQOKILE YEEQKKQ/TETGKNCEIRAVVNKND |
| 6833 | 1 | 1129 | PLMTLSQCGGIPGHGSHGGHGHGHLPGKPRVKSTRPGSSDIN VAPGEQGPQDEETNTLVANTSNNGCLKDPADPENPRSGDTVEV QVNGNLVREPDMHELEDRAQQLNMRGVFLHVLGDALGSVIVVV |

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|------------|--|--|--|
| | | | NALVFYFSWKGCGSEGDFCVNPFCFDPCKAFVEIINSTHASVVEA GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID IRNLIKELRNVEGVVEVHELHVWQLAGSRIIATAHIKCEDPTSY MEVAKTIKDVFNHGHGIIATTIQPEFASVSGSKSSVVPCELCARTQ CALKQCCGTLPQAPSGKDAEKTPAVSISCLLSNNLEKKPRRTK AENIPA\VVIEIKN\IPNK\QPESSL |
| 6834 | 78 | 1151 | AGQERPAPIWRLLWLTPSVSRKAEPAHIPINR*GA*E*RGGLP LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP CSKLVLSGARGIVGTTVQVLEAQPLLLFTGVWGLNLRAGEE SRAL*LIBEVTQVRDAHLGNVAVGCAQLSQGVGSALAKALLE AAAARVDCKEVLTVSGDKQQAQVSVRL*VRDVCVEAGCVEFGQ AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG QQDGEDQAARTRLQAGAHVVAHGRRQGGAPCRPHQEAGVSCHE LQQVVGDAI*ARE*APQIVLLLLLEDVAQLRTGKKA*DLVVDVE QLLRQL |
| 6835 | 1 | 834 | GIPAAADR\EASLELIKLDISRTFPNLCIFQOQGPYHDMLSILG AYTCYRPDVGQVQGMFIAAVLILNLDTADAFIAPSNLLNKPCQ MAFFRVHDGLMLTYFAAEFEVFEENLPKLFPAHFKNLTPDIYL IDWIFTLYSKSLPLDLACRIWDVFCRDGEEFLFRTALGILKLF DILTMDFIHMAQFLTRLPELPAEELFASIIATIQMSRNKKWA QVLTALQKDSREMRGKSVPTLRLQREFALGTNQSPMPRLCC FRLTPGQPRRTDAL |
| 6836 | 1 | 850 | MSCGRPPFDVDMITLKV\DNLTYRTSPDLSRRVFEKYGRVGDV YIPREHTKAPRGFAFVRFHDRRDQDAEAMDGAEIDGRELVR QVARYGRDLPRSRQGRRAAGPEAA/RYGRRSRSYGRRSRSPR RRHRSRSGPSCSRSRSRRYRGSRYSRSPYSRSPYSRYSRS PYSRYSRYRSGSHYSSSGYSNRYSRYSRSHSRSHSKSGSTS SRASSTSKSSSARRSKSSSVSRSRSRSSMTSPPRVSKRKS KSRSRSKRPPKSPREEGQMS |
| 6837 | 1 | 1369 | TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP/SGTSSSGSKASGP PNPAAQGDGTSLSPNYTLSTSGNDGKPVSGGGGRGRGRKRDS GHVSPGTFFDKYSAAPDSGGAPGVSPGQQASGAAGVSSAGET RGAPTPEKALTSPSWKGAEILLGDQPDIGSLDGGAKSDSSS PNVGEFASDEVSTSYANEDEVSSSDNPQALVKASRSPLVTS KLPPRGVAGEHGPAPPPALGLGIMSNSTSTPDSYGGGGPGH PGTPGLEQVVRTPTSSSGAPPDEIHPLLEILQAQIQLRQOFSIS EDQPLGLKGGKKECAVGAQNGDSELGSCCEAVKSAMSTI DLDSLMAEHSAAWMPADKALVDSADDDKTLAPWEKAKPQNPNS KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAAKARASVPTWR SLHSDISNRFGTFVAALT |
| 6838 | 16 | 499 | LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMETITLTWQDEE DQTRDMELVETRPAGDGTQKWAADVVPSSGEE/Q/RYMCHVQHE GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAMC RKKNSDRVSYSEAASSDHAQGSVDVSLTACKV |
| 6839 | 1 | 1195 | AAPAGGGPDEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG RGNFPTLSVQPRQIRAGGPQHGGAG\IHVHRVRLHGSAAASHVL HPESGLGYKDLDLVFRMDLRSEASFQTKAVVLACLLDFLPAGV SRAKITPLTLKEAYVQKLVKCTDSRWSLISLNSKSGKNVELK FVDSVRRQFEFSIDSFQIILDSLLLFQGCSTPMSEAFHPTVTG ESLYGDFTEALEHLRHRVIATRSPEIRGGLLKYCHLLVRGFR PRPSTDVRLQRYMCSRFFIDFPDLVEQRTTLERYLEAHFGGAD AARRYACLVTLHRVNESTVCLMNHERRQTLDLIAALALQALAE QGPATAALAWRPPGTGVPATVNYVTPVQPLLAHAYPTWLP CN |
| 6840 | 4254 | 2061 | ELQGDFSVPDVPKMAWCENSICVGFKRDIYILRVDGKGSIKEL FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW |

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|------------|--|--|---|
| | | | TDIPVAMEHQPPYIIAVALPRYVEIRTFEPRLLVQSIQLQRPFI TSGGSNIIYVANSNHFVWRLIPVPMATQIQQLQDKQFELALQLA EMKDDSDSEKQQQIHHIKNLYAFNLCQKRFDSEMQVFAKLGT PTHVMGLYPDLLPTDYRKQLQYPNPLFVLGAELEKAHLALIDY LTQKRSQVLKLNDSHQSSSTSPMBGTPTIKSKKKLLQIIDTT LLKCYLHTNVALVAPLLRLNNHCHIESEHVLKKAHKYSELI LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIHVWEETGSRFHNCILQYCEKVQGLMKEYLL SFPAGKTPVPAGEEEGELGEYRQKLLMPLFISSYDPRGLICDF PFDGLLEERALLGRMGKHEQALFIYVHILKOTRMABEYCHKHY DRNKDGNKDVLSSLRMYLSPPSIHCLGPIKLELLEPKANLQAA LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLKLENAQKK RFNQVLKNNLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK IGNSAFARYPNGVVVHYFCS\KEVNPADT |
| 6841 | 1 | 3206 | TPSTTGKSNTPSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA REKRDNRNMEVQVTQEMRNVSIGMGSSDEWSDVDIIDSTPELD MCPETRLDRTGSSPTQGI VNKAFGIN TDSL YHELSTAGSEVIGD VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA KVDQLSGEQEVL RGELEAAKQAKV KLENRIKELEELKRVKSEA IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFRVEMARVLM RNQYKERLMELQEA VRWTE MIRASREHPSVQEKKSTIWQFFSR LFSSSSSPPPAKRPYPSPGNIHYKSPPTAGFSQRRNHAMCPI SAG SRPLEFFPDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW SLPAKYQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA AGVNLGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD QFTVCNAHVLCISSIPAA SDDSYPPGEMFLDSDVN PEDPGADGV LAGITLVGCATRCNVRSNCSSRGDTPVL DKGQEVATIANGKV NPSQSTEEATEATEVDPGPSEPETATLRPGPLTEHVFTDPAPT PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSAAPTMWLG AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRLVALAD GTLAI FHRGEDGQWDL SNYHMLDLGHPHHSIRCMV VYDRVWC YKNKVHVIQPKTMQIEKSFDAHPRESQVRQLAWIGDGVVWSIR LDSTLRLYHAHTQHLLQDV DIEPYVSKMLGTGKLGFSFVRIT LVAGSRLWVG TNGVVISIPLTETVVLH RGO\LLG\LRANKTSP TSGE\ARPGG\I IHVYG\DDSSDRAARSFI PYCSMAQAQLCFH GHRDAVKFFVSVPGNVLATLNGSVLDS PAEGPGPAAPASEVEGQ KLRNVVLVSGGEGYIDFRIGDGEDDETEGAGDMSQVKPVL SKA ERSHII VWQVSYTPE |
| 6842 | 3 | 926 | RCQQLSATILTDHQYLERTPLCAILKQKAPQYIRAKLRSYKP RRLFQSVKLHCPKCHLLQEVPHGEDLDIIFQDGATKTPDVKLQ TSLYDSKIWTTKNQKGRKVAHVFKVNGILPLSNECLLIEGGT LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFMFT LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI |
| 6843 | 2 | 851 | NHRKVLGAKRYECNECGKSFAYTSSLIKHRRHTGERPYECSE CGRSPAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLQHQ VHTRERPYECSECGKSFSLRNLIIHQVRVHTGERHECGCGKSF SRKSSLIHLRVHTGERPYECSDCGKSFENSSLIKHLRVHTGE RPYECIDCGKSFHSSSFRHRQVRVHTGMRPYK*SKFWKFCPCGF LLLQGRVHTGSRCECDKWGIFFS*NASFFT*KSAPTEEVFFE CNECEKAFSPSLVTTIFT |
| 6844 | 244 | 642 | EHQLAGFELRKTQTSMSLGTTRKTRDRVKSTAYLSPQLEDVFF QYDVKSEIYSFGIVLWEIATGDI PFQGCNSEKIRKLVAVKQOE |

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|------------|--|--|--|
| | | | PLGEDCPSELREIIDECAHDPSPVRPSVDEILKKLSTFSK*CIK I |
| 6845 | 3 | 1519 | VAVRDECYWRHVFDQDLWMLLFILMCHPETAARLEYYRIRTLG GALENAQNGLGYQGAFAWESADSGLEVCPEDIYGVQEVHVNGAV GLAFELYHTTQDLQLFREAGGWDVVRVAEFWCSPVWSPREE KYHLRGVMSPDEYHSGVNNVSYTNVLVQNSLRFAAALAQDLGLP IPSQWLAVADKIKVPFDVEQNHFPEFDGYPEGEVVKQADVLLG YPVPFSLSPDVRKNLEIYEAVTSPQGPAMTWSMFVAGWMLKD AVRARGLLDRSFANMAEPFKVVTENADGSGAVNFLTGMGGFLQA VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLPGHKVSPFRS AGRIQMSPPKLPSSSSSEFFPGRTFSDVRDPLQSPLVWTLGSSSP TESLTVDPAE*SGTGASETSLQPSLWFRLLHPPLLGLTLLACHPS PAARLSGKVHAAPFEKAFCL |
| 6846 | 213 | 1258 | LYFLKTIK*LNRLAEHP*YENEKLTCLRNTIMEQYTRTEESARG IIFTKTRQSAYALSQWITENEKFAEYGVKKAHLIGAGHSSEFKP MTQNEQKEVISKFRGTGKINLLIATTVAEEGLDIKECNIVIRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDPREKM MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTNRNIAKHK NNPSLITFLCKNCVSLACSGEDIHVIKMHVNMTPFEKELYIV RENKTLQKKCADYQINGEIIICKGQAWGTMMVHKGDLPLCKIR NFVVVFKNNSTKKQYKKWVLPITFPNLDYSECCFLSDED |
| 6847 | 1450 | 348 | SMCWNSDRLEMLDILALILYPPSYVPTGHLSDDSLSRKCYCLT WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ PFAYGTLTVRSLDTRHCLNEFNFPDPYKVKQRENGVALRCF PGVVRSLDALGWEERQALALVKGLLAGNVFDWGAKAVSAVLESDF YPGFEEAKRKLQERPLVDSYSEWLQRLKGPPhKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPAALNDVTHSESLIVAE RIAGMDPVVHSALREERILLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE |
| 6848 | 19 | 16 | AMWWSNLDGIRNTVLSNPKKRNLTSLAMLKSLQSDTLHDADSND LKVIIISAEGPVFSSGHDLEETEEQGRDYHAEVQTCVKMMH IRNHPVPVIAVNGLATAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAEALLHGLLNK VVPEAELEQETMRIARKIASLSRPVVSGLKATFFYKQLPQDLGTA YYLTSQAMVDNLALRDGOEGITAFLOKRPVWSHEPV*VEH |
| 6849 | 70 | 821 | SLGVDGSCLEQGSPPRPQTDTSF*PVGNNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQAERSCSHLGTM VEFAVALGSKLDVINKHSPNNFRLRVGLNHGFPVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQTVEETAWALQSLGYTCYSRG VIKVGKGQLCTYFLNTDLTRTGPPSATLG |
| 6850 | 2 | 1235 | ARGLNHEWTFEKLQHISRNAQDKQELHFLMLSGVDPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCCHPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWVYLLKNLRELYLIGNLNSNNKMI GLESRLRLHLKILHVKSNTLKVPSNITDVAPHLTCLVIHNDGT KLLVLNSLKKMMNVAELELQNCLELRI PHAIFSLSNLQELDLKS NNIRTIEELISFOHLKRLTCLKLWHNKIYVTPPSITHVNKLES YFSNNKLESPLPAVFSLQKLRCLOVSYNNISMIPIEIGLQNLQ HLHITGNKVDILPKQLFKCIKLRTNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI |
| 6851 | 1765 | 660 | VSAQVSAREGENCLGWNADSSQESYKSLLEEABDCYPPSLLTLD LRDLFNQVEQGPILLSCPKAGTDLSMGRAREVGMMAAGLMIGAGA CYCVYKLTIGRDDSEKLEBEGEEWDDQQLDREEDPIWDFPET |

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|------------|--|--|---|
| | | | MARPWTEGDGWTBEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE HKNTWSAQNCNGSCVLDLSKCLFIQGGKLLFAEPKADAGFPFSQD INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM YINEVCRKTVSRCCNSFLQQAGLNLLISMVTVINMLAKSASDLK FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSPMSL FIRNGNREILLETAP |
| 6852 | 1 | 407 | RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT GFIGLNSIAVLNCLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ IAETLWEQVLKPLGDNLMENIRQSVTNSIKAGLTDQVSHHARL KTD |
| 6853 | 3 | 469 | GDSCAVCIELYKPNLVRILTCHNHFHKTCVDPWLLHRTCPMC KCDILKALGIEVDVEDGVSLSQVPVSNEIFNSASSHEEDNRSET ASSGYASVQGTVEPPLLEHVQSTNESLQLVNHEANSVAVDVIPH VDNPTFEEDETPNQETAVEREIKS |
| 6854 | 1148 | 585 | HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLIVYEPSTQAK PVKNTFLRMWYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG IICVEGFKHECEFWHTIRYPNWKHISCKHAESVETEGNGEDLR LFHSFEELLLEAHGDYGLRNDYHMLNGQFLBFLKKHSEHVFI LFGIESKSSDS |
| 6855 | 1913 | 1148 | GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDLLAK EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNILLNDRGHI QLTYFSRWSEVEDSCSDAIERMYCAPEVGAITEETACDWWSL GAVLPELLTGKTLVECHPAGINTHTLNMPEWVSEEARSLIQQL LQFNPLERLGAGVAGVEDIKSHPPFTPDVAELMR |
| 6856 | 1617 | 997 | VTQLYVSVDASTKDSLKKIDRLFKDFWQQFLDSLKALAVKQQR TVYRLTLVKAWNVDLQAYAVLVLGNPDFIEVKGVTYCGESSA SSLTMAHVPHWEEVQFVRELVDLIPEYEIACEHEHNSCLLIAH RKFKIGGEWWTWINYRPFQELIQEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDRHQRKNKS KAISGC |
| 6857 | 1 | 617 | KGPEATAMVVCVSHPCNRQNHKPSHSAQTCWCSFTPASAPNH KLMAEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQLSDEDDGTNMLQLVRQEMAVCEQLSEFLDSLRLQYLRT TGVNRCFHITAVRLSDGFTFVIYEFWETEAWKRHLQSPCLKAF RHVKVDTLSPQALSRILVPAANCTVGRD |
| 6858 | 2 | 669 | RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVBPGIFEWTKWEAGKTPTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLGLPPRECDFPAQLVR KIPSLGMCFCENKECKWELVNPVKTLTGANAFAFNWRNWS GN |
| 6859 | 1 | 1150 | GETMFKKAKTKAKKKPKRSDSSGGYNLSDI IQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGPHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQIPSNRIDTT SSASVWAGSPSPVSPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQKRMIALTTKENNSGMNSMETVLTFTPSKAPKPVN AWASSLHVSSSKSPRDFLLEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTGPEGNHISDLPLDPSNPWLSSSVTAPSM VAPVTFASIVEELQOEALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPGGPLAVPMWNKHGC |
| 6860 | 1889 | 1515 | DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLGQQHMGIRPAGPMSGMGMMNMGMDGQWHYM |
| 6861 | 1889 | 1515 | DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP |

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|------------|--|--|--|
| | | | MGSFVLDGQQHMGIRPAGPMSCGMGMGMMDGQWHYM |
| 6862 | 2 | 471 | EEIDREFHNKLLKEDKLEKQKPVNGEDKGDGSDVTQNSEGNA DEEDPLGPNCCYYDKTKSFFDNISCDNRRRPTWAEERRINAET FGIPLRPNRGRGGYRGRGGLGFRGGRGRGGGRGGTPTAPRGFRG GFRGGRGGREFADFEYRKTTAFGP |
| 6863 | 2216 | 487 | PQEPALKSEFSQVANSNTIPLPLPQNTCKDNGPCKQVCSTVGGSS AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF YCVNHTVLCAAGYILNAHRKCDVINECVTDLHTCSRGEHCVNTL GSFHCYKALTCEPGYALKDGECEDEVDECAMGHTTCQPGFLCQNT KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI NTVGSYTCQRNPLICARGYHASDDGTCKVDVNECETGVHRCGEG QVCHNLPGSYRCDCKAGFQDAFGRGCDVNECWASPGRLCQHT CENTLGSYRCSASCGLLAADGKRCEVNECAQRCSQECANIY GSYQCYCRQGYQLAEDGHTCTDIDECAQAGILCTFRCLNVPGS YQACPEQGYTMTANGRSCKDVDECALGTHNCSEAECHNIQGS FRCLRFECPPNYVQVSKTKCERTTCHDFLECOMSPARITHYQLN FQTGLLVPAHIFRIGPAPAFGTDTIALNIKNGEEGYFGTRRLN AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT TFAL |
| 6864 | 2 | 2933 | LADSSPSNLQIIKELLSMHQPDPAITKEFDYLPFVDSRSSSSG FVGLRNGGATCYMNAVQQLYMQPLPESLLSVDNDDTNPDSDSV FYQVQSLFGHLMESKQLQYYVPENFWKIFKMWKELYVREQQDAY EFTTSLIDQMDEYLLKMGDRDQIFKNTFQGIYSQKICKDCPHRY EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRIITVKRTCIKSLPSVLVIHLMRFGFDWESGRSICYDEQIRFP WMLNMEPYTVSGMARQDSSSEVGENGRSDVQGGGSPRKKVALT ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKWKYKFNDTVIE EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAIMLFY QRVSDQNSPVLPPKSRVSVVRQEAEDLSLAPSSPEISPPSSPR PHRPNNDRLSILTCLVKKGEKKGLFVEKMPARIYQMVREDNLKF MKNRDVYSSDYFSFVLASLASLNLATKLKHPYPYCPMAKVSLLQAIQ FLFQTYLRTKKLRLVDTEEWIATIEALLSKSFDACQWLVEYFIS SEGRELKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKS HQLLEVLALLLDKDVPCNKCAQYFFLNTFVQKQGIKAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPIISAPSSPLPLHEEVEALLFM SEGKPYLLEVMFALRELTSLLALIEVMVYCCPCNEHFSFTMLH FIKNQLETAAPPHELKNTFQLLHEILVIEDPIQVERVKFVFSTEN GLLALMHSHNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSNAVQWLQKKMSEHYWTLQSNVSNSTSTGKTFTQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQSGSESPPMIGEL RSDLDVDP |
| 6865 | 1820 | 1242 | DPERWKHLSKVTPPGSSVSTTFVQVRLQSFQSGSMMPSNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEBIGEGEFLV LDQRAADYNQALGTCLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS |
| 6866 | 1571 | 495 | DCPRPYTLYGLRATCMRDLDWAWINAVSAFAKALEQDLVNIKF IEGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLBEYRNSSR VEKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLLIPLGAVDDGEHSQNEKINRWNYIEGTLFAAFPL EMAQLH |

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|------------|--|--|---|
| 6867 | 2833 | 1704 | GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQSP LQSAESSPTAGKKLEVPPEEEEEQEAOWNALLGRIFWDFLGEK YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF KPYVDHQGLWIDLEMSYNGSFLMTLETMNLTKLGKEPLVEALK VGEIGKEGCRPRAFCLADSDEESSAGSSEEDDAPEPSGGDKQL LPGAEGVVGHRSTSIRMFVDKTKSKYFQKATETEFIKKKIEE VSNTPLLLTVEVQECRGTAVNIPPPPTDRVMYGFRRKPPHVELK ARPKLGEREVLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM HSANDPRSTSCLLKDPPEAADQP |
| 6868 | 1 | 346 | RPTRPPTREPIKNLILPYISDMNFVQDLCEDFYELFKTDKGF KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQ GSQGRIVHLSNSFTQTVNCRKPPFSSW |
| 6869 | 3 | 1619 | MYMERMDKRALISFWESVEHLKANKNEIPQLVGEIYQNFVFS KEISVEKSLYKEIQCLVGNKGIEVFYKIQEDVYETLKDRYPS FIVSDLYEKLKKEEKHASQMISNKDEMGPRDEAGEEAVDDGT NQINEQASFAVNLRELNEKLEYKRALNSIQNAPKPKKIVSK LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE NGEQLPCYFVMVSLQEVGVETKNWTVPKRLEFHNLRKLSEC VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQNLKFLQNLSDER LCQSEALYAFSPSPDYLVKIDVQGGKNSFSLSSFLERLPRDF SHQEEETEEDSDLSLDYDGDVGRKDALAEPCFMLIGEIFELRGM FKWVRRTLIALVQVTFGRITNKQIRDTVSWIFSEQMLVYYINIF RDAFWPNGKLAPPTTIRSKESQETKQRAQQKLENI PDMLQSL VGQQNARHGIKIFNALQETRANKHLLYALMBLLLIELCPELRV HLDQLKAGQV |
| 6870 | 1 | 1566 | MAAVVAATRWQLLLVLSAAGMGASGAPQPPNILLIMDDMGWG DLGVYGEPSRETPNLDRMAEGLLFPNFYSANPLCSPSRAALLT GRLPIRNGFYTTNAHARNAYTPQEIYGGIPDSEQLPELLKKAG YVSKIYVKGWHLGHRPQFHLKHGFDEWFGSPNCHFGPYDNKARP NIPVYRDWEMVGRYYEEFFINLKTGEANLTOIYLQEAALDFIKRQ ARHHPFFLYWAVDATHAFVYASKPFLGTSQRGRYGDVAREIDDS IGKILELLQDLHVADNTFVFFTSNGAALISAPEQGGSGNGPFLC GKQTTTFEGGMREPALAWNPGHVTAGQVSHQLGSIMDLPTTSLAL AGLTPPSDRAIDGLNLLPTLLQGRMLMDRPIFYRGTTLMAATLG QHKAFWFTWTSNWFNFRQIDFCPGQNVSGVTTHNLEDHTKLPL IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQF QLNVNCWAVMNVAPPCEKLGKCLTPPESIPKKCLWSH |
| 6871 | 209 | 1126 | RMSLNPPIFLKRSEENSSKFVETKQSTTSIASDPLQNLCLAS QEVLQKAQQSGRSKCLKCGSRMFYCYTCVVPVENVPYIEQIPLV KLPLKIDI IKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPYBS EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPKPS FKRRTEEQEFCDLNSCKCKGTTLKIIIFIDSTWNQTNKIFTDE RLQGLLQVELKTRKTCFWRHQKGPDTFLSTIEAIYYFLVDYHT DILKEKYRGQYDNLFFYSFMYQLIKNAKCSGDKRTGKLTH |
| 6872 | 880 | 459 | FGLLMVVLSLIFMKGNCVREDLIFNLFKLGLDVRETNGLFGNT KKLITEVVRQKYLEYRRIPYTEPAEYEFNLGCPRAFLETSMMLV LRFLAKLHKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG PISRPPPR |
| 6873 | 1929 | 955 | DEQAVLCSKDKTYDLKIADTSNMLLFI PGCKTPDQLKKEDSHCN IIHTEIFGFSNNYELRRRRPKLKKLLMENPYEGPDSQKEK DSNSSKYTTEDLLDQIQASEEIMTQLQVLNACKIGGYWRILEF DYEMKLLNHVTQLVDSSESWSFGKVP LNTCLQELGLEPEEMIEH CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKNLAEF QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDLPE DNQERFNSLFSLEKRWTEEDIAPYIQDLGCEKQTIGALLTKYSH SSMQNGVKYNSRRPIS |

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|------------|--|--|--|
| 6874 | 1 | 307 | DSIAHDVNSAAVNVEEGTKNLGKAARYKLAALPVAGALIGGMVG GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMKELTS SCPDLPSTQDKKCS |
| 6875 | 1688 | 349 | VIGTGERGNSASEKWEIMFNEELGDPFIIHSISLLNAEEHSIA TLLLRIEKEBELDMKSGFYVSLEWVTISKKNQDNKKYBIIKRDI LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI SEKIKEPLYWQOTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW PELVIGDKQGELIRDSAQCAIAERLMHLLTSEELNPNPDKEKPP CNAQEEECDFFEESSSLCRFDGNTLKTTHVNLGSGNQYLFVS IVDPKEMPCFCLRHVDALLWOPHSSKQDDMWEHIATFNALGYV QASKRDKKFFACAPNYSYAALCECLRRVFIYRQAPAMSTVLVNR KEGRQVGQVAKQVASLETNDPILGFQATNERLFVLTTKNLFIL KVNTEN |
| 6876 | 41 | 1285 | VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS LHTKPRMPPCDFMPERYQVIFLVNSGSEANLAMLARAHSNNI DIISFRGAYHGCSPYTLGLTNVGIYKMLFPGGTGCQPTMCPDVF RGPWGGSHCRDSPVQTIKRCSCAPDCCQAKDQYIEQFKDTLSTS VAKSIAGFFAEPIQGVNVVQYPKGFLKEAFELVRARGGVCIAN EVQTGFGRGLGSHFWGFTHDVLPDIVTMAKIGINGFPMAAVITT PEIAKSLAKCLQHFNFTFGGNPMACAIGSAVLEVIKEENLQENSQ EVGTVMMLKFAKLREDEFIIVGDVVRGKGLMIGIEMVQDKISCRPL PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF AVEVFRSALTQHMERRAK |
| 6877 | 1 | 778 | GTSPSPARAYAPPTERRKRYQNVSIQEGEGFEINLDRKLKTP QAKLFTVPSEALAIATAVEWDSQDDTIKYTYMHLTTLNCTSLDN PTQRNKDQLIRAAVKFLDITDIYRVEEPETLVELQRNEWDPII EWAERKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNWALQG IEFVAAQLKSMVLTGLIDRLTVEQAVLLSRLEEEYQIQKWN IEWAHDYELQELRARTAGTLFIHLCESTTVKHKLLKE |
| 6878 | 931 | 263 | QTLQGDFFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN LEEDTVTLEVLVAPVPSCEVPSSALSSTVVELRCQDKBGNPAP EYTWFKDGIIRLENPRLSQSTNSSYTMNTKTGTLPNTVSKLD TGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVALVIS VCGLGVCYAQRKGYFSKETSFKQSNSSSKATTMSENDFKHTKSF II |
| 6879 | 3 | 845 | IRVIGESDIMQEFLESSENYNGVSDVELRVALPDGTTVTVRVK KNSITDQVYQAIKAVGMDSTTVNYFALFEVISHSVFRKLAPNE FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF FHQAVDDVKGYIKAEKSYQLQKLYEQKVMYLNMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWKIFTYPFNYMHE CFERVFCELKWRKEEY |
| 6880 | 2110 | 1437 | RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRFASVALIFVTAFOGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLSSIFYNAS KPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESD EDTF |
| 6881 | 2638 | 2244 | NDSKWEDIHVITGALKMFFRELPELFTFNHFNDFVNAIKQEP QRVAVKDLIRQLPKPNQDTMQILFRHLRRVIEENGEKNRMITYQS IAIVFGPTLLKPEKETGNIAVHTVYQNVQIVELILLELSSIFGR |
| 6882 | 1 | 850 | GTPEAQLWITYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QBGNMVTAQEPRLVLISLTCDGDTLTLSAAYTKDLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH MRPRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK |

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|------------|--|--|---|
| | | | KVKATNFRPNIVISGCDVYAESDWEDELLIGDVBLKRVMACSRCLTTVDPTDGVMSRKEPLETLKSYRQCDPSEKLYGKSPLEFGQYFVLENPGTIKVGDPVYLLGQ |
| 6883 | 2794 | 2256 | NSKLKLNQNLKLFITLTQVLSLHGWGPGIHLQKEGAFVPTQNRALQLLYDLRYLNLIVLTAKGDEVKSGRSKPDSEKVTDLHLEALIDPFLLDVFTPHLSNLHRLVQRTSVLFGLVGTENQLAPRSSTFNSQEPHNILPLASSQIRFGLPLSMTSTRKAKSTRNIETKAQYDANC |
| 6884 | 2 | 99 | EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL |
| 6885 | 297 | 1554 | STGQFHWHTDLHLDPTYHITDDHTKVCASSKGANANSPGPGFDVLCDSPPYQLILSAFDPIKNSGQEA SFMIWTGDSPPHVPVPELSTD TVINVITNMTTIIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKVYNAVANLWKPWLDEEAISTLRKGGFYSSQKVTTPNPLRIISLNTNLYYGPNIIMTLNKTDPANQFEWLESTLNNQQNKEKVYIIAHVPVGYLPSSQNTAMREYYNEKLIDIFQKYSVDVIAGQFYGHTRDSIMVLSDDKKGSPVNSLFPAPVTPVKS VLEKQTNNPGIRLFQYDPRDYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPESLYGLAKQFTILD SKQFIKYNYFFVS YDSSVTC DKTKCAFQICAIMNLDNISVADCLKQLYIKHNY |
| 6886 | 2 | 1341 | QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAKQARVSQELKKAARTVSISEGPDTLGDGMRRERRETLALAPEPEPVEKEACEKWKRPFRSASATSLTSLHCVDVVKGLLDFKKRRGHSIGGAPEQRQYQIIPVCVAARLPTRAQDVLDAHLSEVN AVRFPGPNSSLLATGGADRLIHLWNVVGSRLEANQTLGAGGSITSVD FPD SGYQVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTA AKFKLTRHQA VTGSRDRTVKEWDLGRAYCSTINVL SYCNDVVC GDHIIISGHN DQKIRFWDSRGPCHTQVIPVQGRVTSLSLSHDQLHLLSCSRDNTLKVIDLRVSNIRQVFRADGFKCGSDWT KAVFSPDRSYALAGSCD GALYIWDVDTGKLESRLQGP HCAAVNAVANCYSGSHMVSVDQGRKVVLWQ |
| 6887 | 1047 | 116 | WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHGQQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLGTYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVYNASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLTFASNNTDMFPDLPFTDELQRQYCLDTWGVWPRPDWLLTSFWGGDLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHLLDLRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRLSL |
| 6888 | 1 | 992 | FVAYVKKIEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVINFIKGRAPNHRLPQAFPEEIGIEYSVLLFHTEMRWLSRGQILTHIFEMYBEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNLSASMQRGTGMNTVSAREKLSAFVRKFPFWQKRIEKNFTNFPFLEEIIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWILDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTPNKNVPEAA LILSDDIRVAISKVPSFLGHH |
| 6889 | 1 | 1534 | LTLNQLKEEREQDNSESPNGRTSPLVSQNNQEGSTLRDLLTTTAGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILLDDIIASVV ENKIPPSKTSKINVKPELKEEPEESIIISAVDENNKLYSDIPHWSICEKHILWLKDYKNSSNWKLFKECNKQGGQPAVVS G VHKKMNISLWKAESISLDFGDHQADLLNCKDSIIISNANVKEFWDGFEVSKRQKNKSGETVVLKLDWPSGEDFKTMMPARYEDLLKSLPLPEYCNPEGKFNLAHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EYSDVNNILVYVGIAGNGILSKAGILKKFEEEDLDDILRKRLKDSSEIPGALWHIYAGKDVDKIRBFLQKISKQBQGLEVLPEHDPIRDQSWYVNNKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ |

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|------------|--|--|---|
| | | | NFHSCIQVTEDFVSPHELVESFHLTQELRLLEEINYDDKLQVK NILYHAVKEMVRALKIHEDEVDDMEEN |
| 6890 | 3 | 667 | THACGMWIPLYLHRLVVKTAETCNSPPCGAKDSLIFGAITCF TGFLGVDTGAGATRWCRLLKTQRADPLVCAVGLGSAIFICLIFV AAKSSIVGAYICIFVGETLLEFSNWAITADILMYVVIPTRRATAV ALQSFTHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA LMLCPFVVVLGGMFFLATALFFVSDRARAQQVQNQLAMPASVK V |
| 6891 | 1980 | 1262 | LRHQELLSKELKLLRGITTESIIHIGLAAGKEQFMQDASNVMO LLKKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCNVND EVLPHWLSWLP LHEDKEEAIQTLSPCLDIESNHPVVIGPNNNSN LPKIIISIIAEGKINETINYEDPCAURLANVVRQVQTSSEDLWLEC VSQLDDEQEQEALQELLNFA |
| 6892 | 3 | 876 | RSVAAASGPGAWGTDHYCLELLRKRDRYEGYLCSLLPAESRSSV FALRAFNVBLAQKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH QPVAIELWKAVERHNLTKRWLMKIVDEREKNLDDKAYRNKELE NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIIVTCLRA TPYHGSRRKVFPLMDICMLHGVSDQEDFLRRNQDKNVRDVIYDIA SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD IFHPSLQQKNTLLPLYLIQSWRKTY |
| 6893 | 1 | 842 | DGERKMSMVERTFSEINKAEEOYSLCQELCSELAQDLQKERLKG RTVTIKLKNVNFVKTRASTVSSVVSTAEEIFAIAKELLKTEID ADFPHEPLRLRLMGVRISSFPNEEDRKHQORSIIIGFLQAGNQALS ATECTLEKTDKDKFVKPLEMSHKKSFFDKRSEKWSHQDTFKC EAVNKQSQTSPFPQVLKKMNENLEISENSDDCQILTCPCVCFR AQCISLEALNKHVDECLDGPSENFKMFSCSHVSATKVNKKE NVPASSLCEKQDYEAH |
| 6894 | 1742 | 1463 | TTLCCKPLVPREHQFYETLPAEMRKFTPOYKGKSQLLEGLPHWRG DVRDRGHGRPWQPSLEPSLPPTLCFPLSSFSSSWPSAQHLTPS VFNPW |
| 6895 | 2379 | 478 | VTVVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKQYTSQT TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLAL VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSEGSISEL EQLSNLSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL AEHDYGLFHLKSSLRKNSSALHSLKRVVSTFSKDTGELASSFL EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAELKQLL QSKEESPENLFLELEKLVLEHSKDDDNLDLSDSVVGLKQMLSE SGDPLPLSDQDVEPVLAPESLQNLFNMRATAYVLADVMDDQLKS MWFTFPQAEEDTDLDLVKVDLIELSEKCCSDFLHSELERFSL SEPSSPGRTKTKGFKLGKHKHETFITSSGKSEYIEPAKRAHV PPPRGRGRGGFGQIRPHDI FRQRKQNTSRPPSMHVDDFVAES KEVVPQDGI PPPKRPVKVSQKISSRGGFSGNRGGRGAFHSQNR FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG PLPPLRPLSSTGYRPSPRDRASRGGLGPSWASANSRGGSGRG KFSVSGSGRGRHVSFTTR |
| 6896 | 1 | 555 | GNIVIQKKKYNKQHIIPLENVTIDSIRDEGDLRNGWLIKTPTKS FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD SEATVCMRCQKAKFTPVNRRHCRKCGFVVCGPCSEKRFLLPSQ SSKPVRICDFCYDLSAGDMATCQPARSDSYSQSLKSPLNDS DDDDDDSSD |
| 6897 | 3 | 920 | GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY AGYEQVTNEDLLTNCTLLCRLLSPMNLISLHTASGLRLFSVL SLAWGFIADVLESEKYRRLGEMRFTLTFLRLAALRTYRGRLA YLPVGRVGSKTPASPVVVQGPVDAHLVPLEEPVPSHWTVPVDE DFVLVLALLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAML |

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|------------|--|--|---|
| | | | LRLFLAMEKGRHMEYECPLYVVPVVAFRLEPKDGKGVFAVDGE LMVSEAVQGQVHPNYFWMVSGCEPPPSWKQPQMPPEEPL |
| 6898 | 919 | 346 | OKTAVASLLKGRQGIYTENERRMGAIVIKIRFFKIMLVLIICW LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTFIMGILNPA QGFLLSLAFYGTGCSLGFQSPRKEIQWESLTSSAEGAHPSPL MPHENPASGKVSQVGGQTSDEALSMLSEGSASTIEHTASESC NKNEGDPALPTHGDL |
| 6899 | 120 | 827 | MKVRKNNDAYLLDNKINMDCFISCFKKMLTTLMFSGIISL LEHGEEYTFSLPCAYARSILTVPWVVELGGKVSVCNCAKTGYSASI TFHTKPFYGGKLHRVTAEVKHNITNTVVCVRVQGEWNSVLEFTYS NGETKYVDLTCLAVTKKRVRLPKQDPFESRRLWKNVTDLSRES EIDKATEHKHTLEERQRTTEERHRTETGTPWKTKYFIKEGDGWVY HKPLWKIIPPTQPAE |
| 6900 | 3 | 451 | TEVLGSKGIHELRSSTSLHHALESASLLTMFWRAALPSTHIP VLPKGVGESTERELLERLTKVSQQEQLLQSTTEHLKNANQKES MEQFIVSQLTRTHDVLKARTNLEVRKLLHQSEAPSLSPTHHP LADLVGDSWPAIRFQEK |
| 6901 | 1 | 201 | DDNMVQRLETFKMTLQQSTLEQWAAWLDNMVQALKPYEGRP SFPKAARQFLKWSFYRYHLGFS |
| 6902 | 2 | 267 | GAPPPPPSPPPPPQQAAPSSHPHSDLTTFNPSALEGQAGAQA SDMPEPSLDLLPELTNPDELLSYLDPDLPNSNDLLSLFENN |
| 6903 | 1 | 149 | RINQVYRQGTGIHILVIDQMVFQNFQDESCFLPSTVKAESSDGI HIILK |
| 6904 | 464 | 2092 | MEASLPVSLSCVLACGDVEGKFDILFNRRVQAIQKKSNGFDLLC VGNFFGSTQDAEWEYKTKIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGITGSSGLQIVYLSGTESLNEPVPYGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYERLPYRNHIILOEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGCPWFCLASPEVEKHLVNVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEVEKYKATL RRFFKSRGKWCVFERNYKSHHLQLQVIVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVDPKSDWRQCQISKEDDETLARR FRKDFEYDFLDD |
| 6905 | 1 | 226 | VSKTGEAETITSHYLFALGVYRTLYLFNWIWRVHFEGFFDLIAI VAGLVQTVLYCDFYLYITKVLKGGKLSLPA |
| 6906 | 3 | 611 | SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPVFTET TEVRKTKIRNGISFTIWRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPMVPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYFSDHDD |
| 6907 | 2 | 2228 | LRGVVVAAGAFRFSSEESTSHLIMSRRSQRLTRYSQGDDGGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYESLVHESWFPFRSSLEELHGDANWGEDLVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSDDYVGYSDVDQQS SSRLRSVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFLVTRRFSSSLKTLFWLLPLLLLTCLTYGAWFYFPGYGL TFHPALVSWAAKDSRRADGWEARDSSPHFQAEQVRMSRVHSL ERRLEALAAEFSSNWQKAMRLERLELRQGAQPGQGGGGLSHBD TLALLEGLVSRREALKEDFRRETAARIQEELSALRAEHQDSE DLFKKIVRASQSEARIQQLKSEWQSMQTESFQESSVKELRRLE DQLAGLQQELAAALAKQSSVABEVGLLPQQIQAVRDDVESQFPA WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGS |

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|------------|--|--|---|
| | | | AREAAASLSLTQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA DYALESGGASVISTRSETYETKTALLSLFGIPLWYHSQSPRVI LQPDVHPGNCWAFQGPQGFVAVRLSARIRPTAVTLEHVPKALSP NSTISSAPKDFAIQGFDELDQOEGTLLGKFTYDQDGEPIQTFHP QAPTMTATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH |
| 6908 | 3 | 780 | QVPSAAWMAVCGLSRLGLSRLGLQGCFAARLLYPRFQSRG PQGVEDGDRPQSSKTPRIKITYTKGDKGFSSTFTGERRPKDD QVFEAVGTDELSSAIGFALELVTEKGHTFAEELQKIQCTLDV GSALATPCSSAREAHLYTTFKAGPILELEQWIDKYTSQLPPLT AFILPSGGKISSALHFCRAVCRAERRVPLVQMGETDANVAKF LNRLSDYLFTLARYAAMKEGNQEKIYKNDPSAESEGL |
| 6909 | 3 | 409 | GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNLLPEKAFSDIP SPYLRTGIKMMQAVRQAFQDQDDRTWDGRPLTMAATFDDCLYA LCVVDITIKRSSQTGEWQNIAMTEPELSPAYLISEAMRRSRMS LYC |
| 6910 | 1 | 1068 | LVPVVVIDSYYYGKLVIAPLNIVLYNIPTPHGPDLYGTEPWYFY LINGFLNPNVAFALALLVPLTSLMEYLLQRPHVQNLGHPYWL LAPMYIWFIIFFIQPHKEERFLFPVYPLICLGAVALSALQHSF LYPQKCYHVFQRYRLEHYTVTSNWLALGTVFLGLLSFSRSVA LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKWNRYF PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ NLEEPSRYIDISKCHYLVDLDTMRETTPREPKYSSNKEEWISLAY RPFLDASRSSKLLRAFYVFFLSDQYTVVNYTILKPRKAKQIRK KSGG |
| 6911 | 1184 | 966 | GEDAEEMETGNVANLISTFGSSFGLLRKSPGGGREGEEEGESG PEAAEPGQICCDKPVLRDMNPWSTAIVAF |
| 6912 | 1 | 844 | AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI SGGTDIISCFMGNHNSLPVYKGEIQARNLGMAVEAWNEEGKAVW GESGELVCTKPIPCQPTHFNDENGKRYKAYFSKFPGIWAHGD YCRINPKTGGIVMLGRSDGTLPNGVRFSGSEIYNIVESFEEVE DSLQVCPQYKREERVILFLKMASGHAFQPDLVKIRDAIRMGL SARHVPSLILETKGIPYTLNGKKVEAVKQIIAGKAVEQGGAFS NPBTLDLYRDIPELQGF |
| 6913 | 1643 | 1558 | KKSHEESHKEELSYGAQASLPLPCSDFR |
| 6914 | 1251 | 615 | ELAAECKSAGYPGTLPYRCDLSNEEDILSMFSAIRSQHSQVDI CINNAGLARPDTLGSGSTSGWKDMFNVNVLALSICTREAYQSMK ERNVDDGHIININMSGHRVLPVSVTHFYSAKYAVTALTEGLR QELREAQTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMK CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT |
| 6915 | 254 | 652 | GRSLSFKTFLIWLISYIYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS |
| 6916 | 254 | 652 | GRSLSFKTFLIWLISYIYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS |
| 6917 | 254 | 652 | GRSLSFKTFLIWLISYIYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS |
| 6918 | 28 | 921 | PEAGTRSWREPDPELRRFLLSAACRSFPQWLPGGGGGQVSSCS DTDVPYLLAVKSEPGRAERQAVRETWGPAPGIRLLFLGSP VGEAGPDLDLSLVAESRRYSDDLWDFLDVFNQTLKDLLLW LGRHCPTVSFVLAQDDAFVHTPALLAHLRALPPASARSLYLGE VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYIAGRLAPW LLRAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT ADHCAFRNLLVRLPGQASIRLWKQLQDPRLQC |

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|------------|--|--|--|
| 6919 | 850 | 41 | QGRRELSGSVFCFFIQOEPKEMLTSEYHERVRSQGGQLOQLQA ELDKLHKEVSTVRAANSERVAKLVFORLNEFVRKPDYALSSVG ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPPTVILEPHVFP NCWAFEGDQGVVQLPGRVQLSDITLQHPPPSVEHTGGANSAP RDFAVFLLSFFTHQGLQVYDETVSLGKFTFDVEKSEIQTFHL QNDPPAAPPKVKIQLSNWGHPRFTCLYRVRAHGVRTSEGAEGS AQGPH |
| 6920 | 1418 | 591 | EAQGPSKVHLTLKKKK |
| 6921 | 2 | 1711 | MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI PAHRLVLSAVSDYFAAMFTNDVLEAKQEVMEGVDPNALNSLV QYAYTGLVQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP SNCLGIRSGDAGQCTELLNVAKHYTMEHFIEVIKNQEFLLLP NEISKLLCDDINVDEETIFHALMQWVGHDVQNRQGLGMLLS YIRLPLLPQLADLETSSMFTGDLECCQKLMAMKYHLLPERR SMMQSPRTKPRKSTVGALYAVGGMDAMKGTITIEKYDLRTNSWL HIGTMNGRRQLQFQVAVIDNKLIVVGGRDGLKTLNTVECFNPVGK IWTVMPPMSTHRLGLGVATLEGPMYAVGGHDGWSYLTNTVERWDP EGRQWNYVASMSTPRSTVGVALNNKLYAIGGRDSSCLKSMY FDPHTNKWLSLCPMSKRRGGVQVATYNGFLYVVGHDAPASNH SRLSDCVERYDPKGDWSVAPLSVPRDAVAVCPGLDKLYVVG YDGHYTLNTVESYDAQRNEWKEVPVNIAGRAGCVVVVCLP LTPPAGIRHEVRDREREREREREREFLLDSTGSELKQNIHSIT GLPPAMQKVMYKGLAPEDKTLREIKVTSKAKIMGGGSTINDVLA VNTPKDAQAQDAKAEENKKEPLCRQKQHRKVLKDGKPEDVMP KGAQERLPTVPLSGMYNKGKVRLLTFLKEDQLWIGTKERTK LPMGSIKNVSEPIEGHEDYHMAFQLGPTSEASYWVWVPTQY VDAIKDTVLGKWQYF |
| 6922 | 1075 | 369 | LGLFCILFIDTLCAVLEDRDLSIRESLFGAVVRNAEACQRRQ LPVTFGNKQKVLGKALSIRFPLMTIEFAAGPAQSGILSDREV VNLFLHFTVNPKEPRVEYIDRPRCLRGKECCINRFQQVESRWGY SGTSDIRFTVNRRIIVGFLYGSIHGPTDYQVNIQIIEYEKK QTLGQNDTGFSKCDGTANTFRVMFKEPIELPNVCTACATLKGP DSHYGTGLKKVHETPAASKTVFFFSSPGNNNGTSIEDGGQIP EIIIFYT |
| 6923 | 2469 | 1660 | FEERVICFVEYYLTAFHEGRKGLAKKPYNEIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPKSKYKLPVABQVSHHPP ISCFYCECEKRLCVNTHVWTKSKFMGMSVGVSMIGEVRLLE HGEEYVFTLPSAYARSILTIIPWVGLGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNN ETKVIDTTLTPVYPKKIRPLEKQGPMSRNLWREVTYRLGLDI DAATEQKRHLEEKQVBERKRENLRTPWKPKYFIQEGDGSILQ SPLESTLMGLEVSFPV |
| 6924 | 2210 | 1235 | RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSSEGNQKEKDLCKIFY DOWSESDQVEFVHLSRMCHYQHGINSYLPMLQDFITALP EQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKI IQDIETIESNWRGGRHNLQRIQCRSENSKGVYCLQYDERVITGSSDS LRDNSIKINDKTSLECLKVLTGHTGSVLCQYDERVITGSSDS TVRVWDVNTGEVLNLIHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVCHRAAVNVDFDKYIVSAGDRTIKWV STSTCFVRTLNHKGRIACQYDRDLVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCRLTLVEHSGRVFRLQDFBQIISSSHDDTILINDFL NVPPSAQNETRSPSTYTYISR |
| 6925 | 2 | 1653 | SGRVAMDGLGLQFPEQGFAPGPFLLPHMGGHYRDCOSLGAFFL |
| 6926 | 1 | 733 | |

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|------------|--|--|--|
| 6927 | 2 | 1484 | DGYPLPTDTSPLDGVDPDPAFFAAMPFGDCPAAGTYSVAQVSD YAGPPEPPAGPMHFRLGPEPAGPSIPGLLAPPSALHVVYGMGS PGAGGGRGFQMPPQHQQHQQHPPGPGGQPTPPPEALPCRDGT DPSQPAELLGVDRTFEQYLHFVCKPEMGLPVQGHDSGVNLPD SHGAISSVSDASSAVYYCNYPDV LTLGGDIQLMLAQNANRAAHLEEFHYQTKEDQEILHSLHRESS CQGFANATDLSTDLSQLSVSCCKYEAAEILQPRDLKSNPEH YVQVLKRMGNIRNEIGVFFYMNQAAALQSERLVSKSVSAEQQLW KKSFSCEFEGIHNFESIEDATNAALLCNTGRIMRICAQAHCA GDELKREFSPEEGLYNKADIDYLLKALRSIGTRDIHPVWDSVN WELSTTYFTMATLQDDYAPLSRKAQEQIEKEVSEAMKSLKYCD VDSVSARQPLCQYRAATIHRLASMYHSLRNQVGEHLRKQHR VLADLHYSKAAKFLQLLKDAPCELLRVQLERVAFAEFQMTSQNS NVGKLKTLGSGALDIMVTEHAFQLIQKELIEFEGQPKSGDAAA ADASPNSLRNEEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN IEDDTILKINKHIYSQLLRATANKTATLLERINVIHLLGQLAA GSAASSNAVQ EATDLINLLQVKMRKRYSDKTLSPHNLQDYQTLWDLRELECK IGERYITHEDDLWEKYAGEQGLQYPHTLINPSASHSDTPETE ETEMKALGERVSIL RDQGVRRDRSPAREPGDVSARTSGGGGGRSATTAMPPFPVNG NLHQHDPQDLRHNGNVVAGRPSCSRGPRRAIQKPPAGRRSG RGPAAGGLCLOPPDGGTCVPEEPVPMDEALEKHLAGLQFRE QEVNRQGGARTNSTSAQKNERESIRQKLAGSFFDDGPGIYTSC SKSGKPSLSRLSQGMNLQICFVNDSSGSDKSDADDSTKTSLD TPLSPMSKQSSSYSDRTTEESSESLDDMDFLTRQKQLQAEAKM ALAMAKPMKMQVEVEKQNRKKSFPVADLLPHMHPHISECLMKRSL KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE QDAMLVDIEDLTHAESQKQKMAEKMPAK FKDTANVFSVLFQMRNNFRHYFIEPSQLKLFYDVTWITVQVAI SYTVVPFVILSIKPSLTFYSSWYVCLHILGLVLLLPVKKTQR RKNTHEINQLSQSKKFDGENSLGQNSFSTNNVCNQNEIASR HSSLKQ FVERLPNRPACLLVASGAAGVSAQSFLHCFTMASTAFNLQVAT PGGKAMEFVDVTEGNARWQDFRLKAYASPAKLESIDGARYHAL LIPSCPGALITLASSGSLARILQHFHSESKEICAVGHGVAALCC ATNEDRSWVDFSYSLTGFSVCELVRAFGFARLPLVVEDFVKDSG ACFSASEPDVAVHVVLDRLHVTGQNASSTVPAVQNLFLCGSRK FVDSFGQGEQAEIEEGGTQMNRMRAHSPAEASVESSSPGPKK SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHQPLFSIVR QACVRSLSCEVCPGREGPIFFGDEQHGFFVSHFFIKDSLARGF QRWYSIITIMMDRIYLINSWFFLLGKVRGIIIDELQKALKVFEA EQFGCPQRAQRMTAFTPFLHQRNGNAARSLTSLTSDNLWACL HTSFAWLLKACGSRLEKLEGAFTEDTLVQMEKLADLEESES WDNSEAEIEEEKAPVLPESTEGRELTCQPAESSLSGCGSWQPRK LPVFKSLRHMQRVGGRTAHHELRRRANHGLCLPTRLASGPSTL KTLQEVTDLSLGGWLMAGVGGII SLNLHCTLPPPPHGYAGYPSDKGKKPKGSKQPSGTTKRP SDDDCPSASKVYKASDSAEAEIAEALTPQQQHLIREDQCNQKLW DEVLSHLVEGPNFLKLEQSFMCVCCQELVYQPVTECFHNVC DCLQRSFKAQVFSCPACRHLGQNYIMIPEILQTLDDLDFPGY SKGR DRDHSQCGGIRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV CWTPFFVQMWVMDANAPKASAFIIVMLLASLNSCCNPWIYM LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKNSSSSVLS HRSSQRSCSQPSTA |
| 6928 | 1086 | 777 | |
| 6929 | 1749 | 607 | |
| 6930 | 131 | 545 | |
| 6931 | 2 | 659 | |
| 6932 | 2 | 1131 | |
| 6933 | 1431 | 890 | |
| 6934 | 3030 | 2588 | |

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|------------|--|--|---|
| 6935 | 886 | 543 | NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL VAMDGNLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS VGAVLELLNFPPSSPTLSVSSTSL |
| 6936 | 1347 | 567 | RSRRQFLSRALLEFFGKSHPPHRLFRKSLNVGLHYSHIPFLT TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS LPSPPLNLGPGQPALTPQEENILHTTQTDCCYNLAACLLQMEPV NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG |
| 6937 | 1 | 727 | AVEFRCCPGRDPACFARGWRLDRVYGTCTCDQACRFTGDCCFDY DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA PCPPLERAGCLEYSTPQGDGCHTVVPAFITTSFNFKERTRQA TSPHWSTHTEDAGYCMFETESLTPHCALENRPLTRWMQYLRG YTVCVDCQPPAMNSVSLRCSGDGLSDGNQLTHWQAIGNPRCQG TWKKVRRVDQCSCPAVHSFIFI |
| 6938 | 3 | 719 | NSRKLELAERVDTFMQLKRRQSSEKENDSGTLDTVGAVVVDH EGNVAAVSSGGLALKHPGRVGGAAALYGCSCWAENTGAHNPYST AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMONKFIS PFLASEDGVGGVIVLRSCRCSEPDSSQNKQTLVFLWSHT ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVABEGGVCRLGEP SELTQAECEASQRHFT |
| 6939 | 3 | 810 | KVTAPRRPQRYSSGHGSDNSSLGELPPAMORTALFHHSGSS GYESLRRDSEATGSASSAPDSMESGAASPGARTSLKSPKKRA TGLQRRRLIPAPLPDPTALGRKPSLPGQWDLPPPLAGSLKEPF EIKVYEIDDERLQRPPTPREAPTQGLACVSTRLLAERRQQR LREVQAKHKHLCEELAETQGRMLLEPGRWLEQFEVDPELEPESA EYLAALERATAALEQCVNLCKAHVMVTCFDISVAASAAIPGPQ EVDV |
| 6940 | 1188 | 496 | GKMAAQPLRHRRCATPPRGDFCGGTERAIDQASFTTSMEDTQ VYKSSPLGPAAGAEPAAGPQLPSWLQPERCAVFOCAQCHAV LADSVHLAWDLRSRLGAVVFSRVNTNVVLEAPFLVGIIEGSLKGS TYNLLFCGSCGIPVGFHYSTHAALALRGHFLCSSDKMVCYLL KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS EVTDPQSKPEN |
| 6941 | 1 | 713 | SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEARQAEALGYQA VVLSAAMQGDVKSMQFYGLLAHVARTRLTPSMAGASVEEDAQL HELAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQSG RGGRNQELALRVGAELRRWPLGPIIDVFLSGGTGQDGPTEAAG AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGAHLHTG MTGTNVMDTHLLFLRPR |
| 6942 | 1 | 246 | GDYVERYDPKTDWTMGAPLSMPTNAVGGCLLDRLVADGGYDG QTYLNTMESYDPQTNEWTQMASLNI GRAGACVVIKQP |
| 6943 | 1 | 739 | PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWRLG HSPAGGSITETLVQGBKTEYLLTALEPKPTYIICMVTMETTNAY VADETPVCAKAETADSYGPTTLNQEQNAGPMASLPLAGIIGGA VALVFLFLVLAICWYVHQAGELLTRERAYNRGSRKKDDYMESG TKKDNSILEIRGPGQLMLPINPYRAKEEYVHTIFPNSGSSLCK ATHTIGYGTTRGYRDGGIPDIDYSY |
| 6944 | 960 | 156 | VANILLNGVKEYSELTGSSERAEQPLSVGRCLSTICNMPKALRT LCVNHFLGWLSEFGMLLFYTFMGVEVVFQGDPKAPHTSEAYQKY NSGVTMGCGMCIYAFSAFYSAILEKLEFLSVRTLYFIAYLA FGLGTGLATLSRNLYVVLSCITYGILFSTLCTLPYSLLCDYQ SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVGLPLTSA VGSANGVMYFSSLVSLGCLYSSLFVIYEIPPSDAADDEHRPLL LNV |

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|------------|--|--|---|
| 6945 | 2067 | 179 | EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAFAQGC HSPKGPAPVPVPLKKRGYDVTNRPHLNKGMAFTLEERLQGIHGL IPPCFLSQDVQLLRIMRYEROQSDLDKYIILMTLQDRNEKLFY RVLTSDEVEKFMPIVYPTTVGLACQHYGLTFRPRGLFITIHDKG HLATMLNSWPEDNIKAVVVTGGERILGLGLGCGYGMGIPVKGKLA LYTACGCVNPQQCLEVLLDVGTNNEELLRDPLYIGLKHQRVHGK AYDDLDEFMQAVTDKFGINCLIQFEDFANANAFRLNKNYRNKY CMFNDDIQGTASVAVAGILAAALRITKNKLSNHVFGGQAGAEAM G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH LNHEKEMFAQD\HPEVNSLEEVRVLPKTAIGVAAIAEA\FTE QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG GDPGHP\DEIFLPSRAKLPQEVSEQHLSQGRLYP\PLST\IR NVFLRIAIVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD YDSFYT/VDSYIWAQKAMNVQTV |
| 6946 | 133 | 2551 | SCEYSGITVAPGDPCCGVAHLLAPSMASDTPESLMALCTDFCLR NLDGTLGYLLDKETLRHHPDIFLSEI\CDRLVNEYVELVNAAC NF\EPHE\SFFNPLFRDPRKQASRR\IHL\RED\LVQD\QD\LE AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG C\TNILLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGPSRLR F\KLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ WKDSL\VSLVL\YNMDLSDDHIR\VVVQLHKLRLHLDISDRRLSS YYKFKLTREVLVSFLVQKLGNLMSLDISG\HMLENCISISKGR EAGQTSI\EPSK\SSIIIPRGFEGGPLQF\LGVF*GIFCGRLTH IPAYKVSQDKNEEQVNAIEAYTEHRPEITSRAINLLFDIARIE RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF QYRRVNEILLSILNPTRQDESIIQRIAVHLCNALVCQVNDNDHEA VGKMGFVVTMLKLTQKLLDKTCDQVMEPSW\SALWNITDETPD NCEMFLNFMNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVEL RPQLMTSQFISVFSNLLSKADGIEVSYNACGVLSHIMFDGPEA WGVCEPQREBEERMWAAIQSWDINSRRNINYSFEPILRLLPQ GISPVSHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM ATARQETKEMARKVIEHCNSNFKEENMDTSR |
| 6947 | 2 | 1682 | TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRLKMLNVP SQSFAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG LKGRLEIEVTEBELKHNKDDCWCICIRGFVYNVSPYMEYHPGGE DELMRAAGSDGTETLFDQVHRWVNYESMLKECLVGRMAIKPAVLK DYREEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFTDLSVTI /EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A MRFRKIFLCGL/CESVKGIEIVLQKKENTSWDFLGHLKNNHNSL IPRKDTGLYRKQQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLNNKYIYFLIK IYPTGLFTPELDRLOIGDFVSVSSPBGNFKISKFQLEDLFLLA AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE KLAPDKRLDVEFVLSAPISEWNGKQGHISPAALLSEFLKRNLDK SKVLVLCICGPVPFTEQGVRLHDLNFSKNEIHSFTA |
| 6948 | 104 | 58 | PDGAHSFPFDEYFTCSSLCLSCGVGCKKSMNHGKEGVPEAKSR CRYSHQYDNRVYTKACYERGEVSVVPKTSASTDSPNMGLAKY AWSGYVIECPNCGVYRSRQYWFNGQDPVDTVVRTETI VHVWPGT DGFLKDNNAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTQDI APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDCSSSK TRPVPERGWGPAPVRVCDNCEYAR/TRPVSCYRGTSGR*RRRRT QETVE |
| 6949 | 152 | 4656 | GLRLCLSRPLTRPGDSDVSGSAMASGAGGVGGGGGGKIRTRRCH QGPIKPYQQGRQHQGILSRVTSVKNI VPGWLQRYFNKNEDVC |

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|------------|--|--|--|
| | | | <p>SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESFALHCQPST SAFFIGSSGSLVKIKDSTSQHDDDNISTSGFSSRASDKDIT VSKNTSLPPLWSPEAERSHLSQHTATSSKKPAFNLSAFGTLSP SLGNSSILKTSQLGDSFPYPGKTTYGGAAAVRQSKLRNTFPYQA PVRROMKAKQLSAQSYGVTSSARRILQSLEKMSSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGKMRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNFSPEITSSSPINSS QALTNKVQMTSPSSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAEALSGSSSTLEPIISSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSLVDILKSPGFASPKIDSVAQAQPTATSPVY TRPAISSFSSSGIGFESLKGAGSQWQCDTCLLQNKVTDNKCAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVI WDCDTCLVQNKPEAIKVCACETPKPGTCVKRALTLTVSESAET MTASSSSCTVTTGTGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGSGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFGFDTSSSSSSNAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSSESKPEEVKDKSKNDNFKFGLSFGL SNPVFLTPFGVSNLQGEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLTGTIETKSVSVAPLKQOTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFLGRTEEKQEPVTSLSLVFGE KLTMKEPKC/QPVFSFGEFORQTKDENSSTFSFMTKPEKE SEQPAKATFAPGAQTNTTADQGAAPDLSYLNSSSSSSTPAT AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLFSQDSKLATTSSTGTAVTFVFGPGASSNNTTSGFGFG ATTTSSAGSSFVFGTGPSASAPAFGANQTPTFGQSQGASQP NPPGFGSISSTALFPTGSQPAPPTFTVSSSSQPPVFGQPSQ SAFGSGTTPNSSSAFQFGSSTTNFTNNSPSGVFTFGANSSTP AASQPSGSGGFPFNQSPAFTVGSNGKIVFSSSGTSFSGRKIK TAVRRRK</p> |
| 6950 | 2585 | 411 | <p>PRPGSRSGLCRRAGERGAVRAGGLSRRTAE*IMDELHYQDTS DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQDWKFLASHFPNR TDQQCYRWRVLRVLPDLVKGPTWKEEDQKVIELVKYGTQKWT IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEDRIICEAHKV LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGLSESKDC KPPVYLLLELEDKDLQSAQPTGEGSLLTNWPSVPTIKEEN SEELAAATTSKEQEPICGTDLDAVRTPEPLEEFPKREDEQESSP ETSLPYKWVVEAANLLIPAVGSSSLSEALDIESDPAWCDLSKF DLPEEPSAEDSINNSLVQLQASHQQVLPQPSA\LVPSVTEY RLDGHITISDLSSSRGELIPISPTSEVGGSGIGTPPSVLKRQRK RRVALSPVTENSTSLFLDSCNSLTPKSTPVKTLFPSPSQFLNF WNKQDTLELESPLTSTPVCSQKVVTTPHLDKTPHQAHAFA VTPDQKYSMDNTPHTTTPFKNALEKYGLKPLPQTPHLEEDLKE VLRSEAGIELIEDDIRPEKQKRKPLRRSPIKKVRKSLALDIV DEDMKLMSTLPKSLSLPTTAPSNSSSLTSGIKEDNSLLNQGF LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTACCGTRDQLFMQE KARQLLGRKPSHTSRTILS</p> |
| 6951 | 1940 | 239 | <p>AGPDDTMKRSLOALYQQLSFLILALTEALAFATQEPSPRESL QVLPSGTTPGTMVTAPHSSSTRHTSVMLTNPDPGPPSQAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPIKAP/SSTGPAPAMAT TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPRTTTRPPRP PGSSRKAGAGNSRPVPPAPGGHSRSKEGQGRNPSSTPLGQKRP LGKIPQIYKGNFTGSVEPEPSTLTPRTPLWYSSSPQQTVAAT</p> |

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|------------|--|--|--|
| | | | TVPSNTSWAPTITSLGPAKDKPGLRRAAQGGSTFTSQGGTPDA TAASGAPVSP/PSCPSAFSAPPPR*PTGWQP**LLAYCYP\CT SRPLSTSSGVFTAAATGPTPAADTSVSAPSQGI PQGASTTPQAP THPSRVSESTISGAKEETVA\PS*PTGCPVLSQWYPPQQAIS STAWSPPGPGSLGQQGTS PMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEEEEEEDRQPGEQPEAYGNNTHTHPT TFQQAC\RGAAPEIPVPLKPLRLQLSEPRSPANGDYRDTGMVPC |
| 6952 | 658 | 304 | PESEGESGEMTDRTYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLHGLPLRPSQLLRHCGE*EQSASPLQLDGKDSALWT ASRQARGELRLCLTTAVRGTSPPSVSPVCSS |
| 6953 | 1512 | 349 | NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC GRALSSPGSLGRHLIHSQDQRSNCAVCGARFTSHATFNSEKLP EVLNMESEPTVHNEGPSSAEGKDIAFSPVYPAGILLVCNNCAA YRKLLAEQTPSVRKWALRRQNEPLEVRLQRLEERTAKKSRDND ETPEEREVRMRDREAKRLQRMQETDEQARRLQDRREAMRLKR AIETPEKRQARLIREREAKRLKRRLEKMDMLRAQFGQDPSAMA ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH |
| 6954 | 819 | 1 | PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAQON *PQR*RWTEGNSPQASAVATPGOGASPAAPRCTP*PSRRHRLP PGARPPAG*AAPAPT KPWLAGPASAPQGAAPLSPPAPPLIRTR *CAGAAARGPRRDRSPRPTPGGCSWSEPTPPAVSASAQTPS DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSRRREGTIPGNPHPR AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGGAPPNQVGSS VMQAMSTGI |
| 6955 | 1968 | 782 | PPGRRQVRAQVAGAPVGHWGTRARQVKTGRRRRARRTMPFLGQD WRSPGWSWIKTEDGWKRCESCSQKLERENNHCHNISHSIILNSD GEIFNNEEHEYASKKRKKDHFNDTNTQSFYREKWIYVHKESTK ERHGYCTLGEAFNRLDFSAIQDIRRFNVVKLLQLIAKSQLS LSGVAQKNYFNILDKIVQKVLDDHNPRLIKDLLQDLSSTLCIL /N*RSREVCISGKHQYLDLPIRNYRLATTATGSSDD*ASE\NG LTLSDLPLHMLNLIYRPSDGDNDIITLGQVTPPLYMLSEDRQLW KKLCQYHFAEKQFCHRLILSEKGHIEWKLMYFALQKHYPKEQY GDTLHFCRHCSILFWKDSGHPCTAADPDSCTFVSPQHFIDLFK F |
| 6956 | 8605 | 3839 | QTSSTIFASPTSPVVLGESVLQDNSFDLNNGSDAEQEEMETQSS DFPPSLTQPAPDQSSSTIQLHPATSPAVSPPTSPAVSLVSPAAS PEISPEVCPAASTVVPVSPVSPASSAVLPVSLVPLTASV TSPKASPVTSPAAFPATSPANKDVSSFLETTADVVEITGEGLT ASGSGDVMRRRIATPEEVRLPLQHGWRREVR IKKGSRRNQGETW YYPGCGKRMKQFPEVIKYLNRNVHVSRRHFSFSRMPVGDFF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV PKVKRGRGRPPKVKITELLNKTNDNRLKLEAQETLNEEDKAKI AKSKKKMRQKVQRGECQTTIQGQARNKRQETKSLKQKEAKKKS KAEKEKGKTKQEKLEKVKREKKEKVKMKEKEEVTAKAPACKAD KTLATQRRLEERQRMILEEMKKPTEDMCLTDHQPLPDFSRVP GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEBL LCQGDLSLGEVQDLLVRLKALHDPGFPSYCSLKLGEKVSFI PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQKAAV LAFLVHELNGSTLIINEIDKTLESMSYRKNKWIIEGRLRLRLKT VLAKRTGRSEVEMEGPEECGLRRRSSRIMEVTSMEEEEEES AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRLFFRKLLH SSQMLRAVSLGQDRYRRYVWLPYLAGIFVEGTENLVPEEVIK KETDSLKVAHASLNPALFSMKMELAGSNTTASSPARARGPRK |

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|------------|--|--|---|
| | | | TKPGSMQPRHLKSPVRGQDSBPQAQLQPEAQLHAPAPQPQLOLQQLQSHKGFLEQEGSPLSLGQSQHDLQSASFLSWLSQTQSHSSLSSSVLTPDSSPGKLDPAQSPPEEPEDAESSPDQALWFNISAQMPCNAAPTPPPAVSEDQPTSPQQLASSKPMNRPANPCSPVQFSSTPLAGLAPKRAGDPGEMPQSPPTGLGQPKRRGRPFESKFQKMEQRYLTQLTAQPVPPMCMCSGWWWIRDPEMLDAMLKALHPRGIREKALHKHLNKHRLDFLQEVCLRPADPIFEPRQLPAFQEGIMSWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDSTREDLAYCEHLSDSQEDITWRGREGRLAPQRKTNPDLAVMRLAALQNVRRYLRPLWPTHEVVLEKALLSTPNGAPEGTTTETISYEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVTCIVCRKGDNDFFLLCDGCDRGCHYCHRPKMEAVPEGDWFCVCLAQQVEGEFTQKGFPGKRGQKRKSGYSLNFSSEGDGRRRRVLLRGESPAAGPRYSEEGLSPSKRRRLSMRNHSDLTFCIILMEMESHDAAPWFLEPVNPRLVSGYRRIKKNPMDFTMRERLLRGGYTSSEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEFYQKQGGSVRQGRWGVTLWHLPTFTQTKTCHFLMLPLPVVQTQVRYNPDF |
| 6957 | 82 | 3514 | HLIVAMPEPTKKEENEVPAPAPPEPEPSKEKEAGTTPAKDWTLVETPPGEEQAKQANSQSLFIEKPPQGGTVKVGEDITFIKVKAEIDLSEKPTINGSRKWMDLASKAGKHLQLKSTFERHSRVYTFEMQIIKAKDNFAGNYRCEVTYKDKFDSCSFDLVBHSTGTTPNIDIRSAFKRSQEGQEDAGELDFSGLLKRRVKKQEEEPQVDVWELLKN TKPSEYEKIAFYQESPTCSGMLKRLKRSIREKKSAAPAKILDPVYQVDKGRVRFVVELADPKLEVKNKNGQELRPSTKYIFEDTRCQSILNIDNCQMTDDSEYVVTAGDEKCTELLVREPPIMVTQKLEDTDYCGERVELECEVSEDDAQVWKFKNGBEIILVQTRYRIRVEGKKHILIEGATKADAADYSVMTGGQSSAKLSVDLKLKILITPLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVHKGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPKVVHIDPPKII LDGLDADNTVTVIAGNKLRLIEPISGEPKKAMWSRGDKAIMEGSGRIRTESYPPDSTLVIDIAERDDSGVYHINLKNEAGAHASIKVKVVDFFDPPVAPTVEVGDDWCIMNWEPPAYDGGSPILGYFIERKKKQSSRWMLNFDLCKETTFFPKKMEGVAYEVRIFAVNA\IGISKSPMSRPFVPLAVTSPPTLLTVDSVTDTTVMRWRPDPDII GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKDLIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPIVKEIIEPPKIHSPKHLKQTYIRRVGDRVILVIPFGKPRPELTWKKDGAIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAITGYTIQKADKKSMEWLRVIEHIEVPVHTELIVIGNEYFYFRVFSENMCGLSEDAWTMTKESAVIARDGKIYKNPVYEDDFSEAPMFTQPLVNRLCHSGYMATLNCSSVRGNPKPKITWMKNKVAIVDDPRYRMFSNQGVCLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ |
| 6958 | 274 | 1663 | PRTSRVKTEGSGSSAMDFSVKVDIEKEVTCPICLELLTEPLSLDCGHSFCQACITAKIKESVII SRGESSCPVCQTRFQPGNLRPNRHLANIVERVKEVKMSPOEGQKRDVCEHHGKKLQIFCKEDGKVICWVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAELLEDIRQERTAWKNYI QIBRQKILKGFNEMRVILDNEEQRELQKLEEGEVNVLNLAATDQLVQQRQDASTLISDLQRLRGSSVEMLQDVIDVMKRSESWTLKKPKSVSKLKVFRVFDLSGMLQVLKE LTDVQYVWVDMNLNPGSATSNAISVDQRQVKTVRTCTFKNSNPCDFSAGVFGCQYFSSGKYWEVDVSGKIAWILGVHSKISSLNKRKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAPEDSSSDPKVLTFLMAV\LPVVLGFS |
| 6959 | 1 | 1469 | SLVHVVEFGRGIEDFPYLFQQLTHCQQRICSVTQAGVQWCDHSS |

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|------------|--|--|---|
| | | | LQPQTPGLNQSSHLSSLSSRDYRMLSSFNWFQDRFWLPPNVT WTELEDRDGRVYPHPODLLAALPLALVLLAMRLAFERFIGLPLS RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKPEQLSLLAQCGL TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSFVGGLSV LYHESWLWAPVMCWDYRPNQLTSCPAADSEA\SLYWYLLLELG FYLSLLIRLPFDVKRKGSGPSSIKPRPHYDPPSTA\DFKEQVIH HFVAVILMTFYSANLLRIGSLVLLLDSSDYLLLEACKMVNYMO YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPF GYFFNGLLMLLQLLHVFWSCILRLMYSFMKKGQMEKDIRSDV EEDSDSEEAQAQEPQLKNGTAGGPRPAPTDPGRSRVAGRLTN RHTTAT |
| 6960 | 387 | 2068 | AKWAREKEMQEF\TRSF\RCRDPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEPLKMQVDEAASREDKLDLTKKGRKPT PCSDPERKRRFRNBSSESGSEASSPDYFGPAKNGVASRSHTHP KEENPRRA\SKAVESSDEERQDLPAQRGESESEEEKGYKKG TRKKPVVKKQAPGKASVSRKQAREESESEAEVPQRTAKKVEGN KGTKSLKESESESEEEILAKKKEQREEVEEKEEDEEKGDWK PRTRNGRRKSAREERSCKQKSAKRLLDSDSEEBQKEAASSG DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKEPTA KGSRKMARLGSTSGEEDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPKAGGKAGSGRRGEDHPAVMLRKRYIR ACGAHRNYKKLLGSCSHKERLSILRAELEALGMKGTPSLGKCR ALKEQREEAEEVASLDVANIISGSGRPRRTAWNPLGEAAPPG LYRRTLDSDEERPRPAPPDWSHMRGISSDGESN |
| 6961 | 340 | 1646 | RPWSSPTMKPNFSLRLRIFNLNCWGPYLSKXHRADRMRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDFWFGKAVGLLVHL SGMVLNAYVTHLAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQLKFPFGVRIYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDEALMATLFVRHSPQNPSSSTHGP\AERS PL/MCVCLKEALDGSGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELOHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ |
| 6962 | 340 | 1646 | RPWSSPTMKPNFSLRLRIFNLNCWGPYLSKXHRADRMRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDFWFGKAVGLLVHL SGMVLNAYVTHLAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQLKFPFGVRIYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDEALMATLFVRHSPQNPSSSTHGP\AERS PL/MCVCLKEALDGSGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELOHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ |
| 6963 | 374 | 2618 | RVTPLYLKLKPKTAENQKASEENEITQPGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFNSVLETLEQNRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSVSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPQIDSGQDTPRG TPESGTSGQSSDTEGSLQSHPOHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHMEDPSWITRIHERSQMERYL STITPETHCRKQPRPVRIQTLVGNIIHKQEMEDDYDYGGQVRQ ILERNESEECTEDTQAEGETESEPKGESFDSGVSSSIGTEPDSV EQFGPGAARDSQAEPQPEQAEEAPAEAGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQPPSVNTSIGQLPSTQLYLR QTETILTSNLRMLTLTSNTQVIGTAGNTYLPALFTTQAGSGPK |

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|------------|--|--|---|
| | | | PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPOLASSAGH STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI CWRFSFLKDYLIK\HMTHTGVRAQCSICNKRFTQKSSLNVMH RLHRGEKSYBCYICKKKFSKHTLLERHVALHSASNGTPPAGTTP GARAGPPGVVACTEGTIVCVSCPAKFDQIEQFNDHMRMHVSDG SGRFFFFSNTDVYFIKKVTNRWTAGSSYKMRMKSIGKILL QIFIG\NCSMFVLVI |
| 6964 | 1 | 178 | NVFIEPRIQGFMTSAHPGQKHDFSMGLLPFLAALVCSGGS SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFCLKDRSDFRF PQEKVEVSLQKA\QAMFLYDVLQVFNFSHKALL\CCMEHDL PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQVIEGSTLALRRY PQESISTLE |
| 6965 | 757 | 208 | IITALGVRCMPGCPGCGMAGPRLLFLTALALELLGRAGGSQP ALRSRGATACRLDNKESSESWGALLSGERLDTWICSLGLSMVG LSGVFPLLVIPLEMTMLRSEAGAWRLKQLLSFALGGLIGNVFL HLLPEAWAYTCSASPGGEGSQLQQQQQLGLWVLAGILTFLALEK /HVPQQQGGDQPGPQQRPHCCRRARQWRPLSGPAGCRARPCR GP\DIKVSGLNLLANTIDNFTHGLAVAASFLVSKIGLLTTMA ILLHEIPHEVGDFAILLRAGFDRWSAAKQLSTALGGLLGAGFA ICTQSPKGVEETAAVVLFPTSGGFLYIALVNVLPDLLEEDPW |
| 6967 | 162 | 633 | TFPFKYWILDLSASSRMETDCNPMELSSMSGFEESLNGFEG TMDKMRLEAEAVNDVLFVANNMFVSKSLRCADDVAYINVETK ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLDLTL\ SPAYREAFGR\LLQRLALKRDGQS |
| 6968 | 1 | 2265 | RGGGGGRCGPGARERERPEPERTMEAAAGRGCFQPHPLQKT LEQFHLSSMSLGGPAAFSARWAQEAYKKEAKEAGAAVPAVP PAATEPPVHLPAIQPPVLPVPFFMPSPDRSTERCETVLEGE TISCFFVVGGEKRLCLPQILNSVLRDFSLLQINAVCDELHIYCSR CTADQLEILKVMGILPFSAPSCGLITKTDARLCNALLYGGAYP PPCKKELAAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS SPSAACIQCLD\CRMLYPPHKFVVHSHKALENRTCHWGF\DSA\ NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP RVSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS LGCVHPRQLSAFRPWSPAVSASEKELSPHLPALIRDSFYYSKS FETAVAPNVALAPPQKQVSSPPCAAASVRAPEPLATCTQPRK RKLTVDTPGAPETLAPVAPEEDKDSAEVEVESREEFTSSLS LSSPSFTSSSSAKDLGSPGARALPSAVPDAAPADAPSGLEAEL EHLRQALEGGDLTKEAKEFLHEVVKMRVQKEKLSAALQAKRS LHQELEFLRVAKKEKLEATEAKRNLKEIERLRAENEKMKKEA NESRLRLKRELEQARQARVCDKGCEAGRIRAKYSAQIEDLQVKL QHAADREQLRADLLREAREHLEK\VVK\ELQEQWLWPRARPE AAGSEG\AAELEP |
| 6969 | 1855 | 118 | AGTMHGRLLKVKTSSEEAQAEAKRLEREQKLLYQSATOAVFQKRA GELDESVLELTSQILGANPDPFATLWNCREVLQOLETQKSPEEL AALVKAELGFLESLRVNPKSYGTWHHRCWLLGRLEPNWTRREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFDLSLITR NFSNYSWHYRSCLLPQLHPQDPSGPQGRLPEDVLLKELELVQN AFPTDPNDQSAWFYHRWLLGRADPDALRCLHVSDEACTVVSF SRPLLVGSRMEILLMVDDSLIVWRTPDGRNRP SHVWLCDL AASLNDQLPQHTFRVIWTAGDVOKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIIILM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDLRSKFLLENS VLKMEYAEVRLHLAHKDLTVLCHLEQLLVTHLDLSHNRRLTL PPALAAALRCLEDPPT\VLQASDNATESLDGVTNLPRLQELL CNNRLQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL PSVSSVLT |

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|------------|--|--|--|
| 6970 | 3 | 1528 | SFPPLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLRPLNE GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSSEDEVEILGPFPA QTPPWLMASRSSDKDGSVHTASEVPLTPRTNSPDGRRSSDTS KSTYSLTRRISSLESRRPSSPLIDIKPIBFVLSAKKEPIQPSV LRRTYNPDDYFRKFEPHLYSLSDNSDDVDSLTDDEILSKYQLGM LHFSTQYDLLHNLTVRVIEARDLPPPISHDGRSQDMAHSPYV KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL LTVVDFDKFSRHCVIGKVSVPVLCVLDLVKGGHWWKALIPSSQNE VELGELLLSLNLYPSAGRLNVDVIRAKQLLQTDVVSQGSDFPVKI QLVHGLKLKTKTSFLRGITIDPFYNESPSFKVPQELENASLV FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRLNTHRT AVEQWHSLSRAECDRVSPASLEVT |
| 6971 | 37 | 3702 | ACFYVPGSRSEFKLIPRHGLVMGRSGKLFSGVSAKLKRWKKGHS SDSNPAICRHRQAARSFRSRSRSDLTVDVAVKLHNELOSGSL RLGKSEAPETPMEEAEVLVTEKSSGTFSLSDCTNVTFSKVQ RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEFPAALIRKA AQHGVCVSLKGSFMEFKAHPAAISTAKFCIQEIEKSGGSK EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA CAMQAFHSLFHARPGSLTSLAELNAQIITALYDVVPSENDLQPL LAWLKVMKHAHINLVRLQWDLGLHLPRFFGTAVTCLLSPHSQV LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRV EEGLTYKFHAAWSSVLQLLCVFEACGRQAHPVMRKCLQSLCDL RLSPHFPHTAALDQAVGAAVTSMGPEVVQLQAVPLEIDGSEETLD FFRSWLLPVIDHVQETRLGFFTTYFLPLANTLKSAMDLAQAG STVESKIYDTLQWQMTLLPGFCTRPTDVAISFKGLARTLGMAI SERPDLRVTVQALRTLITKGCQAEADRAEVSRAKNFLPILEN LYQGPVAAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK VLDPASSDFTRLVLDLVVALAPCADEAAISKLYSTIRPYLESK AHGVQKKAYRVLEEVCAAPQGGALFVQSHLEDLKKTLDSLSRS TSSPAKRPRCLKLHIVRKLSAEHKEFITALIPEVILCTKEVSV GARKNAFALLVEMGHAFRLFGSNQEEALQCYLVLIYPGLVGAVT MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLASRTRDVV KSAIGFIKVAVTVMVAHLAKHVQLVMEAGKLSDDMRHFRMK LRNLT\KFIPK\FGILTWGKKAAGVPKEYHRVLVNIKAEARAK RHRALSQAABEEEEEEEPAGQKGSIEEILADSEDEEDNE EEERSRGKEQRLARQRSRAWLKEGGDEPLNFDLPKVAQRVLA TQPGPGRGRKKDHSFKVSAAGRLIIREADGNKMEEEGAKGED EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGSGGI HRPVAKKAMPAGAEYKAKKAGDVKKGRPDYAYIPLNRSKLN RKKMKLQGFKGLVKAQGRSGVGHKNRRKDRR |
| 6972 | 2179 | 973 | PGGAILLPLWRRTRPREATVPRGAAQRGRARSAGRI PSSQSPS PAEAGGATRSPPPRPPRPPGSPAPPLLRSDAGPGATVSA AAATERARRGATMGAQLSTLGHMVLPPVNFYSLLMKLFQRSTP AITLESPIKYLRLIDREIISHDTRFRFALPSPQHILGLPVG QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK FPAGGKMSQYLESQIGDTIEFRGPGSLVYQGGKFAIRPDKK SNPIIRTVKSVMIAAGGTITPMLQVIRAIMKDPDDHTVCHLLF ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPAWDYQGG\ FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPLN\DHVGH PTERCFFV |
| 6973 | 1 | 1964 | LQPRCAHRLRAQKGRFAPGVDMVLCVPVIGKLLHKRVVLASA SPRRQEILSNAGLRFVVPKFKKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVQKQDAY RMLSRFE/SGREHSVFTGVAIVHCSKDHQLDTRVSEFYEETKV KFSSELSEELLWEYVHSGEPMKAGGYGIQALGMLVESVHGDFL NVVGFPNLHFCKQLVKLYPPRPEDLRRSVKHDSPAADTFEDL |

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|------------|--|--|---|
| | | | SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEACHRTRETLP PFPTRLLELIEGFMLSKGLLTACKLVDFLLKDEAPQKAADIAS KVDASACGMERLLDICAAMGLLEKTEQGYSTETANVYASDGE YSLHGFIMHNNDLTWNLFYLEFAIREGTNQHHRALGKKAEDLF QDAYVQSPETRLRFMRAMHGMKTLTACQVATFNLRSFSSACDV GGCTGALARELAREYPRMQVTTFDLDPDIIELAAHFQPPGPAQAV IHFAAGDFFRDPLPSAELYVLICRILHDWDDKVHKLSSRVAESC KPGAGLLLVETLLDEEKRAQRALMQSLNMLVQTEGKERSLGEY QCLLELHGFHQVQVHVLGGVLDAIL\PKWPPEAQAACSL |
| 6974 | 3082 | 2172 | RSCAASFASFARPPLELFAPPGSHRSPPGRGVATSAQCALSVRK LLAARPGGLGTYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV SLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNNSVLPVTASAP TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH LTTTLEHSLGTPEAGVAATLSQSAEPPPTLISQAPASSPSSL STSPPEVFSASVTNHSSTVTSQTPTGAPTAPESPTESSSDHT PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPFPFG |
| 6975 | 2 | 500 | RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSRS SLPPAPQPPPYL*LSAVPFFIHLPLPLPPQAQKDVDAVDKVMK BLDENGDEGEVDFQBYVVLVAALTACNNFFWENS |
| 6976 | 1216 | 970 | GCQL*VAYGTTENSPTFAHPPEDTVEQKAESVGRIMPHTEAR NMMEAGTLAKLNTPGELCIRGYCVMGLGYWGEPOKTEEAVDQDKW YWTGDVATMNEQGCKIVGRSKDMIIRGGENIYPAELEDFPHTH PKVQEVQVGVKDDRMGEEICACIRLKDGBETTVEEIKAPCKGK ISHFKIPKIYVFTNYPLTISGKIQKFKLREQMERHNL*IKQQ ACPGRLA |
| 6977 | 1298 | 588 | SLFINTNLLSNQIRKTSFGMCSEPISDNTEQKGLKTPDFA* ANKKSKHHVNGNRTVEPPEGTQMAVFGMGCFWGAERKFWVLKG VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVYQPEHMSFE ELLKVFWEHNDPTQGMQRQNDHGTQYRSAYPTSQAKQMEALSS KENYQKVLSEHGFGPITTDIREGQTFYAEYHQYLSKNPNNGY CGLGGTGVSCPVGIKK |
| 6978 | 3 | 242 | SFPFRDSRRRCCKGSSLRHTAVAMVLSKEAKQRLQQLFKGSQ FAIRWGFIPLYIYLGFKRGADPGMPEPTVLSLLWG |
| 6979 | 3917 | 1146 | DEARVRGEAVAAAILSRCHWSGPPPPPPSPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALAEAEPPDERELDADDEPGRPGHINEEVETEGLSLEGT AQPPPPGLQPHAEPPGGYSGPDGHYAMDNITRQNFYDTQVIKQE NESGYERRPLEMEQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRGRSPQPPAEDEDDDF DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEDPHVVRIGWSLDS CSTQL GEEFFSYGYGGTGKSTNSRFENYGDKFAENDVIGCFADFECCGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKYNILGTNAIMDKMRVMGLRRQR NYAGRNDVLIQATQCLNRLIQAARKRNYILDQTNVYGSQAQ RKMRFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVDPHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEGRKAGP PPEKRFNDRGGGGFRGRGGGGGQRYENRGPFGNRRGGFQNRGG GSGGGGNYRGGFNRRGGGGYSQNRWGNMNRDNMNSNNRGSYNRA PQQQPPPPPPPPPPPPPPPPPPPSYS PARNPFGASTYNKNSNI PGSSANTSTPTVSSYSPQSGFFPSTFQPSYSQPPYNQGGYSQ GTTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPPTAQTYPQPSY NQYQYAAQWQNYQYQNGQWPPYGNIDYGSYSGNTQGGTSTQ GTRGRKTGRVAAPSTRRTTGNMQKLQTRSPAMSLSDPGLGYHPT |
| 6980 | 1 | 420 | |

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|------------|--|--|--|
| | | | CWTLRWFPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA GGSCACAGSCCKKCKCTSCCKSCCSCPLGCAKCAQGCICKGA SEKSCCA |
| 6981 | 10 | 1054 | PGRGFRRLRPAFAARGVFQGGGLGQAKQARTRACAALPTPHPS APRLLEPQGVFSLFPPPPGPWPMILTKAQYDEIAQCIVSVPT RQSLRLKQRFPSQSQTALLSIFSQYQKHKTHAKHHTSEAI ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQ EHEETPPSKSIINSMRLDPSQIPDGVLANQVYQCIVNDCCYGPL VDCIKHAIGHEHEVLLRDLLEKNLSFLDEDLRAKGYDKTPDF ILQVPVAVEGHIHWISEKASFGDECSHHAYLHDQFWSYWNRF PGLVIYWGFIQELDCNRERGILLKACFPPTNIVTLCHSIA |
| 6982 | 153 | 1285 | FFQQDCSAPAAPGLAGSEFRRRLRAYRRRRQRARGLKRVAWLAPP PSLLQGLQGWAPVDGTLGPDERSASSPMIQNSRPSLLQPDQV GDTVETLMLHPVIKAFLCGSIISGTCSTLLFQPLDLLKTRLTQLQ PSDHGSRVRGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI YFGTLYSLKQYFLRGHPPTALESVMLGVGSRVAGVCMSPITVI KTRYESGKYGESIYAALRSIYHSEHGRGLFSGLTATLLRDAPP SGIYLMFYNTKNIVPHDQVDATLIPITNFCGIFAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA LRRTLMAAMAWTVYEEMAKMGLKS |
| 6983 | 82 | 773 | EMSFLLQDPSFPTMGWSTGAGALGAALALLANTDVFLSKPKQK AALEYLEDIDLKLEKEPRTFKAKELWEKNAGVIMAVRRPGCFL CREEAADLSLKSMLDQLGVPLYAVVKEHIRTVEVKDFQPYFKGE IFLDEKKKFFYGPQRKMMFMGFIRLGVWYFFRAWNGGFSGNLE GBGFILGGVPVVGSGKGILLHEHREKEFGDKVNLLSVLEAAKMI KPQTLASEKK |
| 6984 | 1845 | 1282 | GGRSAYSLPAGSLFRVPATAAAKMASGVQVADEVCRIFYDMKVR KCSTPEEIKRRKKAVIFCLADKKCIIEEGKEILVGDVGVITIT DPFKHFVGMLEPKDCRYALYDASFETKESRKEIMFFLWAPELA PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNACIAEKL GSLIVAFEGCPV |
| 6985 | 1887 | 1324 | RRTAGIYPCFPKGRTRHALCSVLLLLTGQLAFDDFQESCAMM WQKYAGSRRSMPGARIILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFDIVDAKLL IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGGQIIPVFK LSGENGDEVKKE |
| 6986 | 642 | 1350 | YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQDFKMYIAF VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVDRDSSYSLESSL ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWKESDEPPRPVQAKFEFHGDYEQQLFHLVLSRKDKTGIV VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTWH AVGTIEDHLRPYME |
| 6987 | 1623 | 341 | LEAAEKASRAPKESQRQTDKSNYETENWSPQKSQRRYDMYNTAC FLGEIEVGLYTIQILQLTPFFHKENELSKGHMVQFLSGKWTIPP DPRNECYLALSFKTSHLKNLQSDLKRCDFDFIDYMLVKMRYTQ KEIABIMLSKKVSRCFRKYTELFCCLDPCLLQSKESQLLQBEHC RKKLEALRADRFAGLLEVLNPNYKDATTMESIVNEYAFLQONS KKPMTNEKQNSILANIIISCLKPNSKLIQPLTLKKQLREVLFQ VGLSHQYPGPYFLACLLFWPENQELDQDSKLEKYVSSLNRSFR GOYKRMCRSKQASTFLYLGKRKGLNSIVHKAKIEQYFDKQNTN SLWHSBGDVNKKNEVKDLRLRLTGQAEGLISVEYGTTEEKIKIPV ISVYSGPLRSGRNIERVSFYLGFSEIEGPPGL |
| 6988 | 3 | 689 | TQLLRPAVFGSAASGIRSLWSASSGHWCAAGRAHAPVPR LVRLGLAATAAPQDAQTPQPMPRADCMRHLPHYFCRGQVVRG FGRGSKQLGIPTANFPEQVVDNLPADISTGIYGWASVSGSDVH KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL |

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|------------|--|--|---|
| | | | RPEKNFDSLESLSIAIQGDIBEAKKRLPEHLKIKEDNFFQVS KSKIMNGH |
| 6989 | 2 | 1118 | LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFSGSKSNMATL KDQLIYNLLKEEQTPQNKITVVGVGAVGMACISILMKDLADEL ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNTVANSKLV IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV SNPVDILTIVAWKISGFPPKNRVIGSGCNLDSARFRLMGERLGV HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK EQWKEVHKQVVESAYEVIKLGYSWAIGLSVADLAESIMKNLR RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE EARLKKSAADTLWGIQKELQF |
| 6990 | 719 | 258 | THASGMASVVLALRTRTAVTSLSPPTALAVRYASKKSGGSS KNLGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAPKEGTFKLVLAM |
| 6991 | 169 | 451 | RRSSDFHNPGLSRPVSLRENTHHQVICSTKNRRNPKKIAYLL SLLMTNLNPNSTENQPVDAWAFDLDQEFITYACVEGTGCLF CGRHVH |
| 6992 | 944 | 510 | RQAPGCSSLALRQVRQVYCGLVRAQVQTRPLSSRFVVERRGALY RSPMNQENPPYPGPGPTAPYPPYPQPMGPGMGPPYPPQGY PYQGYPYQGWQGGPQEPKPTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLDWMLT |
| 6993 | 1 | 374 | QWCVTCPQHNRQGPVAPPGIQAYGAAPPEDLQVDFTEMSKCRG DRVWIKNWNVASLCPWLKGPQTVVLSPPATAVKVEGIPAWIHSH VKPAARETWEARSPDNPFRTVLKKTSPAPVTPGS |
| 6994 | 346 | 1100 | QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR RDFAPPQQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSGIAAQLNALGLAGDYLAQGLKLS PGQVQTFLLWGAGALVVYWLSSLLGLVLALLGRILWGLKLVIF LAGFVALMRVDPSTRALLLLALLILYALLSRLTGSRASGAQL EAKVRGLERQVEELRWRQRRRAAGARSVEEE |
| 6995 | 144 | 1346 | GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIRKAYLEDFTYRMHECYQIWAQL EHEAGTQLHRQTGLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWRMVPGSYGVSAFFCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPLDKPEPAVIESCMYTNTPDEQFILDHRPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTSPSYDLAPFRISRFPSLG KAH |
| 6996 | 543 | 1942 | ETANAEEAAARKSAMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYSEWKGRKNTNEFYKTIIPRFYRLPAENEVLQLKL R EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEAMIN YENFLKVBKAGAKCKQFFTAQVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESOLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAFSAALRVYGGYLNLDKDHNGMLK EELSRYGATMTNVFLDRVFQECITYGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLVNVSFNYFFRAIQELMKITHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDVTVTILIDL NGFWTYENREALVANDSENSADLDDT |
| 6997 | 370 | 1104 | AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFYFLVRF TVIYNEQMAKKRELFSNLQEFAGPSGKLSLLEVCGTGANFKF YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH |

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|------------|--|--|--|
| | | | QVADGSVDVVVCTLVLCVSKQERILREVCRVLRPGGAFYFMEH VAAECSTWNYFWQVLDPAHLLFDGCNLTRESWKALERASF LKLOHIQAPLSWELVRPHIYGAVK |
| 6998 | 2 | 616 | FVSRALLRVRSRRHPABERAAAPGRFEDAPIECPGATNCPEPLWC SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTAKVPPAADGK APLTKPSKKEAPAEKQPPAAPTAPAKKTSADKADPALLNNHNSN LKPAPTVPSSPDATPEPKPGDGAEEDEAASGGPGGRGPWSCN FNPLLAVAGVAVAAIALILGVAFLVRKK |
| 6999 | 14 | 1591 | GRAGACSRRTDAMSIEISSDVIRLIMQYLKENS LHRALATLQE ETTVSLNTVDSIESFVADINS GHWDTVLQAIQSLKLPDKTLIDL YEQVVLIELRELGAARSLLRQDPMIMLKQTQPERYIHLENL LARSYFDPREAYPDGSSKEKRAAIAQALAGEVSVVPFSLMAL LQQALKWQKHQGLLPPGMTIDLFRGKAAYKDVEEEKFTQLSRH IKFGQKSHVECARFSPDQYLVTVGSVDGFIEVWNFTGKIRKDL KYQAQDNFMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKISG QCLRRFERAHSKGVTCLSFSKDSQILSASFQDQIRIHGLKSGK TLKEFRGHSSFVNEATPTQDGHYIISASSDGTVKIWNMKTTECS NTFFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVMNQ GQIVRSFSSGKREGGDFVCCALSPRGEWIVCVGEDFVLYCFSTV TGKLERLTVEKDVIGIAHHPQNLATYSSEGLLKLWK |
| 7000 | 2 | 827 | GPGVVFLLEMESEGPPESESEFFSQREBENEEEAQEPETGP KNPLLQPALTGDEGLQKIFEDPENPHHEQAMQLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTRGYTLHCAAAGRL ETLKALVELDVIDEALNFREERARDVAARYSQTECVFELDWADA RLTLKKYIAKVS LAVTDTEKSGSKLLKEDKNTILSACRAKNEW ETHTEASINELFEQRQQLIEDIVTPIFTKMTTPCQVKSASVTSH DQKRSQDDTSN |
| 7001 | 2056 | 844 | RRCLIIAFLKGCFFIYFIFIFETEFLLSCCPGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDKSEAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDVAVVSVKHDPLPLPEANGHRSTNSPTI VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPSRIGRLFDGTEPIVLDLSLQ HYFIDRDGMFRYILNFLRTSKLLIPDDFKDYTLLEYEAKYFQL QPMLEMERWKQDRETGRFSRPECCLVVRVAPDLGERITLSGDK SLIEEVFPFEGDVMCNSVAGWNHDS THVIRFPLNGYCHLNSVQ VLERLQQRGFIEVSGCGGVDSQFSEYVLRRLRRTPRVPSVI RIKQEPLD |
| 7002 | 1043 | 498 | PMPSSSTRWITS*TYTDTSSAWACRPTTGCT*TAAPGPTVRWWP TPCSRHQSRRLTCWCSTSRPCGR*GGLCVRTAPTPTTSASSS SWTSAGTSWPAGRRGTATSGTATTSVWPGCGTRMWSTQWSSV PRSRCCSRPATTPPSKPGAPHAPCASSRHLAHLAPSSPGLPA RGAEVC |
| 7003 | 818 | 61 | QGRFRAFQWQDFLQPPGMRLSALLALASKVTLFPHYRYGMSPP GSVADKRNPPWIRRRPVVVEPISDEDWYLFCDTVEILBGKDA GKQGVVQVIRQRNVVVGGLNTHYRYIGKTM DYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG |
| 7004 | 121 | 2285 | FLLPVLTSRSLRQPAVPHARLGGVEPAAAMKSARAKTPRKPTVKK G\PKRTLTKQLG/YICRVRLPGFPDQECCEI VINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTSKGKTHMTGSPGEGGLLPRCLDMI FNSIGSF QAKRYVFKSNDNRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKAEVEDEDSVYGVFVSYIEIYNNYIDLL EEVPPDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEBAFE VFWRGQKKRIANTHLNRESSRSHSVFNKLVQAPLDADGDNVL |

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|------------|--|--|---|
| | | | QEKEQITISQLSLVDLAGSERTNRTAEGNRLREAGNINQSLMT LRTCMDVLRNQMYGTNKMVPYRDSKLTFLFKNYFDGEGKVRMI VCVNPKAEDYEENLQVMRFAEVTQEEVEVARPVDKAIICGLTPGRR YRNQPRGP\IGNEPLVTDVVLQSFPLPSCEILDINDEQTLPLRL IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDAVLSKENHMQ GKLNEKEKMSGQKLEIERLEKKNKTLEYKIEILEKTTIYEED KRNLOQEELETQNKQLQRFSDKRRLEARLQGMVTETTMKWEKEC ERRVAAKQLEMONKLVKDEKQLKAIIVTEPKTEKPERPSRER DREKVTQRSVSPSPVPVSYL |
| 7005 | 63 | 876 | RNMALVQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ ISSTLADTAAQAQVNGEPYDLERPLETSDLRFLTFDSPEGKAV FWHSSTHVLGAAAEQFLGAVLCRGPSTBYGFYHDFLKGKERTIR GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL IEEKVTGPTATVYGCGLVDLQCGPHLRHTGQIGGLKLLSNSSS LWRSSG |
| 7006 | 22 | 898 | NAFGRHSTAVKMAAAWLQVLPVILLLLGAHPSPLSPFSAGPAT VAAADRSKWHPIPSGKNYFSFGKILFRNTTIFLKFDPGEPCDLS LNTITWYLSADCYNEIYNFKAEEVELYLEKLEKRGKLSGKYQTS SKLPQNCSELFKTQTFSGDFMHRPLPLGKQEKENGNTNLTFIG DKTAMHEPLQWQDAPYIFIVHIGISSKESKENSLSNLFMT VEVKGPEYELTLEDYPLMIFMVMCIIVYVLFVGLWLWASACYWR DLLRIQFWIGAVIFLGMLEKAVFYAGFQ |
| 7007 | 2 | 1001 | AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA YTQALGLDATPDQAVLHNRNRAACHLKLEDYDKAETEASKAIEK DGGDVKALYRRSQALEKLRDLQAVLDLQRCVSLPEPKNVFQEA LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTETKQKAS QNLVVLAREDAAGABKIFRSNGVQLLQRLDMGETDLMLAALRTL VGICSEHQSRVATLSILGTRRVVSILGVESQAVSLAACHLLQ MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ PGQFFGDQTCSCRLFGIRFGDIILL |
| 7008 | 70 | 1478 | CRSALGHERPPPAHLFAGGRRLQTCPRSCRWLGRPPSGLPFGPR SPPLLAGPGQKMVQKPAELQGFHRSFKGQNPFEALFSLDQDPDH GDSDFGLQCSARPDMPASQPIDIPDAKRGKKKRGRATDSFSG RFEDVYQLQEDVLGEGAHARVQTCINLITSQYAVKIEKQPGH IRSRVPREVEMLYQCGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEASIVDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMFLFESIQEGKYEPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLPPPHCRIHVRPGLVTRTVTVNE |
| 7009 | 1 | 626 | ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLSMPPPKFHDTSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMSKLPDLVL GRVWDLSDIDKDGHLVRDEFAMHLVYRALE |
| 7010 | 79 | 571 | SHTRRVVPETLLSPLCPLLGOGTAMSGGEQKPERYYVGVVDVGT GSVRAALVDQSGVLLAFADQFIKNWEPQFNHHEQSSEDIWAACC VVTKKVVGIDLNQIRGLGFATCSLVVLDDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETHKSVLQYVGG |
| 7011 | 3 | 994 | RIQTLPNQNSQTOPLKTPFAVLQPIAQTTFGVQTPQPOSL LQAQISAASITPLLQTPQPLQPPQKAGLLQPPVRIVSQFPQ ARRLDPPSRFSGRNDRGDQVFNKDDRSRERERERRRSRERSPO RKRSRERSRPRRERSRPRRVRVFRYTVQFSKFSLCDPCSCDMH ELRRRYQNLVIPSDFDAQFTWVDAFPLSRPFQLGNYCNFYVMH |

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|------------|--|--|---|
| | | | REVESLEKNMAILDPPDADHLYSAKVMLMASPSPMEDLYHKSCAL AEDPQBLRDGFQHPARLVKFLVGMKGKDEAMAIGHWSPSLDGP DPEKDPVSLIKT\AIRCKALTG |
| 7012 | 1 | 2661 | RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA AAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVGP VGERTPRKKEPPRASPPGGLAEPGSGAGPQAGPTVVP TGIAETPEG\RRTSRRKRAKVEYREMDSELANLSEDEY NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGA DRMTSQEAAACFPDIISGPQQTQKVFLFIRNRTLQ TPEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLIN PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARD ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKI LYEANGQAVPKEKDEMVEQEFNRLLEATS VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQ NLKEKIKELHQYKEASEVKPPRDTAEFLVKS YDELAETQGLKEELQLEANPPSDVYLSSRDRQILD FANATPLSTLSLKHWDQDDDFBTGSHLTVRNGYSC LDIKLNTAVRQVRYTASGCEVIAVNRSTSTQTFIY PLGVLKQPPAVQFVPPLEWKTSAVQRMGFGNLNK FWDPSVNLFGHVGSTTASRGELFLFNLKAPILLAL RGSYSYVAAGSSGNDYDLMAQPIITPGPSIPGAPQ HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLP AQQSPSM |
| 7013 | 1 | 2661 | RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA AAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVGP VGERTPRKKEPPRASPPGGLAEPGSGAGPQAGPTVVP TGIAETPEG\RRTSRRKRAKVEYREMDSELANLSEDEY NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGA DRMTSQEAAACFPDIISGPQQTQKVFLFIRNRTLQ TPEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLIN PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARD ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKI LYEANGQAVPKEKDEMVEQEFNRLLEATS VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQ NLKEKIKELHQYKEASEVKPPRDTAEFLVKS YDELAETQGLKEELQLEANPPSDVYLSSRDRQILD FANATPLSTLSLKHWDQDDDFBTGSHLTVRNGYSC LDIKLNTAVRQVRYTASGCEVIAVNRSTSTQTFIY PLGVLKQPPAVQFVPPLEWKTSAVQRMGFGNLNK FWDPSVNLFGHVGSTTASRGELFLFNLKAPILLAL RGSYSYVAAGSSGNDYDLMAQPIITPGPSIPGAPQ HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLP AQQSPSM |
| 7014 | 3 | 3950 | DFEVGDKIRILATLEDGWLEGLKGRGTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLNTLGVEEQRHETS CIISEAPTSPLGHLTSEYDTRNSYQDDETAGGPPRSPGV PLATDSPTSDPTEVVNGISSQPQVFPFHPNLQKSQY HSEQYPDLLPLEARTRDYASLPKRMYSQKLTQKPVLP SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSIS PQAQGLVMEAAATHSQDGSTDLDSKLTQQLIEFEKSL DKILRHFSIMDFNSEKDIVRGSSSKLITEQELPERRK PCTFVSTSPHLLVDQNLKPAPPLVVRPSRPAPLP SPKLLSRHPTCETLEKEGPGHMGSRSLDQTSPLV RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCE SNIESLN |

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|------------|--|--|---|
| | | | MELQQLRBMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE ELLQTERDYIRDLEMCIERIMVPMQQAQVFNIDFEGFLFGNMQMV IKVSKQLLALEISDAVGPFVLGHRDELBGTYYKIYCNHDEAIA LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP VQRVMRYPLLMELLNSTPESHDPKVPLTNAVLAKEINVNINE YKRRKDLVLKYRKGDEDSLMKISKLNHISIIKKNRVSSHLKH LTGFAPQIKDEVFEETKFNFRMQLERLIKSFIRDLISLYLQHIRE ACVKVVAVSMWDVCMERGHRLDQFERVHRYISDQLFTNFKER TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAELK DKKTEELQSARNNYEALNAQLLDELDPKFHQYAQGLFTNCVHG AEAHCDFVHQAELQKPLLSLLKVAGREGNLIAIFHEEHSRLVQ QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE ELRASLLARYYPEKLFQAERNFNAQDLVSLLEGLDVGVIKKK DPMGSONRWLIDNGVTGKGFVYSSFLKPYNPRRSHSDASVGS TESEHGSSSPRFPQNSGSTLTFTNPN\S\MAVSFTSGSCQKQ DASPPPKWDQGTLSASLNPSNSESPPSRCPSPDPSTSQPRSGD SADVARDVKQPTATPRSYRNFHPEIVGYSVPGRNGSQDVLVK CARTAQAPEDRSTPDGSEAEGNQYFAVYTFKARNPNELSVSA NQKLKILEFKDVTGNTTEWLLAEVNGKKGYVPSNYIRKTEYT |
| 7015 | 1842 | 513 | RQAWHE\VAAPSWRGARLVQSVLRVWQVGFHVARERVIFFSSLL GFQRRCSVCVAGSAFSGPRLASASRNGQGSALDHFLGFSQDPS SVTPCVPVAVSMNRDEQDVLVHHPDMPENSRVLRVVLGAPNAG KSTLSNQLLGRKVFPVSRKVHTTRCQALGVI TEKETQVILLDTP GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTNR QLSPQLLRCLTKYSQIFSVLVNMKVDCLKQKSVLLELTAALTEG VVNGKKLMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH FKEIFMLSALSQEDVTKLQVLLTQAQPGFWEYHSAVLTSTQTP ETCANIREKLEHLPEBVPYVQVQKTAVWEBGPGGELVIOQKL LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV KLLK |
| 7016 | 167 | 2513 | ILNAPKPPPPRDSVEAVAARKTGGGSGWTGMDVSGQETDWRST AFROKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS LVARLIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM PPRPGQSLGGMGSLGAMGQPMSSGQPPPGTSGMAPHSMVAVS TATPQTQLQLQVAAAAAATARSSSSSSSRRYSSSSSSSNSKQ FQAQSSAMQQ\QFQA\VVQQQQQL\QQQQQQQHLIKLHHQNNQ QIQQQQQQLQRIAQQLQQQQQQQQQQQQQQQALQAQPPFIQPP PMQPPQPPPSQALPQQLQMMHTQHHPPPQPPQPPVAQNQPSQ LPPQSQTQPLVSAQALPGOMLYTQPLKFRVAPMVVQPPVQPP QVQQQQTAVQTAQAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP QSMPPPPQPPSPQPGQSSQPNNSVSSGPAPSPSSFLPSPSPQPF \QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSFAGSSQAEEQQY LDKQLKLSKYIEPLRRMINKIDKNEDRKKDLKMKSLLDILTDP SKRCPLKTLQKCEIALEKLNDAVPTPPPPVPPPTKQQYLCQP LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPLSVLQGEVARLDPKFLVNLDPHSCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTRLLQLPDKHSVTALLNTWAQSVHQAACLSAA |
| 7017 | 1 | 1785 | INLGNTCYMNSVI*ALFMAFDFFRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPWFPTPRSQDCSEYLRFLDDR LHEEEKILKVQASHKPSLEECSETSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGLMQASVPGPSEEPVYVNPITAAF ICDSLNEKTIIGSPNEFYCSENTSVPNESNKILVNKDVDPQKPG GETTPSVTDLNLYFLAPEILTDGNQYYCENCASLQNAEKTMTQIT EEPEYLILTLLRFSYDQKYHVRKILDNVSLPLVLELPVKRITS |

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|------------|--|--|--|
| | | | FSSLSSEWSVDVDFDLSLENLAKKLKPSGTDEASCTKLVPYLLS SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK ITSRFKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPLQKE LMDAITKDNKLYLQEQELNARARALQAASASCSPRPNFGDDNDP PGSCGPTGGGGGGGENTVGRLVF |
| 7018 | 464 | 1066 | SLVFRGNTWSGEAGHHCALFNLAAYHQLFVGTERIRAPEIIFQ PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVLTGGNTMYP GMKARMEKELLEMRPFRSSFQVQLASNPVLDWYCARDWALNHL DDNEVWITRKEYEKGGEYLKEHCASNIYVPIRLFKQASRSSDA QASSKGSAAAGGGGAGEQA |
| 7019 | 1048 | 335 | APGGFLVTMVFPAPSPPPWMLGCCSHEVTAGPPTLCKDMSALVAA RMRHIPLAGSDWRDLPNIEVRLSDGTMARKLRYTHHDKNGRS SSGALRGVCSCEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA GLYGRLEWDGFFSTTVTNPEPMGKQGRVLEHPEQHRVSVRECAR SQGFDPDYRLFGNILDKHRQVGNVPPPLAKAIGLEIKLCMLAK AREASAKIKEEEAAKD |
| 7020 | 1 | 2154 | FADSKRKSVDLKDKNLQVALTSKQQLSLETAMSFVARNTFFKVR NGFLMRKVAVFFSNTPTRASQRLREAVLKLSDAGITPLFLTRQE DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAEITTLFQF NEMKXYLAYLVRQDMSDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIETI ENVFESAPNPRDLKIVVLMLEGEVPEQQLEEAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR FGRLLPSFVSSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ VNVPNVTSSPTSNEPVTITTKPVTITTKPVTITTKPVTITTKPVTI INQPSVKPAAAKPAPAKPVAAPKPVATKTATVRPPVAVKPATAAK PVAAPKPAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPAATKP MYKMSREVQVFEITENSACLHWERPEPPGPYFYDLTVTSAHQDS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT |
| 7021 | 2 | 338 | VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLYSHDNIICG ITSVAFSKSGRLLLAGYDDFN CNVWDTLKGDRAGVLGHNDNRVS CLGVTDDGMAVATGSWDSFLRIWN |
| 7022 | 2 | 856 | VYIGSFWSHPLLIIPDNRLFEAEQDLFRDIQSLPRNAALRKLN DLIKRARLAKVHAYIISSLLKEMPSVFGKDNKKKELVNLAETIY GRIEREHQISPGDFPNLKRMDQLQAQDFSKPQLKSKLLEVVD DMLAHDIAQLMVLVRQEESSORPIQMVKGGAFFGLHGFPGHGYG EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKGMLDDDEFALANHLIKVKLEGH ELPNELPAHLPPSKRKVAE |
| 7023 | 2 | 748 | AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLMLKLTCEVRVANELNARRRSF TAADSKDEEVKAPRRSFLDFDPHFWQWSSFSYVQCVLAFTG VAGYITLSDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLNMTSGDAFKTAYFLKGAFLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHTGTGKAL |
| 7024 | 1207 | 190 | RTGVTGVVAQVWMFGGGVLSSGEQLQMPVKPERGLGPSDGNLV SSRRGSPGTVLGLPFWLLTPVLVSRISIRSMILLTRSPTAWHRLS QLKPPVLPGLTGGQALHLRSWLLSRQQAETGGQGGQPGPGLRT RLILITGLFGAGLGGAWLALRAEKERLQQQKRTALRQAAGVQGD FHLLDHRGRARCKADFRGQVWLMYFGFTHCPDICPDELEKLVQV VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHERLLGL |

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|------------|--|--|--|
| | | | TGSTKQVAQASHSYRVYVYNAGPKDEDQDYIVDHSIATYLLNPDG LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS |
| 7025 | 232 | 832 | ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF KQVIRTCEKRPTFNQHTVFNLHQRNLNTGDKLNEFKELGKAFISG SDHTQHQLIHTSEKFCGDKCEGNTFLPDSEVIQYQTVHTVKKTY ECKECGKSFSLSRLSLTGHKRIHTGEKPFCKDCGKAFRHSQLS VHKRIHTGEKSYECKECGKAFSCG |
| 7026 | 328 | 1146 | NPNPISIGDIKDIIKKAASMLDPAHKSHFHPVTPSLVFLCFIFDG LHQALLSVGVSKRSNTVVGNEENERGTPYASRFKMPNFIALEK SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTNVPKLSNSGKLLG QDEQPHIFG |
| 7027 | 43 | 954 | GRRLOQQRPEDAEDGAEGGGKRGEGAGWEGGYPEIVKENKLFEB YYQELKIVPEGEWQFMDALREPLPATLRITGYKSHAKEILHCL KNKYFKELEDLEMDGQKVEVPQPLSWYPEBLAWHTNLSRKILRK SPHLEKFHQFLVSETESGNISRQEAIVSMIPPLLNVRPHHKILD MCAAPGSKTTQLIEMHADMNVPFPEGFVIANDVDNKRCLLVH QAKRLSSPCIMVVDHASSIPRLQIDVDGRKEILFYDRILCDVP CSGDGTMKRNI DVKKWTTLSNLQLHGLQLRIATRGAEQL |
| 7028 | 189 | 608 | SRPPEPEPGTMEKGSDDSSSEKGGVPGTPTSTQSLGSRNFIRNS KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR EILLQGRLYLSENWICFYSNIPRWETTISIQLKEVTCLKKEKTA KLIPNAIQ |
| 7029 | 1343 | 40 | VLESNTEAKQATGTSSKL RHGTGQEKGREGPRCPSGLAQLRLWG /PCPHAGRETGPASAPIPGS*GHGWHW*RKDGGERSEGPSAL SPHSPSLNNMQAPTHVPGMGSSQRPSSVVEQVGVGSQLSRE RWRA*RLPGAAASERTEMTKERSP/RPCQGYDSSNWFQPGKK TRKNSRRNTMVSRRGGCLLYPLQSIMPE*QLR*GAHASPTTG R*KGGGPRSPLTAKSGTTHIPTFFGSI P/RPTRDSGPGT DNS\ AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW VPGPAEGEQGEGAGLEGRP*PLKGCRLSTLTSPQLSIPMVGKPK PEGTTASFFP\RSCHSE*RKPPSPCPHAPALSLPHPLPLPLPL PLPLPGAGT*HSARSGRPGQSETGSLCHNCHCPCPKCSPGG T |
| 7030 | 2 | 521 | FVCFSPAGSGQGGKRRVNMELSAVGERVFAAEALLKRIRKGRM EYLVKWKGSQKYSTWEPEENILDAALLAAFEEREREMELYGPK KRGPKPKTFLKQAQAKAKAKTYEFRSDSARGIRIPYGRSPQDL ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG*G PGLHFPGGGPKKHGFVPASEQHQQHQLPRRGPSGPGPRPG |
| 7031 | 960 | 59 | HCSVPGAWEPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG /CKPS/RHCDLHEGFSRTAALPCGKPOPKHGVEECG/PCPCLA PRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL SAAAPRPSLGSQNASGLPAASLPPQDSSQPHKTVSPARSVPP LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPTST SGSTASHSRRC*SPR*TPAPPRRDHGRSAAFEVLTAASAQPC ASQGGPRPTGAGRTSPPLGLPFSRGPPAASARPFCHPSL |
| 7032 | 1393 | 2104 | RRPGRTEPVEPPVPPPPPRASNSKSRCR*RNHLAPL*QSFLRK SRQIGTSSLPFGRSAGERPRPAATFCLSRGSSPVFL*PSSSSL EPWMKQFGRLLHSLFWKSWQKMNSFLLTPKLDTSLSMGWRYRQR LPRLHTFLKKSILQMASELAPPLTPAPLASSLPPPPGPPPLPV PLA*LSRSGILVPPNSGFSLSCL\PLGDH*GSSGEVRGSCGSPPP HHCWVLPPPP*LLLPPR |
| 7033 | 689 | 815 | RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA |

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|------------|--|--|---|
| | | | LMPSSCPWRTGALGPSAGSRALGRCTSSVGPGRWLRTSSP GCATRTWRTMRMEPRPLRSRMGESAPGIPAEPLSAAPSGPSAPS AAAPSAPTTPAAAGPNTL*SRRTAENCWPPSCSCCWGWC*SWSA WDWRRPPLQVSPAPSSSCCRASCWCLESIT*SSSTARSATGAS SSSTCPTSRSRGAATP\SPMGAPLLPCSVPLISREALQDPR NPSP*GVCSGSSGHAGLALGKPPVACSVF |
| 7034 | 92 | 1942 | EDTSSMPFRLLIPLGLLCALLPQHGGAPGPDGSAAPDPAHYRERV KAMFYHAYDSYLENAPFDELRLPTCDGHDWTGFSFLTIDALD TLL\TLFFYQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMMPVFQSL EAYWPGLQSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNMFSE FLAETVKYL YLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFP KNTVSSGWPWEPARPPTLFS PENHDAQERERKPAKQKVLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K |
| 7035 | 92 | 1942 | EDTSSMPFRLLIPLGLLCALLPQHGGAPGPDGSAAPDPAHYRERV KAMFYHAYDSYLENAPFDELRLPTCDGHDWTGFSFLTIDALD TLL\TLFFYQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMMPVFQSL EAYWPGLQSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNMFSE FLAETVKYL YLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFP KNTVSSGWPWEPARPPTLFS PENHDAQERERKPAKQKVLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K |
| 7036 | 442 | 761 | CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSP LPRDPHPTTLRPLPP PPPPPPPPRRPPRRNRPG |
| 7037 | 442 | 761 | CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSP LPRDPHPTTLRPLPP PPPPPPPPRRPPRRNRPG |
| 7038 | 155 | 891 | GAGAASDMSSGLRAADFPRWKRHISEQLRRLDRLQRAAFEEIIL QYNKLEKSDLHSVLAQKLAQEKHDVFNREHISPGHDGTWNDNQ LQEMAQLRIKHQELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTIISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTSRGT |
| 7039 | 155 | 891 | GAGAASDMSSGLRAADFPRWKRHISEQLRRLDRLQRAAFEEIIL QYNKLEKSDLHSVLAQKLAQEKHDVFNREHISPGHDGTWNDNQ LQEMAQLRIKHQELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTIISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTSRGT |
| 7040 | 34 | 789 | KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKRSN |

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|------------|--|--|---|
| | | | PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG EPFEIKVYEIDDVERLQRRRGASKEAMCFNAKLKILEHRQQR AEVRKAYEWLMKELEATKQYLM LDPNKLWSEFDLEQVWELDSLE YLEALECVTERLESRVNFCKAHLMMITCFDIT |
| 7041 | 1 | 567 | SGRVAMGRRRAPAGGSLGRALMRHQTRSRSRHRHTDSWLHTSEL NDGYDWGRNLNLSVTEQSSLDLFLATAELAGTEFVAEKLNIKFV PAEARTGLLSFESQRIKKLHEENKQFLCIPRRPNWNQNTTPE LKQAEKDNFLEWRRQL\VRLEEQKLILTPERNLDFWRLWRV IERSDIVVQIVDA |
| 7042 | 7 | 345 | PIHMAAALRAD\ISPLFPHTQGYLLLSASHG\ATSLHTKGAL PLETVTMYTVIPKSKYVLVKPDTQYPYSENLEDFKRLAENSASN DDLMAEVAISDYGDKLTLELREKY |
| 7043 | 2 | 2170 | ARGMAARDSDSEEDLVSYGTGLEPLEBGERPKKPIPLQDQTVRD EKGRYKRFHGFAGSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD KSVLGPEDFMDDEEDLSEFGIAPKAIVTDDFASKTKDRIREKAR QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMKGWKEGGVGP RVKRRPRRQKPDPGVKIYGCALPPGSSEGESEGEDDDYLPDNTVF APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG SERAGDLGEIGLNKGRKLGISGQAFGVGALEEDDDIYATETLS KYDTVLKDEEPDGLYGTAPRQYKNQKSEKDLRYVGKILDGF SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENHLLQV LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF LSQDKKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQSPAA AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCIDPSMTEWERGRBRDEFARAALLYASSHSTLSSRF THAKEEDSDSQVEPRDQENDVGDQKQSAVKMKMFGKLTDRDTEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPK QQSSPLVNKEEHAPELSAN |
| 7044 | 276 | 734 | EVYLTDEFAGRKRVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV |
| 7045 | 3 | 513 | LGFKMEALSRAQEMSLAALKQHDPIYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHHRHFGDAEQSQG |
| 7046 | 3 | 513 | LGFKMEALSRAQEMSLAALKQHDPIYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHHRHFGDAEQSQG |
| 7047 | 103 | 486 | QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGPHSYER |
| 7048 | 92 | 627 | FFCLTLLSSWDYRHHATRRVSSPVFTMEDSGKTFSEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEALETQLQQIETRN RDLLSENNRLRMELETIKKFEVQHSSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW |
| 7049 | 393 | 938 | KRTGSASVGGPPPLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMDFDGNRKYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSDNCRFIGGI PKMKKREIEIEIAKVT EGVLDVIVYASADKMKNRGLRLRGVREPPRGCHWLGRKLIAX ASSLWG |
| 7050 | 393 | 938 | KRTGSASVGGPPPLGGPATXASVAGRCSSVGKIPARRCYEDEL |

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|------------|--|--|---|
| | | | VPVFEAVGRIYELRLMMDFDGKNRGYAFVVMYCHKHEAKRAVREL NNYEIRPGRLLVGCCSVNCRLEFIGGIPKMKREILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAX ASSLWG |
| 7051 | 119 | 816 | KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMMQIQRHCS VRDPAIKGKQVVRQELLEEEYEQVKIVGTLESFKIDKPPDFPV SCQDEFFRDPAVWPPPPVPAEHRAPPQIRR/RQSRSKTSEERNR SRSPGTCRPS\PISKSEKPSRDKDYRARGRDDKGRKNMQDG ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDADIADLEEA KLLREAGVLPMMW |
| 7052 | 467 | 715 | SCPGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVPKDKVLDVSGGTGILSMFAARQGPRR |
| 7053 | 467 | 715 | SCPGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVPKDKVLDVSGGTGILSMFAARQGPRR |
| 7054 | 1 | 1036 | GTSQRSRETDARRRSAGABPTARLPWPAALEEWPSCPCEPLPGP RRCRWDAMEYDEKLARFRQAHLPFNKQSGPRQHEQGGPGEVDP VTPEALPELPPGEPEFRCPERVMDLGLSEDFSRPVGLFLASD VQQLRQAIBECKQVILELPEQSEKQKDAVRLIHLRLKLQELKD PNEDEPNIRVLLSHRFYKEKSKSVKQTCDCNTI IWGLIQWTWT CTGCYYRCHSKCLNLISKPCVSSKVSQAEYELNICPETGLDSQ DYRCACRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDAV IPARVVHNWDFEPRKVSRCMSRYLALMVSRPVLRLREIN |
| 7055 | 2 | 527 | DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLCNLILLPMCRITLLAYLRG SQKVPSSRRTRRLLDKSRTHITCGATICIFSGVHVAHLVNALN FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL M |
| 7056 | 2 | 527 | DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLCNLILLPMCRITLLAYLRG SQKVPSSRRTRRLLDKSRTHITCGATICIFSGVHVAHLVNALN FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL M |
| 7057 | 1368 | 431 | GIYLVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA SGEVPSQASLRGFFTEDEPGCFGEENLPALQNIQDEGTGQQL SPQERISEKQLGOHLPPNPHSGEMSTMWLEEKRETSQKQPPAPM AQKLPTCRECGKTFYRNSQLIFHQRTHGTETYPQCTICKAFILR SSDFVKHQRTHTGKPKCKCDYCGKGFSDPSGLRHHEKIHTGEKP YKCPICEKSFQRSNFRHQRVHTGEKPKYKCSHCCKSFWSSSL DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR GYPC |
| 7058 | 1 | 469 | FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR PEYDLVCIGLTGSGKTSLLSKLCESPDNVSTTGFSIKAVPFQ NAILNVKELGGADNIRKYWSRYQGSQGVIFVLDSASSEDDLEA ARN*SCTQLLQHPQLCTLPFLILA |
| 7059 | 1 | 1178 | WPAFFRQPAAMADALLGTGPRRARGCLGAAGPTSSGRAARTPA APWARPSAWLECVVTFDLELGQALELVYPNDFRLTDKEKSSI CYLSFPDSHSGCLGDTQFSFRMRQCGGQSPWHADDRHYNSRAP VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAAPAGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAAPS PDVSSSEMLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVNTNPFK TLQHNPHILRVGEFKMSGDLPKQVKLKKPFKV*RPWDTKP |
| 7060 | 90 | 1670 | SVNLPPLSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKLVNPSQ YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEMRAS |

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|------------|--|--|---|
| | | | LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN QQFLDLRVAVLGNVDSGKSTLLGVLTQGELENDGRGRARLNLFRH LHEIQSGRTSSISFEILGFNSKGEVHGNGTQWGGQTLRMGW*** RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG VKIKRQGHGPNGLGPGNSEGVGRAGRRH*GPWALQVNVYSDSR TAEIICBSSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLIV SANTGIAGTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR QLERVLPKPGCHKVPMVLTSEDDAVTAAQQAQSPNVTPIFTLS SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV PEVGTVVGGTLSR*IDLLATLPTQPSPIYKSTSWPKGGDGP |
| 7061 | 364 | 710 | ARMPSFLGPPCLFVMDPETTLEEPETARLRFPGFCYQEVAGPRE ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPPEIQAWV RGQRPGSPPEAAALVEGLQHD*ARMPSPLGPPCLFVMDPETTL EEPETARLRFPGFCYQEVAGPREALARLRELCCQWLQPEAHSKE QMLEMLVLEQFLGTLPPPEIQAWVGRGQRPGSPPEAAALVEGLQHD PGQLLG |
| 7062 | 71 | 744 | AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDDKKLERL YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRRA TQCEFSRKEFLDGMTELGCDSEKALKALLPRLEQELKDTAKPKD FYQFTTFPAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL MEHH |
| 7063 | 2 | 562 | LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR LTBYIHCLQPATGRWRMLLIVSVCTATGAWNWLIDPETQKVSF FTSLWNHFFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA EYNMSCDDTGKLLKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS HKGFLRLRLDM |
| 7064 | 300 | 884 | RDTGSDPSSTRRLCTCCTGH*PAEPIASPHPSRGTCPPASSAS SRRTGCWTCPPESGHAQARRSRASASRWGARGAVRSABAARGC SSRAGRWLETGRRRRGPPACAAAAGRLRGAP*AAPPTASVVPAR CRCPAARTGAPAAATWLRRLSGLRAPALGRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS |
| 7065 | 1 | 555 | ATTTHSARRSCRGAAAEAAASAAGGRQKGFDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAAFASMAHSPVAVQVPGMQNNIADPEEL FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI QQEITVLSQCDSSSYVTKYGSYLKSKLWIMEYLGGSALDLL RAGPFDEFQ |
| 7066 | 356 | 676 | PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLEFNAMNRFIGAVNMDQTMVPSLLRDVPLADPGLDND VGVEVGSGGCGLEERTPP |
| 7067 | 152 | 973 | KENITMATEIGSPRRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKMRKAVNRKTIIDYNPSVIKYLENRIWQRDQDRMRAIQ PDAGYYNDLVPPIGMLNPNMAVTTKFVRTSTNKVKCPVFVVRW TPEGRLVTGASSGEFTLWNGLTNFETILQAHDSPVRAMTWSH NDMWMMLTADHGGYVYKQSNMNNVVMFQAHKEAIREARFIHNIP FSVVPIMVVKLFKSCILGAEMHGLCQFLGNLHPINTIFFFVFT HSPFCWAPP |
| 7068 | 222 | 816 | DTMKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDD DDDDDDDDDDNSLFTPREPRSHFFPDLEFMCFFGCGQCSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNKLTKIHPKAFITTKLRLRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQDTPKKK |
| 7069 | 1147 | 1765 | FRDHRRYFYVNEQSGESQWFFPDGEEEEESQAQENRDETAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW TLQSNVPLQPLPLEMPPPPPPPPPPPPPPPPPPPPAPKMPPP |

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|------------|--|--|--|
| | | | EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSEED RVSTAQKRIEHWKQQLVSGMAERNANFEA |
| 7070 | 1 | 547 | DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV LEDEKHHGAQSAALQKVKQGERVRKTSLDLRREIIDVGGIQNLI ELRKKRKQKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK MKVIEKFLADGGSDTCDQFRRTALHRASLEGHMEILEKLLDNG ATVDFQ |
| 7071 | 2 | 921 | ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTIQIFFEVPQYPTGYPPPPPTVPAGVAPCVPRFVRSNNV PESSLPASMPYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPV PSGLYAPVYDSRRIRWPPMYQRDDIIRSNLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWQYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS |
| 7072 | 2 | 921 | ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTIQIFFEVPQYPTGYPPPPPTVPAGVAPCVPRFVRSNNV PESSLPASMPYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPV PSGLYAPVYDSRRIRWPPMYQRDDIIRSNLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWQYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS |
| 7073 | 50 | 504 | LAHGSFGVSDFFAPAAAPAHHTLTSFSGSLSPQFRKPLGRAPAMP LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI VTLGKDEFHLHLDVDTAGQDEYSILPYSFIIGVHGYVLVSVTSL HSFQVIESLYQKLHEGHGK |
| 7074 | 263 | 1003 | VCPVLCSSTRQEPGHSSSLVTYFGKPTRRKEFLGHGICIAAGKMNIS VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM CALLNSGGGVKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSKV MNATAALEFLKDMKKTGRRLYLRLPELLAKRPRVDIQEENNMKAL AGVFFDRTELDREKELTFTESTHVEI |
| 7075 | 598 | 1005 | NYINFFFRKEYPPHVQKVEINPVLRSRLQGVIRIMKKTSEESQ VEPEIKRKVQKQKHCSTYQPTPLSPASKKCLTHLEDLQRNCRQ ATTLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVKVP IDII |
| 7076 | 279 | 1049 | LQSESSNAEAGNEQRHEDEQRSKRGWSKGRKRKKPLRDSNAPK SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKQKSH RQDAARQATHDHEKETEVKERSVFDIPIFTEEFNLHNSKAREAE LQLRKSNMFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQOHLTLRQVLTSSFASMFPEXGETPTVDTIDSYM |
| 7077 | 3 | 1119 | SSMGSNSEINGLALRKTDKYGLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNWDKLSRRFQKVKLCRCRKGIPSSLRKAWQYLSN SKELLEQNPRKFEELEAPGDPKWLVDVIEKDLHRQFPFHEMFAR RGGHGQQLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLBATQLDGEIIFALLRRASPLAHR HLRRQRIDPVLYMTWFMCI FARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMBQLRNLFPQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQPPPLGPSSS |
| 7078 | 483 | 767 | FQQRMMAGEQKPSNNLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQBLAEGANAAYLQLLNLFAFGTYPDYIANKE SLPELY |
| 7079 | 2 | 376 | SVVEFFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ MQARKKRRGII EKRRDRINSSLSLRLVPTAFKQGSSEKLEK |

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|------------|--|--|---|
| | | | AEVLQMTVDHLKMLHATGGTGTALLFQASFIQIIF |
| 7080 | 200 | 595 | VQLPLEAPCLSLSCRDHSGGNRDLRRHRDCRVYGSPODGIPY LTHPLCHQDVVSVGRLQIRALATPGHTQGHVLYLLDGEFPYKGPS CLFSGDLLFLSGCGEFPKRKREELGEBGETEVRAATVPWRALKP |
| 7081 | 213 | 506 | AVTEEEMILNSLSLCYHNKILILAPMVRVGTLPMLLLALDYGADI VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVRVFCEREQN RVVFQMGTS |
| 7082 | 3 | 1137 | APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDGTGCL SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSSEDPMSLS QAQSATEVEERHVSFSCSTSRBRPFQAGELILAETGEGETKFKK LFRLLNNFCLLNSNWGAVPFGKIVGKFPQGIILRSSFGKQYMLRRP ALEDYVVLKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG GMSLFSLKAVGSGQGRVISEFVRKDHDLAKNKYKHWRDSWKLSH VEEWPDNVDFIHKDISGATEDISKSLTFDAVALDMLNPHVTLVPV YPHLKHGGVCPVYVNNITQVIELLD |
| 7083 | 115 | 541 | RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP SPKAPRARPCRVSTADRSVRKIMAYSLEDLLKVRDTLMADK PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKQWPPSEQG TRHPLSLSHK |
| 7084 | 3 | 522 | NSVSVSSQSRFLASVPGTVQVRSAAADMAASTAGKQRI PKVAK VKNKAPAEVQITAEQLLREAKELELELPPPPQOKITDEEELND YKLRRKRTFEDNIRKNRTVISNWKYQWBSLKEIQARRSIYE RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL |
| 7085 | 243 | 1499 | RQLARLRRRRGWSRPFPGAPMAHITINQYLQVYEAIDSRDGASC AELVSFKHPHVANPRLQMASPEEKCCQVLEBPYDEMFAHLRCT YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL DLRVFANNADQQLVKKGKSKVGMLEKAAELLMSCFRVCASDTR AGIEDSKKGMFLVLNQLFKIYFKINKLHLCKPLIRAIIDSSNLK DDYSTAQRVTYKYVGRKAMFDSDFKQAEYLSFAFEHCHRSSQ KNKRMILYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG NLLLLHEALAKHEAFFIRCIFLILEKLKIITYRNLFFKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYYI SHQHQLVVSQKNPFPPLSTGC |
| 7086 | 256 | 525 | ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFRLDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRFTDANGDGTIDFR EF |
| 7087 | 166 | 723 | LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMVSVRTMEDSCBLDLVY VTERIIAVSPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSIKAMDITWLNHP HRCRVLHNKG |
| 7088 | 104 | 759 | GTSASPSSLLEMAEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLVSLLVFLGFMSPMTTTFVIEAMAAANAQLHW KRMENTLKEEEDDDSTASDSVLRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGNLIFYFCIIVYLYGDLAIYA AAVPFSLMQVTCATGNDSCGVEADTKYNDTDRCWGPLRRVD |
| 7089 | 33 | 1775 | SVCWEDRYLKARMEESPLSRAPSRGGVNFNLVARTYIPNTKVEC HYTLPPGTMPASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGVQVCGQSPFPQFRE PRPMDELVTLEADGSDIILLVVPKATVLQNLDESQOERNLDM QKLQLEQVTELRSRVQELERALARQEHTELMEQYKGISRS HGEITEERDILSRQGDHVARILELEDDIQTISEKVLTKVEELD RLRDTVKALTRQEKLGLQKEVQADKEQSEAELOVAQOENHHL NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLQQAQQRVALEP |

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|------------|--|--|--|
| | | | LKEQLRGAQELAASSQQKATLLGEEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKKEKQWSKERAGLLQSVAEKDKILK LSAEILRLKAVQEERTQNVFKTELAREKDSLVQLSESKREL TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDESESPEDMRLHPMAFVSVETQ ASLLLGLE |
| 7090 | 33 | 1775 | SVCWEDRYLKARMEESPLSRAPSRGGVNFVARTYIPNTKVEC HYTLPPGTMPASDWDIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFOASYLKPQAQLYQFRVYVNRQGVCGQSPFPQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNLDESQQERNLDM QLKLQLEGQVTELSRVQELERALARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKVELLD RLRDTVKALTREQEKLGLQKQVADKEQSEAEQVAQQUENHHL NLDLKEAKSWQEEQSAQAQLKDKVAQMKDTLGGQAQQRVALELP LKEQLRGAQELAASSQQKATLLGEEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKKEKQWSKERAGLLQSVAEKDKILK LSAEILRLKAVQEERTQNVFKTELAREKDSLVQLSESKREL TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDESESPEDMRLHPMAFVSVETQ ASLLLGLE |
| 7091 | 186 | 1076 | EGMLTREHRCGRSEEQELEPWSPKKARSGRWLNRNGFKRKMEEP EEPADSGQSLVPVYIYSPYVSMCDLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDHDPD STYGLGYDCPATBGIIDYAAAIGGATITAAQCLIDGMCKVAIN WSGGWHHAKKDEASGFCYLNDVGLILRLRRKFERILYVDLDLH HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY YSVNVPIQDGIQDEKYYQICERYEPPAPNPL |
| 7092 | 522 | 809 | KQGINEDQEESSQKPRLEGCEPISKRMKKLIKQKQWEEQRELR KQKRKEKRKKLERQCMENSDGHRKRVRDRVHSTLRLLII DCSFDXLM |
| 7093 | 454 | 655 | NFGVSGVELAQASMVMSFVIAACQLVLGLLMTSLTESSIONS ECPQLCVCEIRPWFTPQSTYREA |
| 7094 | 2 | 508 | FVRSMHVGVGFASSRPPCVDLWNQSIISFFGWAGSEEPFSFYG DIIAPPLQDYGGIMAGLSDPWWKTLTYLTGGALLAAAYLLHE LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFLCKMETYLRM ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGETEII |
| 7095 | 1 | 411 | IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR SLECVSHEVDSHYCPSCLNMPASABAKLKKNRNCANCFDCPGCMH TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMD KSVGE |
| 7096 | 224 | 2067 | ETRS LAVQEKPSQAGRRSSRISFAGALFLTRFLQELLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDSIEKLFCTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEQSSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQQGF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAGHFA GAI FQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRLVHLKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPQKQSGSEGEDGFQVELELVELTVGTLDLCESEVLPRRR RKRNKKEKSRDQEGAHRTLLQQTQEEEPSTQSSQAVAAPLGL LDEAKAPGQPELWNALLAACRAGDVGVLLKLQ LAPSPADPRVLSL LSAPLGGSGFTLLHAAAAGRGSVVRLLEAGADPTVQCQDH |
| 7097 | 256 | 1228 | IRTKSAATWEAWPQCGREGSRIITEPCANAGSRQELQTRISS FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA |

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|------------|--|--|---|
| | | | SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSPGSHDTMTYC LNKKSPISEESRLQLLNKALPCITRPVVLKWSVTQALDVTEQ LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTALVEDTLTEISE WLERHPREVILACRNFEGLSEDLHEYLVACTKNIFGDMLCPRG EVPTLRQLWSRGGQVIVSYEDESSLRRHHBLWPGVPYWGNNRVK TEALIRYLETMKSCGR |
| 7098 | 82 | 956 | SSFLKRCRKVLGCWGPSEQLSTLEPRDKEIDNYCVMRLQT EARGGFAPNRPVNICRMTAVDGRGSSRETCHFHPSLEA LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG LGSSVIYFLWNLNLLWPRVLAVALFSAFSPSYVALHFLGLWLVL LLWVWLQGTDFMPDPSEWLYRVTVATILYFSWFNVAEGRTGR AIIHFAFLSDSILLVATWVTHSSWLPSPGIPLQLWLPVGGCGCF LGLALRLVYHHLHPSCCWKPDQVD |
| 7099 | 992 | 210 | LFRLAPGFLRLSLARQGYHQIWAFFFLPSGATATWPAASRSRLA ARSLPRSPARPGPNDAALGEHDFRGQGVRAQRFSEBPGGAD GAVLEVHPVQIGAGVSLPGILAACGAEVILSDSSELPHCLEVC RQSCQMNNLPHLQVGLTWGHISWDLALPQDIILASDVFFEP EDFEDILATIIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWD KCVHIPLESDADKEDIAESTLPGRHTVEMLVISPAKDSL |
| 7100 | 205 | 671 | ANGGFWEAAPGSEVSLPLVPTASHSKTTALGIGSAPPHLSVL FLFSPFPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV DWAFLTKTNMQTMYEQSEWGWKDKREEMTDDRAWYLIAWEN SSVPVAFSHFRFDVERGDEVLYW |
| 7101 | 2 | 503 | WRGGPRRAKRLAGGAVGVLLVRGVHVSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEITIPADVTP ERVPTTHVDYSEAEQSDQLHQEISQANVICIVAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVESR |
| 7102 | 2 | 503 | WRGGPRRAKRLAGGAVGVLLVRGVHVSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEITIPADVTP ERVPTTHVDYSEAEQSDQLHQEISQANVICIVAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVESR |
| 7103 | 119 | 438 | GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES LSDKGSELKKSFDVAVFDVLKVTPEYAGQITLMDVPVFKAIQF DELSSCGWNKKEYSSAP |
| 7104 | 1670 | 795 | RLWEHRSVSAGASGWLSSPGCLLLHPSLPEEERVDILINAGV MRCPHWTTEDGFEMQFGVNLGEAWAGAAPVQAILPRRPPKVL GF*V*VKSDLFIILNPGHFLLTNLLLDKLGASAPSRILNLSSLA HVAGHIDFDDLWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIGSTFLQHHN\WAHLLAAS KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAD EEVARRLWAESARLVGLEAPSVREQLPR |
| 7105 | 765 | 143 | GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST SQIPVQMHFLFDVHNPDPYVSSGGGFGPADDHGYGVSYIFMGDG MITFHISKKSTKTDSHRLGQHIEDALLDVASLFQAGQHPKRR FRGSGKENSRRHRCGFLSRQTGASKASMTSTDF |
| 7106 | 14 | 1064 | GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHRMFGT YFRVGFSGSFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCQF GAEFVEVIKDS TPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTHAF PYIKTRISVIQKEEFVLTPIEVAIEDMKKTKLQLAVAINQEPED AKMLQMVLCQSGVATVNGQPLEVAQVPLAEIPADPKLYRHENKL RLCFKEFIMRCGEAVEKNKRLITADQREYQQLKKNYNKLBKBL RPMIERKIPELYKPIFRVESQKRDSEFRSSFRKCETQLSQGS |
| 7107 | 1145 | 591 | *I*WLQTGKKK |

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|------------|--|--|--|
| 7108 | 1 | 942 | VKVALLLTNLEQPRTESEWENSFTLKMPLQFVNLSSTFYIAF FLGRFTGHPGAYLRLINRWLEECPSGCLIDLQMGIIMVLK QTNWFMELGYPLIQNWTRRKVRQEHGPERKISFPQWEKYNL QPMNAYGLPDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI RLDAYKFTVQWRRPLASRAKDGIWYGILEGIGILSVITNAFVI AITSDFIPRLVYAYKYGPCAGQGEAGQCMVGYVNASLSVFRIS DFENRSEPESDGSEFSGTPLKYCRYRDYRDPHSLVPYGYTLQF WHVLAW |
| 7109 | 964 | 102 | WDQRKNSLVPGPAPAGPAQEEPEWKKESLGAQAELSILQPKP TQFPFKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQV SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQESFRQM VVIHKEIPTGKKDHECSECGKTFIYNHSLVHVHQRVHSGEKPYKC SDCGKTFKQSSNLGQHQRHTGKPFECNECGKAFRWGAHLVQH QRIHSGEKPYECNECGKAFSSQSYLSQHRRHISGKPFICKECG KAYGCSELIRHRRVHARKEPSH |
| 7110 | 96 | 697 | RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLFRASITPVLG SPSTKRRGQMLQPIIEGETAHFFEEIKEEEDGVNLSSELGDM KTAVQVQSSLNKSESDVEENQEKALDLRLSSRAASMPLELQ LWKARAEKKLRKTLREFEEAFYQNGRQAQKEDRVPVLEEYRE YKKIKAKLRLEVLISKQDSSKSI |
| 7111 | 2 | 414 | GSGLYRGPTPGGQCIWKPNMPPDHERNFGFTQFALELNELTAE LKRSLPSTDTRLRPDQRYLEBGNIAAEAQKRRIEQLQRDRRKV MEENNIVHQAFFRRQTDSSGKEWVTNNTYWRRAEPGYGNMD GAVLW |
| 7112 | 103 | 495 | PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW FKNDQDIQLSEHFSVKVQAKYVSMTIKGVTSSESGKYSINIKN KYGGEKIDVTVSVYKHGEKIPDMAPPQQAQPKLIPASASAAGQ |
| 7113 | 1 | 824 | KCLRQAWHEAPSSLAFTRWCSREERAEGGNLHRSITRDPKPPG LRFSQRPMDKKKRSKPKCLAQPAQAPGLRRVPVPTSHSGSL ALGLPHLPSPKQRAKFRVGEKCRPVLAGGGSGSAGTPLQHSF I.TEVTDVYEMEGGLNLNDFHSGRLQAQFKECSFEQLEHVREM QEKLARLHFSLDVCGEEEDDEEEDGVTEGLPBEQKKTMDARNL DQLLSNLGSCGALVPGMGRGEGTYSQSHSWALGEKVGVHGSK SSGPLNLPRR |
| 7114 | 3 | 1492 | VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDSESGQCKICRKI IYLNDFVSVKQRLPKYYSWERCCKHHLNLFQGNRSYVRKKDDG CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS QTGEKLYKCTECGVFIQKANLVVHQRTHTGKPYECCECAKAF SQKSTLIAHQRTHTGKPYECSECGKTFIQKSTLIKHQRTHTG KPFVCDKCPKAPKSSYHLIRHEKTHIRQAPYKGIKCTTSSLIYQ RIHTSEKPCSEHGKASDEKPSPTKHWRTHTKENIYECCKGKS FRGKSHLSVHQRIHTGKPYECICGKTFSGKSHLSVHHRTHTG EKPYECRRCGKAFGEKSTLIVHQRMTGKPYKNECGKAFSEK SPLIKHQRIHTGERPYECTDCKAFSRKSTLIKHQRIHTGKPY KCSECGKAFSVKSTLIVHHRTHTGKPYECRCGKAFSGKSTLI KHORSHTGDKNL |
| 7115 | 1 | 947 | NAAHGYNWGLWCMIYIPPDWLDRGDESAPIRTPAMIGCSFVVD REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA HIERTKPYNNIDYAKRNALRAAEVWMDDFKSHVYMAWNIIPM SNPGVDFGDVSRERLALRQLKCRSFKWYLENVYPENRYNNTLT YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSDGL LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD FTQSGPIVSRATGRCLLEVMSKDANFGLRLVVQRCSGQKWMIRN WIKHARH |
| 7116 | 866 | 95 | RVRMRNNAEVIEEKLMSKSWAKFRPGEPWKGYPNIDPETDPYVT PGSVINNLISINTVREVDHLDRNRSGLSSSLNTTLPTSAWSSIR |

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|------------|--|--|---|
| | | | ASNNVPLSSTAQSTARSNSDKLTWSPGSVTNTSLAHELWKVP LPPKNITAPSRPPGLTGQKPLSTWDNSPLRIGGGWNSDARY TPGSSWGESSGRITNWLVLKNTLPQIDGSTLRITLCMQHGPLIT PHNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL |
| 7117 | 695 | 1261 | LLISTPGGCHPPPSSTIEFTYTGAWGKALPAPHMPCAPGALPQGA FVSQAARAIPLLQPSQAQAEGLSQPARACGALCSLPWPLRNWG SPIRLRPGGLRTPNTDRKTRRSAMACWARAQWDTLGPLKLSHR GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPDDL RVKHRCQPTGHLPL |
| 7118 | 49 | 1863 | PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLQPQVE ESVNLGKFKHSIVRLVAFPCPFASSQVALENANAVSEGVVHEDLR LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD NMI IQSISLDDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISADLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRI SRYLANKCSIASRIDCF SEVPTSVFGEKLRQVEERLSFYETGEI PRKNLDVMKEAMVQAE EAAAEITRKLEKQEKRLKKEKRLAALALASSENSSTPEECE EMSEKPKKKKKQKQEVVPQENGMEPPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSI PKRKKSTPKEETVNDPBEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFKHAKSQED |
| 7119 | 49 | 1863 | PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLQPQVE ESVNLGKFKHSIVRLVAFPCPFASSQVALENANAVSEGVVHEDLR LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD NMI IQSISLDDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISADLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRI SRYLANKCSIASRIDCF SEVPTSVFGEKLRQVEERLSFYETGEI PRKNLDVMKEAMVQAE EAAAEITRKLEKQEKRLKKEKRLAALALASSENSSTPEECE EMSEKPKKKKKQKQEVVPQENGMEPPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSI PKRKKSTPKEETVNDPBEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFKHAKSQED |
| 7120 | 1991 | 64 | QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPADLYKFAEEMKFSKKLSAISLGQGGQP RAEAMMRSSIERGKVVFFQNCPLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPPVILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLSLCLPHGNALERRKFGPLGPNIPY EFTDGLDRICISQLKMFLEDDIIPYKVLKYTAGIYNGGRVTD DWDRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHG LSYIKSLPLNDMPFIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREIIVEDVTQNILKVPPEINLQWVMKYPVLYEES MNTVLVQEVIRYNRLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWMDLLQRLDFLQAWIQDG IPAVFWISGFFPPQAFLTGLQNFARKFVISIDTISFDFKVMFE APSELTQRPPQVGCYIHGLFLEGARWDFEAPQLAESQPKELYTEM AVIWLPTPNRKAQDQDFYLCPIYKTLTRAGTSLTGHSTNYVI AVEIPTHQPRHWIKRGVALICALDY |
| 7121 | 2 | 546 | RPLRPWVLSLGSVMGLMTYGRROFQSLDTTMRRLIPPFREASAK LTTLVDADEAFTAYLEAMRLPQNTPEEKDRRTAALQEGRLRAV SVPLTAEVSLWPAQLQELARCGNLACRDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKQIHRVSSLLQEAQTQAALVLDCL |

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|------------|--|--|--|
| 7122 | 2 | 546 | ETRQE RPLRPWVLSLGSVMGLMTYGRRFQSLDITMRRLLIPPPREASAK LTTLVDADEAFATYLEAMRLPKNTPEEKDRRTAALQEGRLRAV SVPLTLAETVASLWLPALQELARCGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKQIHRVSSLLQEAKTQAAALVLDCL ETRQE |
| 7123 | 1 | 1092 | KPAVPEARSAGTSEAGRSGAEVSCGVSVDGAAMRLTPRALCS AAQAAWRENFPICGRDVARWFPGHMAKGLKKMQSSSLKLVDCIIE VHDARIPLSGRNPLFQETLGLKPHLLVLNKMMDLADLTEQQKIMQ HLEGEGLKNVIFTNCVKDENVKQIIPMVTTELIGRSHRYHRKENL EYCIIMVIGVNPVNGKSSLINSLRRQHLRGKATRVGGEGPITRAV MSKIQVSRPLMFLDTPGVLPAPRIESVETGLKLALCGTVLDHL VGEETMADYLLYTLNKHQRFQYVQHYGLGSACDNVERVLKSVAV KLGTQKVKVLGTGNVNVIQPNYPAAARDPLQTFRRGLLGSVM LDLDVLRGHPRV |
| 7124 | 2 | 382 | LPTLLLLAAPPFAHLLLPFGHDQSPCWHPGPALSPGTGLPGLSWAM ANSGLQLLGGYPLALGGWVGIIASTALPQWKQSSYAGDASIQLRS KVFLSEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS |
| 7125 | 166 | 1127 | NCISEKRNYSFSMQKGRGRTSRIRRRKLCGSSSESRGVNESHKSE FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS LPESCLLT\RDVTIRSYLGAYITKWKPPSPPLALCTFLVSEKH AGHRSLLLEA\YLEILPKAYTCPVCLPEPVNLLPKSLKAKAEQ RAHVQEFFASSRDFSSSLQPLFAEAVDSIFSYSALLWAWCTVNT RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSHPHVQVKAANE ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVENPH ACVYVSRGWNQLCS |
| 7126 | 1 | 733 | CRDMAAFIVPSFARRCSQKSLGHLPTQFWLWAAAMSPRGQERGT SHSQAREPQRPGRWNLGSLQSSPGTLGQAGTASRRRGCMVQRWV QVATGRRRAVQVPKGLGLALGETSPGASRGMSGGAGGCWALGWA PSPVLPWLLGPPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC WRGGRIASAEASST*TPGSGSRARSRRSPGSRRRSASAPSPPT PTDACA*SCVARPAGSRSSRPAAA |
| 7127 | 1311 | 277 | GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF AKQKQI*S*NSQKIGASEIDRGRKEADCSAPAAARIGAVSVFR RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV *FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L CQSSLRDQITIVTWRM*RNYSMFRINMISSL*DGSIHPLKLHFI PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRLFL LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV |
| 7128 | 2 | 5228 | GRVDLWTLILGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE DYRGTRDSVKTVLQDERQSQUALILKIADYIYYEERTCILRCVLHL LTYFQDERHPYRVEYADCVDKLEKELVSKYRQCFEELYKTEAPT WETHGNLMTERQVSRWFVQCLREQSMLEIIFLYYAYFEMAPSD LLVLTLMFKEQGFGRQTNRHLVDETMDFVDRIGYFSALILVE GMDIESLHKCALDDREHLHQFAQDGLICQMDCLMLTFGDIPH APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLQ SLASGGNDCTTSTACMCVYGLLSFVLTSLELHGLGNQQDIIDTA CEVLADPSLPFLFWGTPTSGLGIILDSVCGMFPHLLSPLQLL RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR RQTPKLLYPLGGQTNLRIPQGTVGQVMDDRAYLVRWEYSYSSW TLFTCEIEMLLHVSTADVQHCRVKEPIIDLHVKVISTDLSIA DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA KVWTDLRHTGFLPFVAHPVSSLSQMSISAEGMNAGGYGNLLMNSE QPOGEYGVTTIAFLRLITTLVKGLGSTQSQGLVPCVMFVLKEML |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--|--|--|
| | | | PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS LQFLCICSLAYTEAGQTVINIMIGVDTIDMVMAAQPRSDGAE GQGGQQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLAQALSQHG GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP GLIELFLNLEVKG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ QDRYWCPLLHRAAIAFLHALWQDRRDSAMLVLRTPKPFWENLT SPLFGTSPSPSETSEPSILETCALIMKIIICLEIYYVVKGSLDQP LKDTLKKFSIEKRFAYWSGYVKS LAVHVAETEGSSCTSLLEYQM LVSARWMLLIATTHADIMHLTDSVVRRLQFLDVLDTGKALLLV PASVNCRLRSGMKCTLLILLRQWKRELGSVDEILGPLTEILEG VLQADQQLMEKTKAKVFSAFITVLQMKEMKVS DIPQYSQVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRERDQ RDGVCVLGLHLAKELCEVDEDDGDSWLQVTRRLPILPTLLTLE SLRMKQNLHFTTEATLHLLTLARTQQGATAVAGAGITQSI CLPLLSVYQLSTNGTAQTPSASRSLDAPSWPGVYRLSMLSMEQLK TIRYNFLPEALDFGVHQTERTLQCLNAVTVQSLACLEADHTVG FILQLSNFMKEWHFHLPLQMRDIQVNLGYLCQACTSFLHSRKM LQHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA EYNFLFALSFTPTFDSEVAPSGFTLLATVNVALNMLGELDKKK EPLTQAVGLSTQAEGRTRLKSLMFTMENC FYLLISQAMRYLRD PAVHPRDKQRMKQELSELSTLLSSLSRYFRGAPSSPATGVLP SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR |
| 7129 | 1 | 1054 | FRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIK EPRWDQSTFIGRANHFTVTDPNILLTNEQLESARKIVHDYRQ GIVPPGLTENELWRAKYIYDSAFHPDTGEXMILIGRMSAQVPMNMT ITGCMMTFYRTTFAVLFWQWINSFNAVNNYTNRSGDAPLTVNEL GTAYVSATTGAVATAGLNALTKHVSPLIGRFVFPFAA VAANCINIPLMRQRELKVGIPVTDENGRLGESANA AKQAITQVVVSRI LMAAPGMAIPPFIMNTLEKKAFLK RFPWMSAPIQVGLVGFCLVFA TPLCCALFPQKSSMS VTSLEAELQAKIQESHPELRVYFNKGL |
| 7130 | 2 | 780 | HEVPSLQTS DPLPGSVQRCVSVVVSQPNKENWCQDHL YNSLGRKGISAKSPYHRSQSSSVL INKSMDSINYP SDVGKQQLLSLHRSS RCESHQDLLPD IADSHQ QTEKLSDLTLQDSQKV VVNNRNLPLN AQIATQ NYFSNFKETDGEDDYVEIKSEEDSELELSHNR RRKSDSKFVDADFS DNVCSGNTLHSLNSPRTP KKPVNSKLGLSPYLTP YNDSDKLNDYLWRG PSPNQNI VQSLREKFQCLSSSSFA |
| 7131 | 805 | 573 | AAAEHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQ FNHLEVVKLLQDYQDSYTLSETQAEAAAEALS KENLESMV |
| 7132 | 1420 | 1087 | IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGN AHALSTVTA I IDGTGSGVGAALGPLLAGLLSP SGWSNVFYMLMFADACALLFLI RLHKELSCPG SATGDQVPFKEQ |
| 7133 | 2 | 3648 | QQIPGLLPAHGESGDALRKPRLOKPI TGHLDLFF TLYPSLEKFEEELLEHVQDHFQEGCGPLDGGAL EILERRLRVGVHNGLGFVQ RPQVVVLVPEMD VALTRSASF SRKVVSSTSSGSQALVLRSLRL PEMVGHFAFAVIFQLEYVFS SPAGVDGNAASV TSLNLACMH MVRWAVWNPLLEADSGRVTLPLQ GGIQPNPSHCLVYKVPASMS SEEVKQVESG TLRFQFSLGSEHLDAPTEPVSGPKVERRPSR KPTSPSSPPAPVPRVLAAPQNSPVGPGLSIS QLAASPRSPTOHCL ARPTSQLP HGSQASPAQ AEFPLEAGISHLEADLSQTSLVLETS IAEQ LQELPFTPLHAPIVVGTTQTRSSAGQPSRASM VLLQSSGFPEILDANKQPAEAVSATEPVTFNPQ KEESDCLQSNEMVLQFLAFS RVAQDCRGTSW PKTVYFTFQFYRFPATT PRLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVG PGFGLKPGERRCFA RYLAVQTLQIDVWDGDS LLIGSAAVQMKHLLRQGRPAVQASHE |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--|--|---|
| | | | LEVVA TEYEQDNMVVSGDMLGFGVRVPIGVHVS VKGR LHLTLAN VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLTTGSSRR KHVVQAQKLADVDSELAAMLLTHARQGGKGPQDVSRSDATRRRK LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH TVTVEIDNPESLIVDSQEWDRPKGAAGLHTPVEEDMFHLRGSL APQLYLRPHETAHVPPKFQSFAGQLAMVQASPLSNEKGMADV SPWKSSAVPTKHAKVLFASGGKPIAVLCLTVELQPHVVDQVFR FYHPELSFLKKAIRLPPWHTFPGAPVGMGLGDPVHVRCSDPNV ICETQNVGPGEPDIFLKVASGPSPEIKDFVVIYSDRWLATPT QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH PQELKTDPKGVFVLPPRGVQDLHVGVRLRAGSRFVHLNLVDVD CHQLVASWLVLCCCRQLISKAFEMLAAGEGKGVNKRITYTNP YPSRRTFHLHSDHPELLRFREDSFQVGGGETYITGLQFAPSQRV GEEELIYINDHEDKNBEAFCVKVIYQ |
| 7134 | 2115 | 1111 | GGGFSYPPHVGSLGLTGLDPHYVLELVHVDNPTYEEGLIDNSG LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPFQSEGHTL ECLEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKMKL LAYDDDFDNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYPRINLTRCASIPDIMEQLQFIVKKEI YRFTTWPFIKSPKQYKNLSFMDAMNFKWTKKEGLSFNKLVL SLPNNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLSCTLSKSL |
| 7135 | 2 | 2072 | FVPRVTPRSLSLQGPKEGSEVGSITQPLPSSYLIFRAAESDGR WLDLELALRCSLLRLGTCKPGRDGEPTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDADFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQBELGELGEASQVETVSE ENKSLMWTLKQLRPGMDLSRVVLPFTFVLEPRSFNLKLSDYHY ADLSRAAVEEDAYSRMKLVLRWYLSGFYKPKGIKKFPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPFVSNRKGDFCIS GSITAKSRFYGNLSALLDGGKATLTLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLPFFGGSTSIQI SGKITSGEVVLASLSGHWRDVFIEEGSGSSALFWTPSGEVRR QRLQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWPKQLFHLDPITQEWYRYEDHSWPDP LKDIAQFEQDGLRTLQQAARQTTFGLSGPGRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPESLDEEQDGFVPGGESPC PRCKEARRLQALHEAILLSIREAQQLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK |
| 7136 | 2 | 418 | DFVPSFRPSPGNTSQTWLLRAATLEKEVAGLREKTHHLDMLK SQQRKVRQMIQELQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKMPV IRVVET |
| 7137 | 2 | 466 | WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVADTWQA GSFKVATQERNPQRAQMLRRQKGVVFPFGDFTLTELQRLDSAI PDDLGNNTNKRSEKVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP |
| 7138 | 2 | 466 | WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVADTWQA GSFKVATQERNPQRAQMLRRQKGVVFPFGDFTLTELQRLDSAI PDDLGNNTNKRSEKVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP |
| 7139 | 1 | 357 | SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRLGLGWVQFSSEGLRNALQ QENHIIDGVKVQVHTRRPKLPTSDDEKDF |
| 7140 | 1401 | 1957 | RASSLQVLKAWGLIPSSPQQQHTGQYALEELFDLKVYDCFCFSF NMNVSLKQLRPSQPWPRGKCRKTPGWBEARPKAQDLRGDLGKT |

| SEQ ID NO: | Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence | Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence | Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--|--|---|
| | | | QAGPAEAHTRGPPRLPAATGCPHPLGLLSGISVDIDPTGLQSQ WTFKGGDPPLMFSEYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMNTNCGG |
| 7141 | 124 | 1073 | LDSRSCWLDMELEEDVRFIVDETLDGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQSGPGYIWK EALQHEBEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSLSTRKGLRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP |
| 7142 | 658 | 839 | LIFLMLHMEKMLSSVTLHIRAFLYWICLKPTSCLIFQNVNLL KK*SRVGVVVVMCRT/YSSDLQVGVIKPWLLLGSDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSIISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA |
| 7143 | 3 | 773 | SLMSSDGEPLSRMDESDSISSTIMDV DSTISSGRSTPAMNNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDADHRSIHVDGQRGG VFVCLWKGCKVYNTPTSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGRLARHVPHTFSQQNSKVSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI |
| 7144 | 1 | 988 | FRVNMQDGGPSPAHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSIVIRDEVEKYNRNGVNALQLDPAALNRLFTAGRD SIIRIWSVNVQHKQDPYIASMEHHTDWNVDIVLCCNGKTLISASS DTTVKVVNAHKGFCMSTLRTHKDYVKALAYAKDELVASAGLDR QIFLWDVNTLTALTASNNTVTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRCAKLMKLGHTDNVKALLNDRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDFAFTHVYSGG RDRKIYCTDLRNPDIRVLICE |

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

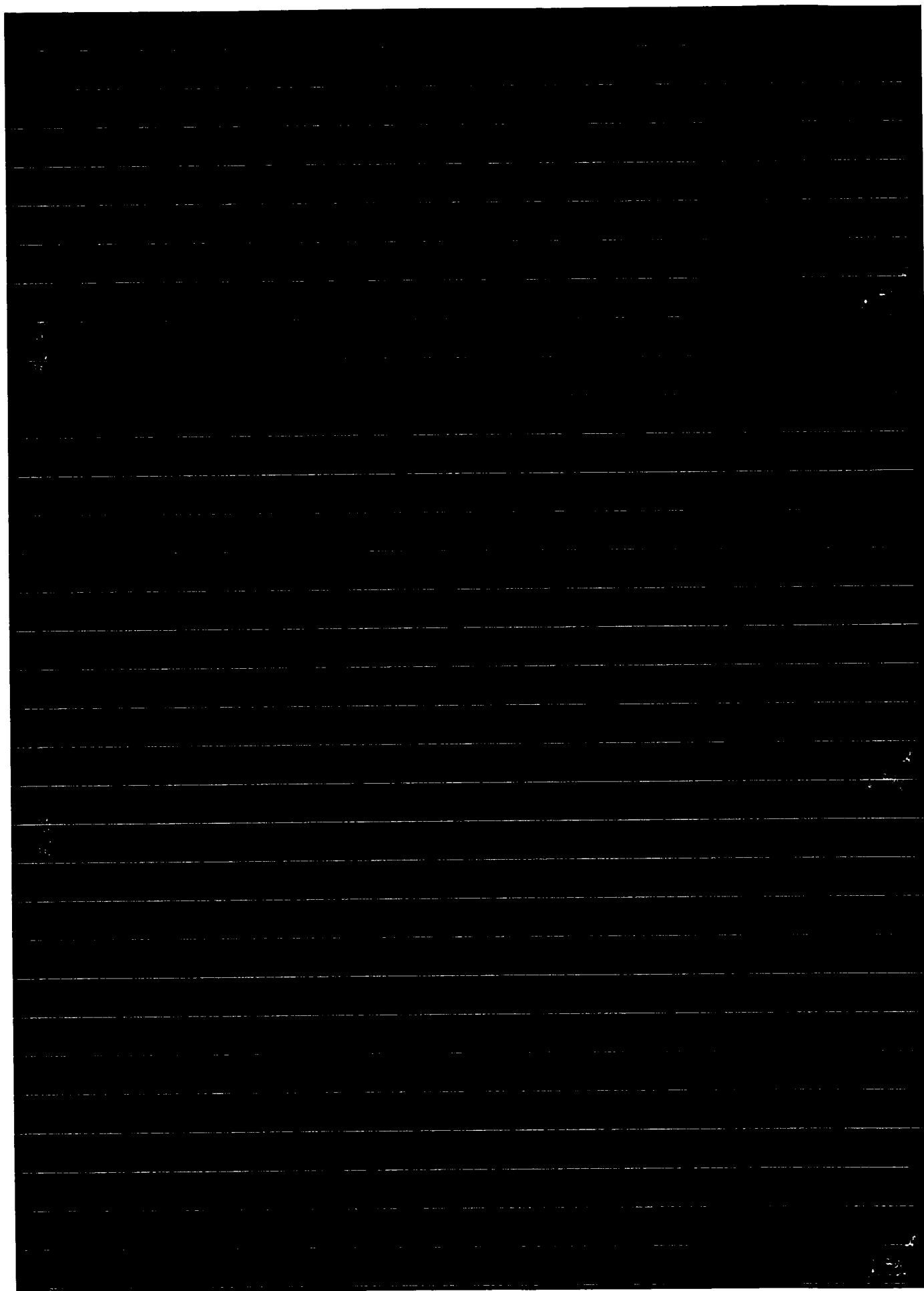
b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MEDLINE, EAST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|------------------------|
| A | WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82 | 1-11, 13-16, and 19-26 |
| A | US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18. | 1-11, 13-16, and 19-26 |
| A | Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract. | 1-11, 13-16, and 19-26 |
| A,P | Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract. | 1-11, 13-16, and 19-26 |
| A | Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract. | 1-11, 13-16, and 19-26 |
| A,P | Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract. | 1-11, 13-16, and 19-26 |

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

| | |
|---|--|
| * Special categories of cited documents: | |
| "A" document defining the general state of the art which is not considered to be of particular relevance | "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| "E" earlier application or patent published on or after the international filing date | "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "O" document referring to an oral disclosure, use, exhibition or other means | "&" document member of the same patent family |
| "P" document published prior to the international filing date but later than the priority date claimed | |

Date of the actual completion of the international search

Date of mailing of the international search report

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This includes 4 invention Groups and 3572 sequence species

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

CORRECTED VERSION

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(15) **Information about Correction:**

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